(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
17 April 2003 (17.04.2003)

PCT

(10) International Publication Number
WO 03/031622 A1

(51) International Patent Classification[7]: C12N 15/29, 15/52, 15/53, 15/55, 15/60, 15/61, A01H 5/00

(21) International Application Number: PCT/AU02/01345

(22) International Filing Date: 4 October 2002 (04.10.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
PR 8113 5 October 2001 (05.10.2001) AU

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 03/031622 A1

(54) Title: MANIPULATION OF FLAVONOID BIOSYNTHESIS IN PLANTS

(57) Abstract: The present invention relates to nucleic acids and nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants.More particularly, the flavonoid biosynthetic enzyme is selected from the group consisting of chalcone isomerase (CHI), chalcone synthase (CHS), chalcone reductase (CHR), dihydroflavonol 4-reductase (DFR), leucoanthocyanidin reductase (LCR), flavonoid 3', 5' hydrolase (F3'5'H), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), phenylalanine ammonia-olyase (PAL) and vestitone reductase (VR), and functionally active fragments and variants thereof.

MANIPULATION OF FLAVONOID BIOSYNTHESIS IN PLANTS

The present invention relates to nucleic acids and nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants.

Flavonoids constitute a relatively diverse family of aromatic molecules that are derived from phenylalanine and malonyl-coenzyme A (CoA, via the fatty acid pathway). These compounds include six major subgroups that are found in most higher plants: the chalcones, flavones, flavonols, flavandiols, anthocyanins and condensed tannins (or proanthocyanidins). A seventh group, the aurones, is widespread, but not ubiquitous.

Some plant species also synthesize specialised forms of flavonoids, such as the isoflavonoids that are found in legumes and a small number of non-legume plants. Similarly, sorghum, maize and gloxinia are among the few species known to synthesize 3-deoxyanthocyanins (or phlobaphenes in the polymerised form). The stilbenes which are closely related to flavonoids, are synthesised by another group of unrelated species that includes grape, peanut and pine.

Besides providing pigmentation to flowers, fruits, seeds, and leaves, flavonoids also have key roles in signalling between plants and microbes, in male fertility of some species, in defense as antimicrobial agents and feeding deterrents, and in UV protection.

Flavonoids also have significant activities when ingested by animals, and there is great interest in their potential health benefits, particularly for compounds such as isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

The major branch pathways of flavonoid biosynthesis start with general phenylpropanoid metabolism and lead to the nine major subgroups: the colorless chalcones, aurones, isoflavonoids, flavones, flavonols, flavandiols, anthocyanins, condensed tannins, and phlobaphene pigments. The enzyme phenylalanine

ammonia-lyase (PAL) of the general phenylpropanoid pathway will lead to the production of cinnamic acid. Cinnamate-4-hydroxylase (C4H) will produce p-coumaric acid which will be converted through the action of 4-coumaroyl:CoA-ligase (4CL) to the production of 4-coumaroyl-CoA and malonyl-CoA. The first committed step in flavonoid biosynthesis is catalyzed by chalcone synthase (CHS), which uses malonyl CoA and 4-coumaryl CoA as substrates. Chalcone reductase (CHR) balances the production of 5-hydroxy- or 5-deoxyflavonoids. The next enzyme, chalcone isomerase (CHI) catalyses ring closure to form a flavanone, but the reaction can also occur spontaneously. Other enzymes in the pathway are: flavanone 3-hydroxylase (F3H), dihydroflavonol 4-reductase (DFR), flavonoid 3'-hydroxylase (F3'H) and flavonoid 3', 5' hydroxylase (F3'5'H).

The *Arabidopsis BANYULS* gene encodes a DFR-like protein that may be a leucoanthocyanidin reductase (LCR) that catalyzes an early step in condensed tannin biosynthesis. Condensed tannins are plant polyphenols with protein-precipitating and antioxidant properties, synthesized by the flavonoid pathway. Their chemical properties include protein binding, metal chelation, anti-oxidation, and UV-light absorption. As a result condensed tannins inhibit viruses, micro-organisms, insects, fungal pathogens, and monogastric digestion. Moderate amounts of tannins improve forage quality by disrupting protein foam and conferring protection from rumen pasture bloat. Bloat is a digestive disorder that occurs on some highly nutritious forage legumes such as alfalfa (*Medicago sativa*) and white clover (*Trifolium repens*). Moderate amounts of tannin can also reduce digestion rates in the rumen and can reduce parasitic load sufficiently to increase the titre of amino acids and small peptides in the small intestine without compromising total digestion.

Vestitone reductase (VR) is the penultimate enzyme in medicarpin biosynthesis. Medicarpin, a phytoalexin, has been associated with plant resistance to fungal pathogens.

While nucleic acid sequences encoding some flavonoid biosynthetic enzymes CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR have been isolated for certain species of plants, there remains a need for materials useful in

modifying flavonoid biosynthesis; in modifying protein binding, metal chelation, anti-oxidation, and UV-light absorption; in modifying plant pigment production; in modifying plant defense to biotic stresses such as viruses, micro-organisms, insects or fungal pathogens; in modifying forage quality, for example by disrupting protein foam and/or conferring protection from rumen pasture bloat, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

It is an object of the present invention to overcome, or at least alleviate, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the flavonoid biosynthetic enzymes CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species and functionally active fragments and variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins which are related to CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR and functionally active fragments and variants thereof. Such proteins are referred to herein as CHI-like, CHS-like, CHR-like, DFR-like, LCR-like, F3'5'H-like, F3H-like, F3'H-like, PAL-like and VR-like, respectively.

The individual or simultaneous enhancement or otherwise manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants may enhance or otherwise alter flavonoid biosynthesis; may enhance or otherwise alter the plant capacity for protein binding, metal chelation, anti-oxidation or UV-light absorption; may enhance or reduce or otherwise alter plant pigment production; may modify plant defense to biotic stresses such as viruses, micro-organisms, insects or fungal pathogens; and/or may modify forage quality, for example by disrupting protein foam and/or conferring protection from rumen pasture bloat.

The individual or simultaneous enhancement or otherwise manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants has significant consequences for a range of applications in, for example, plant production and plant protection. For example, it has applications in increasing plant tolerance and plant defense to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; in improving plant forage quality, for example by disrupting protein foam and in conferring protection from rumen pasture bloat; in reducing digestion rates in the rumen and reducing parasitic load; in the production of plant compounds leading to health benefits, such as isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

Methods for the manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; altered pigmentation in flowers; forage legumes with enhanced herbage quality and bloat-safety; crops with enhanced isoflavonoid content leading to health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses, respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

The term “isolated” means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid present in a living plant is not isolated, but the same nucleic acid separated from some or all of the coexisting materials in the natural system, is isolated. Such nucleic acids could be part of a vector and/or such nucleic acids could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment.

Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term “consensus contig” refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHI or CHI-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 122 and 127 hereto (Sequence ID Nos: 1, 3 to 7, 8, 10 to 12, 13, 15 and 16, 17, 19 to 22, 307, and 309, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHS or CHS-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 13, 15, 16, 18, 19, 21, 22, 24, 25, 27, 28, 30, 31, 33, 34, 137, 142, 147, 152, 157 and 162 hereto (Sequence ID Nos: 23, 25 to 63, 64, 66 to 68, 69, 71 to 77, 78, 80 to 90, 91, 93 and 94, 95, 97 to 100, 101, 103 to 105, 106, 313, 315, 317, 319, 321, and 323, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHR or CHR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 36, 38, 40, 41, 43 and 132 hereto (Sequence ID Nos: 108, 110, 112 to 116, 117, 119 to 134, and 311, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a DFR or DFR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 44, 46, 47, 49, 50, 52, 54, 55, 57, 59, 61, 62, 64, 101, 103, 104, 106, 117 and 167 hereto (Sequence ID Nos: 135, 137 to 146, 147, 149 to 152, 153, 155, 157 and 158, 159, 161, 163, 165 to 167, 168, 170 to 184, 286, 288 to 292, 293, 295 to 297, 305, and 325, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an LCR or LCR-like protein includes a nucleotide sequence selected from the group

consisting of (a) sequences shown in Figures 65 and 67 hereto (Sequence ID Nos: 185 and 187 to 193, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3'5'H or F3'5'H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 68, 70 and 72 hereto (Sequence ID Nos: 194, 196, and 198 to 201, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3H or F3H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 73, 75, 76, 78, 107, 109, 111 and 172 hereto (Sequence ID Nos: 202, 204 to 244, 245, 247, 298, 300 to 302, 303, and 327, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3'H or F3'H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 80 and 82 hereto (Sequence ID Nos: 249, and 251 and 252, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an PAL or PAL-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 83, 85, 86, 88, 89, 91, 93, 95, 97, 177, 182 and 187 hereto (Sequence ID Nos: 253, 255 to 257, 258, 260 to 267, 268, 270, 272, 274, 276 and 277, 329, 331, and 333, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an VR or VR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 98, 100 and 192 hereto (Sequence ID Nos: 278, 280 to 285, and 335, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

By "functionally active" in relation to nucleic acids it is meant that the fragment or variant (such as an analogue, derivative or mutant) encodes a polypeptide which is capable of modifying flavonoid biosynthesis in a plant. Such variants include naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the relevant part of the above mentioned nucleotide sequence, more preferably at least approximately 90% identity, even more preferably at least approximately 95% identity, most preferably at least approximately 98% homology. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least

10 nucleotides, more preferably at least 15 nucleotides, most preferably at least 20 nucleotides.

Nucleic acids or nucleic acid fragments encoding at least a portion of several CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR have been isolated and identified. The nucleic acids or nucleic acid fragments of the present invention may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. Isolation of homologous genes using sequence-dependent protocols, such as methods of nucleic acid hybridisation, and methods of DNA and RNA amplification as exemplified by various uses of nucleic acid amplification technologies (e.g. polymerase chain reaction, ligase chain reaction), is well known in the art.

For example, genes encoding other CHI or CHI-like, CHS or CHS-like, CHR or CHR-like, DFR or DFR-like, LCR or LCR-like, F3'5'H or F3'5'H-like, F3H or F3H-like, F3'H or F3'H-like, PAL or PAL-like and VR or VR-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in amplification protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or

RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol [Frohman *et al.* (1988) *Proc. Natl. Acad Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference] to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated [Ohara *et al.* (1989) *Proc. Natl. Acad Sci USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference]. Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a second aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CHI and CHI-like, CHS and CHS-like, CHR and CHR-like, DFR and DFR-like, LCR and LCR-like, F3'5'H and F3'5'H-like, F3H and F3H-like, F3'H and F3'H-like, PAL and PAL-like, VR and VR-like; and functionally active fragments and variants thereof.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CHI or CHI-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 11, 123 and 128 hereto (Sequence ID Nos: 2, 9, 14, 18, 308, and 310, respectively), and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated CHS or CHS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 14, 17, 20, 23, 26, 29, 32, 35, 138, 143, 148, 153, 158 and 163 hereto (Sequence ID Nos: 24, 65, 70, 79, 92, 96, 102, 107, 314, 316, 318, 320, 322, and 324, respectively), and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated CHR or CHR-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 37, 39, 42 and 133 hereto (Sequence ID Nos: 109, 111, 118, and 312, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated DFR or DFR-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 45, 48, 51, 53, 56, 58, 60, 63, 102, 105, 118 and 168 hereto (Sequence ID Nos: 136, 148, 54, 156, 160, 162, 164, 169, 287, 294, 306, and 326, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated LCR or LCR-like polypeptide includes an amino acid sequence shown in Figure 66 hereto (Sequence ID No: 186), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3'5'H or F3'5'H-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown

in Figures 69 and 71 hereto (Sequence ID Nos: 195 and 197, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3H or F3H-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 74, 77, 79, 108, 112 and 173 hereto (Sequence ID Nos: 203, 246, 248, 299, 304, and 328, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3'H or F3'H-like polypeptide includes an amino acid sequence shown in Figure 81 hereto (Sequence ID No: 250), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated PAL or PAL-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 84, 87, 90, 92, 94, 96, 178, 183 and 188 hereto (Sequence ID Nos: 254, 259, 269, 271, 273, 275, 330, 332, and 334, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated VR or VR-like polypeptide includes an amino acid sequence shown in Figures 99 and 193 hereto (Sequence ID Nos: 279 and 336, respectively), and functionally active fragments and variants thereof.

By “functionally active” in relation to polypeptides it is meant that the fragment or variant has one or more of the biological properties of the proteins CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like, respectively. Additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally

active fragment or variant has at least approximately 60% identity to the relevant part of the above mentioned amino acid sequence, more preferably at least approximately 80% identity, even more preferably at least approximately 90% identity most preferably at least approximately 95% homology. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are well known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide

sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 40, 43, 46, 49, 54, 61, 64, 67, 72, 75, 82, 85, 88, 97, 100, 103, 106 and 109 hereto (Sequence ID Nos: 3 to 7, 10 to 12, 15 and 16, 19 to 22, 25 to 63, 66 to 68, 71 to 77, 80 to 90, 93 and 94, 97 to 100, 103 to 105, 112 to 116, 119 to 134, 137 to 146, 149 to 152, 157 and 158, 165 to 167, 170 to 184, 187 to 193, 198 to 201, 204 to 244, 251 and 252, 255 to 257, 260 to 267, 276 and 277, 280 to 285, 288 to 292, 295 to 297, and 300 to 302, respectively).

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention or complements or sequences antisense thereto, and functionally active fragments and variants thereof.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragments may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to biotic stresses such as viruses, micro-organisms, insects, fungal pathogens; in relation to forage quality; in relation to bloat safety; in relation to condensed tannin content; in relation to plant pigmentation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct including a nucleic acid or nucleic acid fragment according to the present invention.

The term “construct” as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some

cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present invention.

The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

By "operatively linked" is meant that said regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids

and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter and derivatives thereof, the maize Ubiquitin promoter, and the rice Actin promoter.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*), the octopine synthase (*ocs*) and the rbcS genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene and the gentamycin acetyl transferase (*aacC1*) gene], and reporter genes [such as beta-glucuronidase (GUS) gene (*gusA*) and green fluorescent protein

(gfp)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The constructs and vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as Arabidopsis, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the constructs and vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the constructs and vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the constructs and vectors of the present invention into plant cells (for example by transduction, transfection or

transformation) are well known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the constructs and vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a construct, vector, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), even more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying flavonoid biosynthesis in a plant; said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying protein binding, metal chelation, anti-oxidation, and/or UV-light absorption in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying pigment production in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying plant defense to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

By "an effective amount" it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately

skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

Using the methods and materials of the present invention, flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety; and/or isoflavonoid content leading to health benefits, may be increased or otherwise modified, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise modified, for example by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of TrCHIa (Sequence ID No: 1).

Figure 2 shows the deduced amino acid sequence of TrCHIa (Sequence ID No: 2).

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHIa (Sequence ID Nos: 3 to 7).

Figure 4 shows the consensus contig nucleotide sequence of TrCHIb (Sequence ID No: 8).

Figure 5 shows the deduced amino acid sequence of TrCHIb (Sequence ID No: 9).

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHIb (Sequence ID Nos: 10 to 12).

Figure 7 shows the consensus contig nucleotide sequence of TrCHIc (Sequence ID No: 13).

Figure 8 shows the deduced amino acid sequence of TrCHIc (Sequence ID No: 14).

Figure 9 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHIc (Sequence ID Nos: 15 and 16).

Figure 10 shows the consensus contig nucleotide sequence of TrCHId (Sequence ID No: 17).

Figure 11 shows the deduced amino acid sequence of TrCHId (Sequence ID No: 18).

Figure 12 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHId (Sequence ID Nos: 19 to 22).

Figure 13 shows the consensus contig nucleotide sequence of TrCHSa (Sequence ID No: 23).

Figure 14 shows the deduced amino acid sequence of TrCHSa (Sequence ID No: 24).

Figure 15 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSa (Sequence ID Nos: 25 to 63).

Figure 16 shows the consensus contig nucleotide sequence of TrCHSb (Sequence ID No: 64).

Figure 17 shows the deduced amino acid sequence of TrCHSb (Sequence ID No: 65).

Figure 18 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSb (Sequence ID Nos: 66 to 68).

Figure 19 shows the consensus contig nucleotide sequence of TrCHSc (Sequence ID No: 69).

Figure 20 shows the deduced amino acid sequence of TrCHSc (Sequence ID No: 70).

Figure 21 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSc (Sequence ID Nos: 71 to 77).

Figure 22 shows the consensus contig nucleotide sequence of TrCHSd (Sequence ID No: 78).

Figure 23 shows the deduced amino acid sequence of TrCHSd (Sequence ID No: 79).

Figure 24 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSd (Sequence ID Nos: 80 to 90).

Figure 25 shows the consensus contig nucleotide sequence of TrCHSe (Sequence ID No: 91).

Figure 26 shows the deduced amino acid sequence of TrCHSe (Sequence ID No: 92).

Figure 27 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSe (Sequence ID Nos: 93 and 94).

Figure 28 shows the consensus contig nucleotide sequence of TrCHSf (Sequence ID No: 95).

Figure 29 shows the deduced amino acid sequence of TrCHSf (Sequence ID No: 96).

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSf (Sequence ID Nos: 97 to 100).

Figure 31 shows the consensus contig nucleotide sequence of TrCHSg (Sequence ID No: 101).

Figure 32 shows the deduced amino acid sequence of TrCHSg (Sequence ID No: 102).

Figure 33 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSg (Sequence ID Nos: 103 to 105).

Figure 34 shows the consensus contig nucleotide sequence of TrCHSh (Sequence ID No: 106).

Figure 35 shows the deduced amino acid sequence of TrCHSh (Sequence ID No: 107).

Figure 36 shows the nucleotide sequence of TrCHRa (Sequence ID No: 108).

Figure 37 shows the deduced amino acid sequence of TrCHRa (Sequence ID No: 109).

Figure 38 shows the consensus contig nucleotide sequence of TrCHRb (Sequence ID No: 110).

Figure 39 shows the deduced amino acid sequence of TrCHRb (Sequence ID No: 111).

Figure 40 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHRb (Sequence ID Nos: 112 to 116).

Figure 41 shows the consensus contig nucleotide sequence of TrCHRc (Sequence ID No: 117).

Figure 42 shows the deduced amino acid sequence of TrCHRc (Sequence ID No: 118).

Figure 43 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHRc (Sequence ID Nos: 119 to 134).

Figure 44 shows the consensus contig nucleotide sequence of TrDFRa (Sequence ID No: 135).

Figure 45 shows the deduced amino acid sequence of TrDFRa (Sequence ID No: 136).

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRa (Sequence ID Nos: 137 to 146).

Figure 47 shows the consensus contig nucleotide sequence of TrDFRb (Sequence ID No: 147).

Figure 48 shows the deduced amino acid sequence of TrDFRb (Sequence ID No: 148).

Figure 49 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRb (Sequence ID Nos: 149 to 152).

Figure 50 shows the nucleotide sequence of TrDFRc (Sequence ID No: 153).

Figure 51 shows the deduced amino acid sequence of TrDFRc (Sequence ID No: 154).

Figure 52 shows the consensus contig nucleotide sequence of TrDFRd (Sequence ID No: 155).

Figure 53 shows the deduced amino acid sequence of TrDFRd (Sequence ID No: 156).

Figure 54 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRd (Sequence ID Nos: 157 and 158).

Figure 55 shows the nucleotide sequence of TrDFRe (Sequence ID No: 159).

Figure 56 shows the deduced amino acid sequence of TrDFRe (Sequence ID No: 160).

Figure 57 shows the nucleotide sequence of TrDFRf (Sequence ID No: 161).

Figure 58 shows the deduced amino acid sequence of TrDFRf (Sequence ID No: 162).

Figure 59 shows the consensus contig nucleotide sequence of TrDFRg (Sequence ID No: 163).

Figure 60 shows the deduced amino acid sequence of TrDFRg (Sequence ID No: 164).

Figure 61 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRg (Sequence ID Nos: 165 to 167).

Figure 62 shows the consensus contig nucleotide sequence of TrDFRh (Sequence ID No: 168).

Figure 63 shows the deduced amino acid sequence of TrDFRh (Sequence ID No: 169).

Figure 64 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRh (Sequence ID Nos: 170 to 184).

Figure 65 shows the consensus contig nucleotide sequence of TrLCRa (Sequence ID No: 185).

Figure 66 shows the deduced amino acid sequence of TrLCRa (Sequence ID No: 186).

Figure 67 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrLCRa (Sequence ID Nos: 187 to 193).

Figure 68 shows the nucleotide sequence of TrF3'5'Ha (Sequence ID No: 194).

Figure 69 shows the deduced amino acid sequence of TrF3'5'Ha (Sequence ID No: 195).

Figure 70 shows the consensus contig nucleotide sequence of TrF3'5'Hb (Sequence ID No: 196).

Figure 71 shows the deduced amino acid sequence of TrF3'5'Hb (Sequence ID No: 197).

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3'5'Hb (Sequence ID Nos: 198 to 201).

Figure 73 shows the consensus contig nucleotide sequence of TrF3Ha (Sequence ID No: 202).

Figure 74 shows the deduced amino acid sequence of TrF3Ha (Sequence ID No: 203).

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3Ha (Sequence ID Nos: 204 to 244).

Figure 76 shows the nucleotide sequence of TrF3Hb (Sequence ID No: 245).

Figure 77 shows the deduced amino acid sequence of TrF3Hb (Sequence ID No: 246).

Figure 78 shows the nucleotide sequence of TrF3Hc (Sequence ID No: 247).

Figure 79 shows the deduced amino acid sequence of TrF3Hc (Sequence ID No: 248).

Figure 80 shows the consensus contig nucleotide sequence of TrF3'Ha (Sequence ID No: 249).

Figure 81 shows the deduced amino acid sequence of TrF3'Ha (Sequence ID No: 250).

Figure 82 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3'Ha (Sequence ID Nos: 251 and 252).

Figure 83 shows the consensus contig nucleotide sequence of TrPALa (Sequence ID No: 253).

Figure 84 shows the deduced amino acid sequence of TrPALa (Sequence ID No: 254).

Figure 85 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALa (Sequence ID Nos: 255 to 257).

Figure 86 shows the consensus contig nucleotide sequence of TrPALb (Sequence ID No: 258).

Figure 87 shows the deduced amino acid sequence of TrPALb (Sequence ID No: 259).

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALb (Sequence ID Nos: 260 to 267).

Figure 89 shows the nucleotide sequence of TrPALc (Sequence ID No: 268).

Figure 90 shows the deduced amino acid sequence of TrPALc (Sequence ID No: 269).

Figure 91 shows the nucleotide sequence of TrPALd (Sequence ID No: 270).

Figure 92 shows the deduced amino acid sequence of TrPALd (Sequence ID No: 271).

Figure 93 shows the nucleotide sequence of TrPALe (Sequence ID No: 272).

Figure 94 shows the deduced amino acid sequence of TrPALe (Sequence ID No: 273).

Figure 95 shows the consensus contig nucleotide sequence of TrPALf (Sequence ID No: 274).

Figure 96 shows the deduced amino acid sequence of TrPALf (Sequence ID No: 275).

Figure 97 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALf (Sequence ID Nos: 276 and 277).

Figure 98 shows the consensus contig nucleotide sequence of TrVRa (Sequence ID No: 278).

Figure 99 shows the deduced amino acid sequence of TrVRa (Sequence ID No: 279).

Figure 100 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrVRa (Sequence ID Nos: 280 to 285).

Figure 101 shows the consensus contig nucleotide sequence of LpDFRa (Sequence ID No: 286).

Figure 102 shows the deduced amino acid sequence of LpDFRa (Sequence ID No: 287).

Figure 103 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpDFRa (Sequence ID Nos: 288 to 292).

Figure 104 shows the consensus contig nucleotide sequence of LpDFRb (Sequence ID No: 293).

Figure 105 shows the deduced amino acid sequence of LpDFRb (Sequence ID No: 294).

Figure 106 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpDFRb (Sequence ID Nos: 295 to 297).

Figure 107 shows the consensus contig nucleotide sequence of LpF3Ha (Sequence ID No: 298).

Figure 108 shows the deduced amino acid sequence of LpF3Ha (Sequence ID No: 299).

Figure 109 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpF3Ha (Sequence ID Nos: 300 to 302).

Figure 110 shows a plasmid map of the cDNA encoding perennial ryegrass F3OH.

Figure 111 shows the full nucleotide sequence of perennial ryegrass F3OH cDNA (Sequence ID No: 303).

Figure 112 shows the deduced amino acid sequence of perennial ryegrass F3OH cDNA (Sequence ID No: 304).

Figure 113 shows plasmid maps of sense and antisense constructs of LpF3OH in pDH51 transformation vector.

Figure 114 shows plasmid maps of sense and antisense constructs of LpF3OH in pPZP221:35S^2 binary transformation vector.

Figure 115 shows screening by Southern hybridisation for RFLPs using LpF3OH as a probe.

Figure 116 shows a plasmid map of the cDNA encoding white clover BANa.

Figure 117 shows the full nucleotide sequence of white clover BANa cDNA (Sequence ID No: 305).

Figure 118 shows the deduced amino acid sequence of white clover BANa cDNA (Sequence ID No: 306).

Figure 119 shows plasmid maps of sense and antisense constructs of TrBANa in pDH51 transformation vector.

Figure 120 shows plasmid maps of sense and antisense constructs of TrBANa in pPZP221:35S^2 binary transformation vector.

Figure 121 shows a plasmid map of the cDNA encoding white clover CHIa.

Figure 122 shows the full nucleotide sequence of white clover CHIa cDNA (Sequence ID No: 307).

Figure 123 shows the deduced amino acid sequence of white clover CHIa cDNA (Sequence ID No: 308).

Figure 124 shows plasmid maps of sense and antisense constructs of TrCHIa in pDH51 transformation vector.

Figure 125 shows plasmid maps of sense and antisense constructs of TrCHIa in pPZP221:35S^2 binary transformation vector.

Figure 126 shows a plasmid map of the cDNA encoding white clover CHId.

Figure 127 shows the full nucleotide sequence of white clover CHId cDNA (Sequence ID No: 309).

Figure 128 shows the deduced amino acid sequence of white clover CHId cDNA (Sequence ID No: 310).

Figure 129 shows plasmid maps of sense and antisense constructs of TrCHId in pDH51 transformation vector.

Figure 130 shows plasmid maps of sense and antisense constructs of TrCHId in pPZP221:35S^2 binary transformation vector.

Figure 131 shows a plasmid map of the cDNA encoding white clover CHRc.

Figure 132 shows the full nucleotide sequence of white clover CHRc cDNA (Sequence ID No: 311).

Figure 133 shows the deduced amino acid sequence of white clover CHRc cDNA (Sequence ID No: 312).

Figure 134 shows plasmid maps of sense and antisense constructs of TrCHRc in pDH51 transformation vector.

Figure 135 shows plasmid maps of sense and antisense constructs of TrCHRc in pPZP221:35S^2 binary transformation vector.

Figure 136 shows a plasmid map of the cDNA encoding white clover CHSa1.

Figure 137 shows the full nucleotide sequence of white clover CHSa1 cDNA (Sequence ID No: 313).

Figure 138 shows the deduced amino acid sequence of white clover CHSa1 cDNA (Sequence ID No: 314).

Figure 139 shows plasmid maps of sense and antisense constructs of TrCHSa1 in pDH51 transformation vector.

Figure 140 shows plasmid maps of sense and antisense constructs of TrCHSa1 in pPZP221:35S^2 binary transformation vector.

Figure 141 shows a plasmid map of the cDNA encoding white clover CHSa3.

Figure 142 shows the full nucleotide sequence of white clover CHSa3 cDNA (Sequence ID No: 315).

Figure 143 shows the deduced amino acid sequence of white clover CHSa3 cDNA (Sequence ID No: 316).

Figure 144 shows plasmid maps of sense and antisense constructs of TrCHSa3 in pDH51 transformation vector.

Figure 145 shows plasmid maps of sense and antisense constructs of TrCHSa3 in pPZP221:35S^2 binary transformation vector.

Figure 146 shows a plasmid map of the cDNA encoding white clover CHSc.

Figure 147 shows the full nucleotide sequence of white clover CHSc cDNA (Sequence ID No: 317).

Figure 148 shows the deduced amino acid sequence of white clover CHSc cDNA (Sequence ID No: 318).

Figure 149 shows plasmid maps of sense and antisense constructs of TrCHSc in pDH51 transformation vector.

Figure 150 shows plasmid maps of sense and antisense constructs of TrCHSc in pPZP221:35S^2 binary transformation vector.

Figure 151 shows a plasmid map of the cDNA encoding white clover CHSd2.

Figure 152 shows the full nucleotide sequence of white clover CHSd2 cDNA (Sequence ID No: 319).

Figure 153 shows the deduced amino acid sequence of white clover CHSd2 cDNA (Sequence ID No: 320).

Figure 154 shows plasmid maps of sense and antisense constructs of TrCHSd2 in pDH51 transformation vector.

Figure 155 shows plasmid maps of sense and antisense constructs of TrCHSd2 in pPZP221:35S^2 binary transformation vector.

Figure 156 shows a plasmid map of the cDNA encoding white clover CHSf.

Figure 157 shows the full nucleotide sequence of white clover CHSf cDNA (Sequence ID No: 321).

Figure 158 shows the deduced amino acid sequence of white clover CHSf cDNA (Sequence ID No: 322).

Figure 159 shows plasmid maps of sense and antisense constructs of TrCHSf in pDH51 transformation vector.

Figure 160 shows plasmid maps of sense and antisense constructs of TrCHSf in pPZP221:35S^2 binary transformation vector.

Figure 161 shows a plasmid map of the cDNA encoding white clover CHSh.

Figure 162 shows the full nucleotide sequence of white clover CHSh cDNA (Sequence ID No: 323).

Figure 163 shows the deduced amino acid sequence of white clover CHSh cDNA (Sequence ID No: 324).

Figure 164 shows plasmid maps of sense and antisense constructs of TrCHSh in pDH51 transformation vector.

Figure 165 shows plasmid maps of sense and antisense constructs of TrCHSh in pPZP221:35S^2 binary transformation vector.

Figure 166 shows a plasmid map of the cDNA encoding white clover DFRd.

Figure 167 shows the full nucleotide sequence of white clover DFRd cDNA (Sequence ID No: 325).

Figure 168 shows the deduced amino acid sequence of white clover DFRd cDNA (Sequence ID No: 326).

Figure 169 shows plasmid maps of sense and antisense constructs of TrDFRd in pDH51 transformation vector.

Figure 170 shows plasmid maps of sense and antisense constructs of TrDFRd in pPZP221:35S^2 binary transformation vector.

Figure 171 shows a plasmid map of the cDNA encoding white clover F3Ha.

Figure 172 shows the full nucleotide sequence of white clover F3Ha cDNA (Sequence ID No: 327).

Figure 173 shows the deduced amino acid sequence of white clover F3Ha cDNA (Sequence ID No: 328).

Figure 174 shows plasmid maps of sense and antisense constructs of TrF3Ha in pDH51 transformation vector.

Figure 175 shows plasmid maps of sense and antisense constructs of TrF3Ha in pPZP221:35S^2 binary transformation vector.

Figure 176 shows a plasmid map of the cDNA encoding white clover PALa.

Figure 177 shows the full nucleotide sequence of white clover PALa cDNA (Sequence ID No: 329).

Figure 178 shows the deduced amino acid sequence of white clover PALa cDNA (Sequence ID No: 330).

Figure 179 shows plasmid maps of sense and antisense constructs of TrPALa in pDH51 transformation vector.

Figure 180 shows plasmid maps of sense and antisense constructs of TrPALa in pPZP221:35S^2 binary transformation vector.

Figure 181 shows a plasmid map of the cDNA encoding white clover PALb.

Figure 182 shows the full nucleotide sequence of white clover PALb cDNA (Sequence ID No: 331).

Figure 183 shows the deduced amino acid sequence of white clover PALb cDNA (Sequence ID No: 332).

Figure 184 shows plasmid maps of sense and antisense constructs of TrPALb in pDH51 transformation vector.

Figure 185 shows plasmid maps of sense and antisense constructs of TrPALb in pPZP221:35S^2 binary transformation vector.

Figure 186 shows a plasmid map of the cDNA encoding white clover PALf.

Figure 187 shows the full nucleotide sequence of white clover PALf cDNA (Sequence ID No: 333).

Figure 188 shows the deduced amino acid sequence of white clover PALf cDNA (Sequence ID No: 334).

Figure 189 shows plasmid maps of sense and antisense constructs of TrPALf in pDH51 transformation vector.

Figure 190 shows plasmid maps of sense and antisense constructs of TrPALf in pPZP221:35S^2 binary transformation vector.

Figure 191 shows a plasmid map of the cDNA encoding white clover VRa.

Figure 192 shows the full nucleotide sequence of white clover VRa cDNA (Sequence ID No: 335).

Figure 193 shows the deduced amino acid sequence of white clover VRa cDNA (Sequence ID No: 336).

Figure 194 shows plasmid maps of sense and antisense constructs of TrVRa in pDH51 transformation vector.

Figure 195 shows plasmid maps of sense and antisense constructs of TrVRa in pPZP221:35S^2 binary transformation vector.

Figure 196 shows A, infiltration of Arabidopsis plants; B, selection of transgenic Arabidopsis plants on medium containing 75 μg/ml gentamycin; C, young transgenic Arabidopsis plants; D, E, two representative results of real-time PCR analysis of Arabidopsis transformed with chimeric genes involved in flavonoid biosynthesis.

Figure 197 shows the genetic map detailing the relation of perennial ryegrass genes involved in flavonoid biosynthesis.

EXAMPLE 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1

cDNA libraries from white clover (*Trifolium repens*)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 &28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated plants
04wc	Cut leaf and stem collected after 0, 1, 4, 6 &14 h after cutting
05wc	Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at –80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

TABLE 2

cDNA libraries from perennial ryegrass (*Lolium perenne*)

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescing leaves from mature plants

Library	Organ/Tissue
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (*rbcL*, *rbcS*, *cab*, *wir2A* subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR

cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2

DNA sequence analyses

The cDNA clones encoding CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the *e*Bioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

EXAMPLE 3

Identification and full-length sequencing of cDNAs encoding perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins

To fully characterise for the purposes of the generation of probes for hybridisation experiments and the generation of transformation vectors, a set of

cDNAs encoding perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins was identified and fully sequenced.

Full-length cDNAs were identified from our EST sequence database using relevant published sequences (NCBI databank) as queries for BLAST searches. Full-length cDNAs were identified by alignment of the query and hit sequences using Sequencher (Gene Codes Corp., Ann Arbor, MI 48108, USA). The original plasmid was then used to transform chemically competent XL-1 cells (prepared in-house, $CaCl_2$ protocol). After colony PCR (using HotStarTaq, Qiagen) a minimum of three PCR-positive colonies per transformation were picked for initial sequencing with M13F and M13R primers. The resulting sequences were aligned with the original EST sequence using Sequencher to confirm identity and one of the three clones was picked for full-length sequencing, usually the one with the best initial sequencing result.

Sequencing was completed by primer walking, i.e. oligonucleotide primers were designed to the initial sequence and used for further sequencing. In most cases the sequencing could be done from both 5' and 3' end. The sequences of the oligonucleotide primers are shown in Table 2. In some instances, however, an extended poly-A tail necessitated the sequencing of the cDNA to be completed from the 5' end.

Contigs were then assembled in Sequencher. The contigs include the sequences of the SMART primers used to generate the initial cDNA library as well as pGEM-T Easy vector sequence up to the EcoRI cut site both at the 5' and 3' end.

Plasmid maps and the full cDNA sequences of perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins were obtained (Figures 110, 116, 121, 126, 131, 136, 141, 146, 151, 156, 161, 166, 171, 176, 181, 186 and 191).

TABLE 2

List of primers used for sequencing of the full-length cDNAs

gene name	clone ID	sequencing primer	primer sequence (5'>3')
LpF3OH	08rg1YsF07	08rg1YsF07.f1	TTGAGAGCTTCGTCGACC
		08rg1YsF07.r1	AACTCCTCGTAGTACTCC
TrCHRc	11wc1IsD03	11wc1IsD03.f1	TTCAATTGGAGTACTTGG
		11wc1IsD03.r1	ACTCCTTGTTCATATAACC
TrCHSa1	02wc2FsD07	02wc2FsD07.f1	ACATGGTGGTGGTTGAGG
		02wc2FsD07.f2	TGCTGCACTCATTGTTGG
		02wc2FsD07.f3	ACATTGATAAGGCATTGG
TrCHSa3	05wc1RsB06	05wc1RsB06.f1	AGGAGGCTGCAGTCAAGG
		05wc1RsB06.f2	TGCCTGAAATTGAGAAACC
		05wc1RsB06.f3	AAAGCTAGCCTTGAAGCC
TrCHSc	07wc1TsE12	07wc1TsE12.f1	TCGGACATAACTCATGTGG
		07wc1TsE12.f2	TTGGGTTGGAGAATAAGG
		07wc1TsE12.r1	TGGACATTTATTGGTTGC
		07wc1TsE12.r2	TATCATGTCTGGAAATGC
TrCHSd2	07wc1XsD03	07wc1XsD03.f1	TTTATGTGAGTACATGGC
		07wc1XsD03.f2	AGCAGCTGTGATTGTAGG
		07wc1XsD03.f3	TGAGAAAGCTCTTGTTGAGG
TrCHSf	07wc1UsD07	07wc1UsD07.f1	AGATTGCATCAAAGAATGG
		07wc1UsD07.r1	GGTCCAAAAGCCAATCC
TrCHSh	13wc2IsG04	13wc2IsG04.f1	TAAGACGAGACATAGTGG
		13wc2IsG04.r1	TATTCACTAAGCACATGC
TrDFRd	12wc1CsE09	12wc1CsE09.f1	TTACCTCGTCTGTCTCG
		12wc1CsE09.r1	AACACACACATGTCTACC
TrF3Ha	07wc1LsG03	07wc1LsG03.f1	TGAAGGATTGGAGAGAGC
		07wc1LsG03.r1	TACACAGTTGCATCTGG
TrPALa	04wc1UsB03	04wc1UsB03.f1	ATCGGAATCTGCTAGAGC
		04wc1UsB03.f2	TGTTGGTTCTGGTTTAGC
		04wc1UsB03.r1	TTCATATGCAATCCTTGC
		04wc1UsB03.r2	TCTTGGTTGTGTTGTTCC

TrPALb	05wc1PsH02	05wc1PsH02.f1	TGGGACTGATAGTTATGG
		05wc1PsH02.f2	TCTTGCTCTTGTTAATGG
		05wc1PsH02.r1	AGCACCATTCCACTCTCC
		05wc1PsH02.r2	TTCTCTTCGCTACTTGGC
TrPALf	13wc2AsD12	13wc2AsD12.f1	ATAGTGGTGTGAGGGTGG
		13wc2AsD12.f2	TCTTGTTAATGGTACTGC
		13wc2AsD12.r1	ATTTATCGCACTCTTCGC
		13wc2AsD12.r2	AAAGTGGAAGACATGAGC
TrVRa	11wc1NsA07	11wc1NsA07.f1	AAGAACAGTGGATGGAGC
		11wc1NsA07.r1	TCAACTCATCTACTGATAG

EXAMPLE 4

Development of transformation vectors containing chimeric genes with cDNA sequences from perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa

To alter the expression of the proteins involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa, through antisense and/or sense suppression technology and for over-expression of these key enzymes in transgenic plants, a set of sense and antisense transformation vectors was produced.

cDNA fragments were generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained recognition sites for appropriate restriction enzymes, for example EcoRI and XbaI, for directional and non-directional cloning into the target vector. After PCR amplification and restriction digest with the appropriate restriction enzyme (usually

XbaI), the cDNA fragments were cloned into the corresponding site in pDH51, a pUC18-based transformation vector containing a CaMV 35S expression cassette. The orientation of the constructs (sense or antisense) was checked by DNA sequencing through the multi-cloning site of the vector. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins in sense and antisense orientations under the control of the CaMV 35S promoter were generated (Figures 113, 119, 124, 129, 134, 139, 144, 149, 154, 159, 164, 169, 174, 179, 184, 189 and 194).

TABLE 3

List of primers used to PCR-amplify the open reading frames

gene name	clone ID	primer	primer sequence (5'->3')
LpF3OH	08rg1YsF07	08rg1YsF07f	GAATTCTAGAAGCAGAAAGTACGGACATCAGC
		08rg1YsF07r	GAATTCTAGAACCATATGGCGACACATCG
TrBANa	05wc2XsG02	05wc2XsG02f	GGATCCTCTAGAGCACTAGTGTGTATAAGTTTCTTGG
		05wc2XsG02r	GGATCCTCTAGACCCCCTTAGTCTTAAAATACTCG
TrCHIa	06wc2AsF12	06wc2AsF12f	GAATTCTAGAGATCTGAAACAACATAGTCACC
		06wc2AsF12r	GAATTCTAGATCAATCTTGTGCTGCAATGC
TrCHId	12wc1FsG04	12wc1FsG04f	GAATTCTAGAAAGTTCAACGAGATCAATGG
		12wc1FsG04r	GAATTCTAGATTCCGCTTGGTCTTTATTGC
TrCHRc	11wc1IsD03	11wc1IsD03f	GAATTCTAGAACATGGGTAGTGTTGAAATTCC
		11wc1IsD03r	GAATTCTAGAAGATATTGAGTGAGCTTAAGG
TrCHSa1	02wc2FsD07	02wc2FsD07f	GACGTCGACATTACATACATAGCAGGAAC
		02wc2FsD07r	GACGTCGACAGTCTCTCATTCTCATATAGC
TrCHSa3	05wc1RsB06	05wc1RsB06f	GAATTCTAGAAGATATGGTGAGTGTAGCTG
		05wc1RsB06r	GAATTCTAGAATCACACATCTTATATAGCC
TrCHSc	07wc1TsE12	07wc1TsE12f	GAATTCTAGAAGAAGAAATATGGGAGACGAAGG
		07wc1TsE12r	GAATTCTAGAAAGACTTCATGCACACAAGTTCC
TrCHSd2	07wc1XsD03	07wc1XsD03f	GAATTCTAGAATAACCTATCAGTACTCACC
		07wc1XsD03r	GAATTCTAGAATCTAGGCAATTTAAGTGGC

TrCHSf	07wc1UsD07	07wc1UsD07f	GAATTCTAGATGATTCATTGTTTGTTTCCATAAC
		07wc1UsD07r	GAATTCTAGAACATATTCATCTTCCTATCAC
TrCHSh	13wc2IsG04	13wc2IsG04f	GAATTCTAGATCCAAATTCTCGTACCTCACC
		13wc2IsG04r	GAATTCTAGATAGTTCACATCTCTCGGCAGG
TrDFRd	12wc1CsE09	12wc1CsE09f	GACGTCGACACAACAGTCTTCCACTTGAGC
		12wc1CsE09r	GACGTCGACTCTATACTCTGGTAACTATAGG
TrF3Ha	07wc1LsG03	07wc1LsG03f	GAATTCTAGAACCACACAACACACAAACACC
		07wc1LsG03r	GAATTCTAGAACCAAGCAGCTTAATACACG
TrPALa	04wc1UsB03	04wc1UsB03f	AGTACTGCAGAGATATGGAAGTAGTAGCAGCAGC
		04wc1UsB03r	AGTACTGCAGTAGCAAACCAGTTCCCAACTCC
TrPALb	05wc1PsH02	05wc1PsH02f	AGTACTGCAGATAATGGAGGGAATTACCAATGG
		05wc1PsH02r	AGTACTGCAGTGCTAATTAACATATTGGTAGAGG
TrPALf	13wc2AsD12	13wc2AsD12f	AGTACTGCAGATAATGGAGGGAATTACCAATGG
		13wc2AsD12r	AGTACTGCAGTGCTAATTAACATATTGGTAGAGG
TrVRa	11wc1NsA07	11wc1NsA07f	AGTACTGCAGATAAAGAGAGTCAAAAATGGC
		11wc1NsA07r	AGTACTGCAGAACACATACTTAGAGATAGCC

EXAMPLE 5

Development of binary transformation vectors containing chimeric genes with cDNA sequences from perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa

To alter the expression of the proteins involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa, through antisense and/or sense suppression technology and for over-expression of these key proteins in transgenic plants, a set of sense and antisense binary transformation vectors was produced.

cDNA fragments were generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained recognition sites for appropriate restriction enzymes, for example EcoRI and XbaI, for directional and non-directional cloning into the target vector. After PCR amplification and restriction digest with the appropriate restriction enzyme (usually XbaI), the cDNA fragments were cloned into the corresponding site in a modified pPZP binary vector (Hajdukiewicz *et al.*, 1994). The pPZP221 vector was modified to contain the $35S^2$ cassette from pKYLX71:$35S^2$ as follows. pKYLX71:$35S^2$ was cut with ClaI. The 5' overhang was filled in using Klenow and the blunt end was A-tailed with Taq polymerase. After cutting with EcoRI, the 2kb fragment with an EcoRI-compatible and a 3'-A tail was gel-purified. pPZP221 was cut with HindIII and the resulting 5' overhang filled in and T-tailed with Taq polymerase. The remainder of the original pPZP221 multi-cloning site was removed by digestion with EcoRI, and the expression cassette cloned into the EcoRI site and the 3' T overhang restoring the HindIII site. This binary vector contains between the left and right border the plant selectable marker gene aaaC1 under the control of the 35S promoter and 35S terminator and the pKYLX71:$35S^2$-derived expression cassette with a CaMV 35S promoter with a duplicated enhancer region and an rbcS terminator.

The orientation of the constructs (sense or antisense) was checked by restriction enzyme digest. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins in sense and antisense orientations under the control of the CaMV $35S^2$ promoter were generated (Figures 114, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190 and 195).

EXAMPLE 6

Production and analysis of transgenic Arabidopsis plants carrying chimeric perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa genes involved in flavonoid biosynthesis

A set of transgenic Arabidopsis plants carrying chimeric perennial ryegrass and white clover genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, were produced.

pPZP221-based transformation vectors with *Lp*F3OH and *Tr*BANa, *Tr*CHIa, *Tr*CHId, *Tr*CHRc, *Tr*CHSa1, *Tr*CHSa3, *Tr*CHSc, *Tr*CHSd2, *Tr*CHSf, *Tr*CHSh, *Tr*DFRd, *Tr*F3Ha, *Tr*PALa, *Tr*PALb, *Tr*PALf and *Tr*VRa cDNAs comprising the full open reading frame sequences in sense and antisense orientations under the control of the CaMV 35S promoter with duplicated enhancer region ($35S^2$) were generated as detailed in Example 6.

Agrobacterium-mediated gene transfer experiments were performed using these transformation vectors.

The production of transgenic Arabidopsis plants carrying the perennial ryegrass F3OH and white clover BANa, CHIa, CHId, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa cDNAs under the control of the CaMV 35S promoter with duplicated enhancer region ($35S^2$) is described here in detail.

Preparation of Arabidopsis plants

Seedling punnets were filled with Debco seed raising mixture (Debco Pty. Ltd.) to form a mound. The mound was covered with two layers of anti-bird netting secured with rubber bands on each side. The soil was saturated with water and

enough seeds (*Arabidopsis thaliana* ecotype Columbia, Lehle Seeds #WT-02) sown to obtain approximately 15 plants per punnet. The seeds were then vernalised by placing the punnets at 4 ºC. After 48 hours the punnets were transferred to a growth room at 22 ºC under fluorescent light (constant illumination, 55 μmolm^{-2}s^{-1}) and fed with Miracle-Gro (Scotts Australia Pty. Ltd.) once a week. Primary bolts were removed as soon as they appeared. After 4 – 6 days the secondary bolts were approximately 6 cm tall, and the plants were ready for vacuum infiltration.

Preparation of *Agrobacterium*

Agrobacterium tumefaciens strain AGL-1 were streaked on LB medium containing 50 μg/ml rifampicin and 50 μg/ml kanamycin and grown at 27 ºC for 48 hours. A single colony was used to inoculate 5 ml of LB medium containing 50 μg/ml rifampicin and 50 μg/ml kanamycin and grown over night at 27 ºC and 250 rpm on an orbital shaker. The overnight culture was used as an inoculum for 500 ml of LB medium containing 50 μg/ml kanamycin only. Incubation was over night at 27 ºC and 250 rpm on an orbital shaker in a 2 l Erlenmeyer flask.

The overnight cultures were centrifuged for 15 min at 5500 xg and the supernatant discarded. The cells were resuspended in 1 l of infiltration medium [5% (w/v) sucrose, 0.03% (v/v) Silwet-L77 (Vac-In-Stuff, Lehle Seeds #VIS-01)] and immediately used for infiltration.

Vacuum infiltration

The *Agrobacterium* suspension was poured into a container (Décor Tellfresh storer, #024) and the container placed inside the vacuum desiccator (Bel Art, #42020-0000). A punnet with *Arabidopsis* plants was inverted and dipped into the Agrobacterium suspension and a gentle vacuum (250 mm Hg) was applied for 2 min. After infiltration, the plants were returned to the growth room where they were kept away from direct light overnight. The next day the plants were returned to full direct light and allowed to grow until the siliques were fully developed. The plants were then allowed to dry out, the seed collected from the siliques and either

stored at room temperature in a dry container or used for selection of transformants.

Selection of transformants

Prior to plating the seeds were sterilised as follows. Sufficient seeds for one 150 mm petri dish (approximately 40 mg or 2000 seeds) were placed in a 1.5 ml microfuge tube. 500 μl 70% ethanol were added for 2 min and replaced by 500 μl sterilisation solution (H_2O:4% chlorine:5% SDS, 15:8:1). After vigorous shaking, the tube was left for 10 min after which time the sterilisation solution was replaced with 500 μl sterile water. The tube was shaken and spun for 5 sec to sediment the seeds. The washing step was repeated 3 times and the seeds were left covered with approximately 200 μl sterile water.

The seeds were then evenly spread on 150 mm petri dishes containing germination medium (4.61 g Murashige & Skoog salts, 10 g sucrose, 1 ml 1 M KOH, 2 g Phytagel, 0.5 g MES and 1 ml 1000x Gamborg's B-5 vitamins per litre) supplemented with 250 μg/ml timetin and 75 μg/ml gentamycin. After vernalisation for 48 hours at 4 ºC the plants were grown under continuous fluorescent light (55 μmol m-2s-1) at 22 ºC to the 6 – 8 leaf stage and transferred to soil.

Preparation of genomic DNA

3 – 4 leaves of Arabidopsis plants regenerated on selective medium were harvested and freeze-dried. The tissue was homogenised on a Retsch MM300 mixer mill, then centrifuged for 10 min at 1700xg to collect cell debris. Genomic DNA was isolated from the supernatant using Wizard Magnetic 96 DNA Plant System kits (Promega) on a Biomek FX (Beckman Coulter). 5 μl of the sample (50 μl) were then analysed on an agarose gel to check the yield and the quality of the genomic DNA.

Analysis of DNA using real-time PCR

Genomic DNA was analysed for the presence of the transgene by real-time PCR using SYBR Green chemistry. PCR primer pairs (Table 4) were designed

using MacVector (Accelrys). The forward primer was located within the 35S^2 promoter region and the reverse primer within the transgene to amplify products of approximately 150 - 250 bp as recommended. The positioning of the forward primer within the 35S^2 promoter region guaranteed that homologous genes in Arabidopsis were not detected.

5 μl of each genomic DNA sample was run in a 50 μl PCR reaction including SYBR Green on an ABI (Applied Biosystems) together with samples containing DNA isolated from wild type Arabidopsis plants (negative control), samples containing buffer instead of DNA (buffer control) and samples containing the plasmid used for transformation (positive plasmid control).

Plants were obtained after transformation with all chimeric constructs and selection on medium containing gentamycin. The selection process and two representative real-time PCR analyses are shown in Figure xx.

TABLE 4

List of primers used for Real-time PCR analysis of Arabidopsis plants transformed with chimeric perennial ryegrass genes involved in flavonoid biosynthesis

construct	primer 1 (forward)	primer 2 (reverse)
pPZP221LpF3OHsense	TTGGAGAGGACACGCTGAAATC	AGGAGAGGGTTGGACATCGC
pPZP221LpF3OHanti	CATTTCATTTGGAGAGGACACGC	ACGAGGAGTTCTGGAAGATGGG
pPZP221TrBANasense	TTGGAGAGGACACGCTGAAATC	GCAACAAAACCAGTGCCACC
pPZP221TrBANaanti	TCATTTGGAGAGGACACGCTG	GATGATTGCCCCAGCAAGG
pPZP221TrCHIasense	CATTTCATTTGGAGAGGACACGC	CAAGGTTCTCGACTTGGATTGC
pPZP221TrCHIaanti	TCATTTGGAGAGGACACGCTG	AGATTACCTGCCTTGTTGAACGAG
pPZP221TrCHIdsense	TCATTTGGAGAGGACACGCTG	GACGGTAGGAGGGAATAGATTGTTC
pPZP221TrCHIdanti	TCATTTGGAGAGGACACGCTG	CCAGGTTATCCGAGTTATTCAACG
pPZP221TrCHRcsense	CCACTATCCTTCGCAAGACCC	TCCCATTCCAACCACAGGC
pPZP221TrCHRcanti	TCATTTGGAGAGGACACGCTG	CAAGCCAGGACTCAGTGACCTATG
pPZP221TrCHSa1sense	TCATTTGGAGAGGACACGCTG	CTGGTCAACACGATTTGCTGG
pPZP221TrCHSa1anti	TCATTTGGAGAGGACACGCTG	AACCACAGGAGAAGGACTTGACTG

pPZP221TrCHSa3sense	CATTTCATTTGGAGAGGACACGC	AACACGGTTTGGTGGATTTGC
pPZP221TrCHSa3anti	TCATTTGGAGAGGACACGCTG	ACAACTGGAGAAGGACTTGATTGG
pPZP221TrCHScsense	TTGGAGAGGACACGCTGAAATC	ACAAGTTGGTGAGGGAATGCC
pPZP221TrCHScanti	TCATTTGGAGAGGACACGCTG	GGGATTGATACTTGCTTTTGGACC
pPZP221TrCHSd2sense	CCCACTATCCTTCGCAAGACC	AGTTGCAGTGCCGATTGCC
pPZP221TrCHSd2anti	CATTTCATTTGGAGAGGACACGC	AAGATGGACTTGCCACAACAGG
pPZP221TrCHSfsense	CATTTCATTTGGAGAGGACACGC	TCGTTGCCTTTCCCTGAGTAGG
pPZP221TrCHSfanti	TCATTTGGAGAGGACACGCTG	GATTGGCTTTTGGACCAGGG
pPZP221TrCHShsense	TCATTTGGAGAGGACACGCTG	CGGTCACCATTTTTTTGTTGGAGG
pPZP221TrCHShanti	TCATTTGGAGAGGACACGCTG	TGTTGTTTGGGTTTGGACCG
pPZP221TrDFRdsense	CATTTCATTTGGAGAGGACACGC	ATTGAGATTTTGGACGGTGGC
pPZP221TrDFRdanti	CATTTCATTTGGAGAGGACACGC	CGCAACCTGGATTGTTGAGAGC
pPZP221TrF3Hasense	TCATTTGGAGAGGACACGCTG	TCTTCCCTAACGAAACTTGACTCG
pPZP221TrF3Haanti	TCATTTGGAGAGGACACGCTG	GAACAACAACTTAGGGACTTGGAGG
pPZP221TrPALasense	ATGACGCACAATCCCACTATCC	TTGCCTCAGCAGCCACACC
pPZP221TrPALaanti	GGAGAGGACACGCTGAAATCAC	TGCCAAAAGAGGTTGAAAGTGC
pPZP221TrPALbsense	ATCCCACTATCCTTCGCAAGACCC	AATGACTCCCCATCAACGACTCCG
pPZP221TrPALbanti	TTGGAGAGGACACGCTGAAATC	GACAAATTGTTCACAGCTATGTGCC
pPZP221TrPALfsense	ATCCCACTATCCTTCGCAAGACCC	CACCATACGCTTCACCTCATCC
pPZP221TrPALfanti	TCATTTGGAGAGGACACGCTG	TTGTTAGAGAGGAGTTAGGAACCGC
pPZP221TrVRasense	CCACTATCCTTCGCAAGACCC	GCTTACATCCCTCTTACGTTCTGG
pPZP221TrVRaanti	CCACTATCCTTCGCAAGACCC	AAAAGCTCGTGGACGCTGG

EXAMPLE 7

Genetic mapping of perennial ryegrass genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits

The cDNAs representing genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens;

pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, were amplified by PCR from their respective plasmids, gel-purified and radio-labelled for use as probes to detect restriction fragment length polymorphisms (RFLPs). RFLPs were mapped in the F_1 (first generation) population, NA_6 x AU_6. This population was made by crossing an individual (NA_6) from a North African ecotype with an individual (AU_6) from the cultivar Aurora, which is derived from a Swiss ecotype. Genomic DNA of the 2 parents and 114 progeny was extracted using the 1 x CTAB method of Fulton et al. (1995).

Probes were screened for their ability to detect polymorphism using the DNA (10 μg) of both parents and 5 F_1 progeny restricted with the enzymes DraI, EcoRI, EcoRV or HindIII. Hybridisations were carried out using the method of Sharp et al. (1988). Polymorphic probes were screened on a progeny set of 114 individuals restricted with the appropriate enzyme (Figure 115).

RFLP bands segregating within the population were scored and the data was entered into an Excel spreadsheet. Alleles showing the expected 1:1 ratio were mapped using MAPMAKER 3.0 (Lander et al. 1987). Alleles segregating from, and unique to, each parent, were mapped separately to give two different linkage maps. Markers were grouped into linkage groups at a LOD of 5.0 and ordered within each linkage group using a LOD threshold of 2.0.

Loci representing genes involved in flavonoid biosynthesis mapped to the linkage groups as indicated in Table 5 and in Figure 197. These gene locations can now be used as candidate genes for quantitative trait loci associated with flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits.

TABLE 5

Map locations of ryegrass genes involved in flavonoid biosynthesis across two genetic linkage maps of perennial ryegrass

Probe	Polymorphic	Mapped with	Locus	Linkage group	
				NA_6	AU_6
*Lp*DFRb	Y	*Hind* III	*Lp*DFRb	6	6

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Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

CLAIMS

1. A substantially purified or isolated nucleic acid or nucleic acid fragment encoding a flavonoid biosynthetic enzyme selected from the group consisting of chalcone isomerase (CHI), chalcone synthase (CHS), chalcone reductase (CHR), dihydroflavonol 4-reductase (DFR), leucoanthocyanidin reductase (LCR), flavonoid 3', 5' hydrolase (F3'5'H), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), phenylalanine ammonia-olyase (PAL) and vestitone reductase (VR) from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or a functionally active fragment or variant thereof.

2. A nucleic acid or nucleic acid fragment according to Claim 1, wherein said clover species is white clover (*Trifolium repens*) and said ryegrass species is perennial ryegrass (*Lolium perenne*).

3. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHI or CHI-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 122 and 127 hereto (Sequence ID Nos: 1, 3 to 7, 8, 10 to 12, 13, 15 and 16, 17, 19 to 22, 307, and 309, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

4. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHS or CHS-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 13, 15, 16, 18, 19, 21, 22, 24, 25, 27, 28, 30, 31, 33, 34, 137, 142, 147, 152, 157 and 162 hereto (Sequence ID Nos: 23, 25 to 63, 64, 66 to 68, 69, 71 to 77, 78, 80 to 90, 91, 93 and 94, 95, 97 to 100, 101, 103 to 105, 106, 313, 315, 317, 319, 321, and 323, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

5. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHR or CHR-like protein and including nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 36, 38, 40, 41, 43 and 132 hereto (Sequence ID Nos: 108, 110, 112 to 116, 117, 119 to 134, and 311, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

6. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a DFR or DFR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 44, 46, 47, 49, 50, 52, 54, 55, 57, 59, 61, 62, 64, 101, 103, 104, 106, 117 and 167 hereto (Sequence ID Nos: 135, 137 to 146, 147, 149 to 152, 153, 155, 157 and 158, 159, 161, 163, 165 to 167, 168, 170 to 184, 286, 288 to 292, 293, 295 to 297, 305, and 325, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

7. A nucleic acid or nucleic acid fragment according to Claim 1, encoding an LCR or LCR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 65 and 67 hereto (Sequence ID Nos: 185 and 187 to 193, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

8. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a F3'5'H or F3'5'H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 68, 70 and 72 hereto (Sequence ID Nos: 194, 196, and 198 to 201, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

9. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a F3H or F3H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 73, 75, 76, 78, 107, 109, 111 and 172 hereto (Sequence ID Nos: 202, 204 to 244, 245, 247, 298, 300 to 302, 303, and 327, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

10. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a F3'H or F3'H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 80 and 82 hereto (Sequence ID Nos: 249, and 251 and 252, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

11. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a PAL or PAL-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 83, 85, 86, 88, 89, 91, 93, 95, 97, 177, 182 and 187 hereto (Sequence ID Nos: 253, 255 to 257, 258, 260 to 267, 268, 270, 272, 274, 276 and 277, 329, 331, and 333, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

12. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a VR or VR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 98, 100 and 192 hereto (Sequence ID Nos: 278, 280 to 285, and 335, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

13. A construct including a nucleic acid or nucleic acid fragment according to Claim 1.

14. A vector including a nucleic acid or nucleic acid fragment according to Claim 1.

15. A vector according to Claim 14, further including a promoter and a terminator, said promoter, nucleic acid or nucleic acid fragment and terminator being operatively linked.

16. A plant cell, plant, plant seed or other plant part, including a construct according to claim 13 or a vector according to Claim 14.

17. A plant, plant seed or other plant part derived from a plant cell or plant according to Claim 16.

18. A method of modifying flavonoid biosynthesis in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

19. A method of modifying protein binding, metal chelation, anti-oxidation, and/or UV-light absorption in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

20. A method of modifying pigment production in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

21. A method of modifying plant defense to a biotic stress, said method including introducing into said plant an effective amount of a nucleic acid or nucleic

acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

22. A method according to claim 21 wherein said biotic stress is selected from the group consisting of viruses, microorganisms, insects and fungal pathogens.

23. A method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

24. Use of a nucleic acid or nucleic acid fragment according to Claim 1, and/or nucleotide sequence information thereof, and/or single nucleotide polymorphisms thereof as a molecular genetic marker.

25. A substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of ASR and ASR-like, A22 and A22-like, CYS and CYS-like, LEA and LEA-like, DHN and DHN-like and PKABA and PKABA-like; and functionally active fragments and variants thereof.

26. A polypeptide according to Claim 25, wherein said clover species is white clover (*Trifolium repens*) and said ryegrass species is perennial ryegrass (*Lolium perenne*).

27. A polypeptide according to Claim 25, wherein said polypeptide is CHI or CHI-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 11, 123 and 128 hereto (Sequence ID Nos: 2, 9, 14, 18, 308, and 310, respectively); and functionally active fragments and variants thereof.

28. A polypeptide according to Claim 25, wherein said polypeptide is CHS or CHS-like and includes an amino acid sequence selected from the group

consisting of sequences shown in Figures 14, 17, 20, 23, 26, 29, 32, 35, 138, 143, 148, 153, 158 and 163 hereto (Sequence ID Nos: 24, 65, 70, 79, 92, 96, 102, 107, 314, 316, 318, 320, 322, and 324, respectively); and functionally active fragments and variants thereof.

29. A polypeptide according to Claim 25, wherein said polypeptide is CHR or CHR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 37, 39, 42 and 133 hereto (Sequence ID Nos: 109, 111, 118, and 312, respectively); and functionally active fragments and variants thereof.

30. A polypeptide according to Claim 25, wherein said polypeptide is DFR or DFR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 45, 48, 51, 53, 56, 58, 60, 63, 102, 105, 118 and 168 hereto (Sequence ID Nos: 136, 148, 54, 156, 160, 162, 164, 169, 287, 294, 306, and 326, respectively); and functionally active fragments and variants thereof.

31. A polypeptide according to Claim 25, wherein said polypeptide is LCR or LCR-like and includes an amino acid sequence shown in Figure 66 hereto (Sequence ID No: 186); and functionally active fragments and variants thereof.

32. A polypeptide according to Claim 25, wherein said polypeptide is F3'5'H or F3'5'H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 69 and 71 hereto (Sequence ID Nos: 195 and 197, respectively); and functionally active fragments and variants thereof.

33. A polypeptide according to Claim 25, wherein said polypeptide is F3H or F3H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 74, 77, 79, 108, 112 and 173 hereto (Sequence ID Nos: 203, 246, 248, 299, 304, and 328, respectively); and functionally active fragments and variants thereof.

34. A polypeptide according to Claim 25, wherein said polypeptide is F3'H or F3'H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figure 81 hereto (Sequence ID No: 250); and functionally active fragments and variants thereof.

35. A polypeptide according to Claim 25, wherein said polypeptide is PAL or PAL-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 84, 87, 90, 92, 94, 96, 178, 183 and 188 hereto (Sequence ID Nos: 254, 259, 269, 271, 273, 275, 330, 332, and 334, respectively); and functionally active fragments and variants thereof.

36. A polypeptide according to Claim 25, wherein said polypeptide is VR or VR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 99 and 193 hereto (Sequence ID Nos: 279 and 336, respectively); and functionally active fragments and variants thereof.

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                        *        20         *        40         *        60
TrCHIa : GCATTAAACANTGAAANTTGACCAGTCCCAACAAAGATCTGAAACACATAGCTCCCCATT :  60

                        *        80         *       100         *       120
TrCHIa : TTTTAACATTAAACTAAAAATATGTCGGCCATCACCGCAATCCAAGTCGAGAACCTTGAA : 120

                        *       140         *       160         *       180
TrCHIa : TTTCCGGCTGTGATTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 180

                        *       200         *       220         *       240
TrCHIa : GAGAGAGGTTTGACTATTGAAGGAAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG : 240

                        *       260         *       280         *       300
TrCHIa : GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG : 300

                        *       320         *       340         *       360
TrCHIa : CTTGAGACCCTTGACTTCTACAGAGATATCATTTCAGGACCATTTGAGAAGTTGATTCGA : 360

                        *       380         *       400         *       420
TrCHIa : GGATCGAAGATTAGGGAATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGT : 420

                        *       440         *       460         *       480
TrCHIa : GTGGCACACTTAAAATCTGTTGGGACTTATGGAGATGCAGAAGTTGAAGCTATGCAAAAA : 480

                        *       500         *       520         *       540
TrCHIa : TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAA : 540

                        *       560         *       580         *       600
TrCHIa : TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAA : 600

                        *       620         *
TrCHIa : GCTGCAGTAATAGAGAACAAGGGAGCTTCATCGGCG : 636
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FIGURE 1

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                       *       20         *        40         *        60
TrCHIa : MSAITAIQVENLEFPAVITSPATGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDVAVAS :  60

                       *       80         *       100         *       120
TrCHIa : LATKWKGKSSEELLETLDFYRDIISGPFEKLIRGSKIRELSGPEYSRKVNENCVAHLKSV : 120

                       *      140         *       160         *       180
TrCHIa : GTYGDAEVEAMQKFVEAFKPINFPPGASVFYRQSPDGILGLSFSQDASIPEKEAAVIENK : 180

TrCHIa : GASSA : 185
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FIGURE 2

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                    *        20         *        40         *        60
TrCHIa1: GCATTAAACATTGACA-NAGT-CCNAAT-AAAAAAGATCTGAAACACATAGTNCCCCATT :  57
TrCHIa2: ---------------GNTTGCCCGGTCCCAACAAAGATCTGAAACACATAGCCCCCCATT :  45
TrCHIa3: ----------------------------------GGATCTGAAACACATAG-TNCCCC-- :  23
TrCHIa4: ---------------------------------CNGATCTGAAAAACNTAG-TACCCA-- :  24
TrCHIa5: ---------CNTTAAANTTGACCAGTCCNAACAAAGATCTGAAACACATAGCCCCCCATT :  51

                    *        80         *       100         *       120
TrCHIa1: TTTTAACATTAAACTAAAAATATGTCGGCCATCACCGCAATCCAAGTCGAGAACCTTGAA : 117
TrCHIa2: TTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAAGTCGAGAACCTTGAA : 105
TrCHIa3: TTTTAACATTAAACTAAAAATATGTCGGCCATCACCGCAATCCAAGTCGAGAACCTTGAA :  83
TrCHIa4: TTTTAANATTAAACTAAAAATATGTCGGCNATCACCGCAATCCAAGTCGAGAACCTTGAA :  84
TrCHIa5: TTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAAGTCGAGAACCTTGAC : 111

                    *       140         *       160         *       180
TrCHIa1: TTTCCGGCTGTGCTTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 177
TrCHIa2: TTCCCGGCCGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 165
TrCHIa3: TTTCCAGCTGTGATTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 143
TrCHIa4: TTTCCAGCTGTGATTACTTCTCCGGCCACCGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 144
TrCHIa5: TTCCCGGCCGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTTCTTGGTGGTGCAGGG : 171

                    *       200         *       220         *       240
TrCHIa1: GAGAGAGGTTTGACTATTGAAGGAAACTTNNTCAANGCCGCTGGNATACGACCGTNTTNG : 237
TrCHIa2: GAGAGAGGTTTGACTATTGAAGGAAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG : 225
TrCHIa3: GAGAGAGGTTTGACTATTGAAGGAAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG : 203
TrCHIa4: GAGAGAGGTTTGACTATTGAAGGAAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG : 204
TrCHIa5: GAGAGAGGTTTGACTATTGAAGGAAACTTCATCAAGTTCACTGCCATAGGAGTATATTTG : 231

                    *       260         *       280         *       300
TrCHIa1: TACNACN----------------------------------------------------- : 244
TrCHIa2: GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG : 285
TrCHIa3: GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGTAAATCCTCTGACGAGTTG : 263
TrCHIa4: GAAGATGNANNANCGGNTNCNNTN------------------------------------ : 228
TrCHIa5: GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG : 291

                    *       320         *       340         *       360
TrCHIa1: ------------------------------------------------------------ :   -
TrCHIa2: CTTGAGACCCTTGACTTCTACAGAGATATCATTTCAGGACCATTTGAGAAGTTGATTCGA : 345
TrCHIa3: CTTGAGACTCTTGACTTCTATAGAGACATCATTTCAGGACCCTTTGAAAAGTTGATTCGA : 323
TrCHIa4: ------------------------------------------------------------ :   -
TrCHIa5: CTTCAGACCCTTGACTTCTACAGAGATATCATTTCAGGACCATTTGAGAAGTTGATTCGA : 351

                    *       380         *       400         *       420
TrCHIa1: ------------------------------------------------------------ :   -
TrCHIa2: GGATCGAAGATTAGGGAATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGT : 405
TrCHIa3: GGATCGAAGATTAGGGAATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGC : 383
TrCHIa4: ------------------------------------------------------------ :   -
TrCHIa5: GGATCCAAGATTAGGGAATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGT : 411
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FIGURE 3

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                    *       440         *       460         *       480
TrCHIa1: ------------------------------------------------------------ :   -
TrCHIa2: GTGGCACACTTAAAATCTGTTGGGACTTACGGAGATGCAGAAGTTGAAGCTATGCAAAAA : 465
TrCHIa3: GTGGCCCACTTAAAATCTGTTGGGACTTATGGAGATGCTGAAGCTGAAGCTATGCAAAAA : 443
TrCHIa4: ------------------------------------------------------------ :   -
TrCHIa5: GTGGCACACTTAAAATCTGTTGGGACTTATGGAGATGCAGAAGTTGAAGCTATGCAAAAA : 471

                    *       500         *       520         *       540
TrCHIa1: ------------------------------------------------------------ :   -
TrCHIa2: TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAA : 525
TrCHIa3: TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAA : 503
TrCHIa4: ------------------------------------------------------------ :   -
TrCHIa5: TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAA : 531

                    *       560         *       580         *       600
TrCHIa1: ------------------------------------------------------------ :   -
TrCHIa2: TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAA : 585
TrCHIa3: TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAG : 563
TrCHIa4: ------------------------------------------------------------ :   -
TrCHIa5: TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGN-- : 589

                    *       620         *
TrCHIa1: ------------------------------------ :   -
TrCHIa2: GCTGCAGTAATAGAGAACANN--------------- : 606
TrCHIa3: GCTGCAGTAATAGAGAACAAGGGAGCTTCATCGGCG : 599
TrCHIa4: ------------------------------------ :   -
TrCHIa5: ------------------------------------ :   -
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FIGURE 3 (cont)

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                    *        20         *        40         *        60
TrCHIb : TTAAAATTGACACAGTCCCAACCTTAAANTTGACCNGGTCCCAAACAAAGATCTGAAACA :  60

                    *        80         *       100         *       120
TrCHIb : ACATAGCCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 120

                    *       140         *       160         *       180
TrCHIb : GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTT : 180

                    *       200         *       220         *       240
TrCHIb : CTTGGTGGTGCAGGGGAGAGAGGTTNGACTATTGAAGGAAACTTCATCAAGTTCACTGCC : 240

                    *       260         *       280         *       300
TrCHIb : ATAGGAGTATATTTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGCAGA : 300

                    *       320         *
TrCHIb : TCCTCTGAAGAGNGCTTGAGACCCTNGACTNC : 332
```

FIGURE 4

```
                        *         20          *         40          *         60
TrCHIb : MSAITAIQVENLEFPAVITSPVNGKSYFLGGAGERGXTIEGNFIKFTAIGVYLEDVAGAS : 60

                        *
TrCHIb : LATKWKGRSSEEXLRPXT : 78
```

FIGURE 5

```
                    *        20         *        40         *        60
TrCHIb1 : TTAAAATTGACCNAGTCCNAACCTTAAANTTGACCNGGTCCCAAACAAAGATCTGAAACA :  60
TrCHIb2 : -TTAANTTGACACAGTCCCAACCTTAAANTTGACCNGGTCCCAAACAAAGATCTGAAACA :  59
TrCHIb3 : --------------------GCGTTAAAATTGACCCAGT-CCNAACAAAGATCTGAAAC- :  38

                    *        80         *       100         *       120
TrCHIb1 : ACATAGCCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 120
TrCHIb2 : ACATAGCCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 119
TrCHIb3 : ACATAGCCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA :  98

                    *       140         *       160         *       180
TrCHIb1 : GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTT : 180
TrCHIb2 : GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTTT : 179
TrCHIb3 : GTCGAGAACCTTGANTTCCCGGCGGAGATTACTTCTNCGGGCAANGGCAAGGGATATTNT : 158

                    *       200         *       220         *       240
TrCHIb1 : CTTGGTGGTGCAGGGGAGAGAGGTTNGACTATTGAAGGAAACTTCATCAAGTTCACTGCC : 240
TrCHIb2 : CTTGGTGGTGCAGGGGAGAGAGGTTNGACTATTGAAGGAAACTTCATCAAGTTCACTGCC : 239
TrCHIb3 : CTTGGTGGNGNAGGNNAGANNGNNTNGN-------------------------------- : 186

                    *       260         *       280         *       300
TrCHIb1 : ATAGGAGTATATTTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGNAGA : 300
TrCHIb2 : ATAGGAGTATATTTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGCANA : 299
TrCHIb3 : ------------------------------------------------------------ :   -

                    *       320         *
TrCHIb1 : TCCTCTGAANAGNGNTTGANACCNTNGACTNN : 332
TrCHIb2 : TNCTCTGAAGAGNGCTTGAGACCCTNGACTNC : 331
TrCHIb3 : -------------------------------- :   -
```

FIGURE 6

```
                  *        20         *        40         *        60
TrCHIc : GTTAGNAGNAGNATNTCNGGCACCCTTTGAAAAGTTGATTCGAGGATCGAAGATTAGGGA :  60

                  *        80         *       100         *       120
TrCHIc : ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGCGTGGCACACTTAAAATC : 120

                  *       140         *       160         *       180
TrCHIc : TGTTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 180

                  *       200         *       220         *       240
TrCHIc : GCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAATCACCTGATGGAATATT : 240

                  *       260         *
TrCHIc : AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 274
```

FIGURE 7

```
                     *        20          *        40          *        60
TrCHIc : APFEKLIRGSKIRELSGPEYSRKVNENCVAHLKSVGTYGDAEAEAMQKFVEAFKPINFPP : 60

                     *        80          *
TrCHIc : GASVFYRQSPDGILGVSIANSFFLTILIRVRFDC : 94
```

FIGURE 8

```
                    *        20         *        40         *        60
TrCHIc1: GTTAGNAGNATNNTTTCNGGCACCCTTTGAAAAGTTGATTCGAGGATCGAAGATTAGGGA :  60
TrCHIc2: ----------GNATNTTTNGGACCCTTTGAAAAGTTGATTCGAGGATCGAAGATTAGGGA :  50

                    *        80         *       100         *       120
TrCHIc1: ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGCGTGGCACACTTAAAATC : 120
TrCHIc2: ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAACTGCGTGGCACACTTAAAATC : 110

                    *       140         *       160         *       180
TrCHIc1: TGTTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 180
TrCHIc2: TGTTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 170

                    *       200         *       220         *       240
TrCHIc1: GCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAATCACCTGATGGAATATT : 240
TrCHIc2: GCCTATTAATTTTCCACCTGGTGCCTCTGTTTTTTACAGGCAATCACCTGATGGAATATT : 230

                    *       260         *
TrCHIc1: AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 274
TrCHIc2: AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 264
```

FIGURE 9

```
                    *        20         *        40         *        60
TrCHId : TTNANTNNNNTTNNCGGGCAATTACAACTACACAACACCTTCTCCATTACCATCTATCTT :  60

                    *        80         *       100         *       120
TrCHId : CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTCACCGCTTTGAATATCGAGAAC : 120

                    *       140         *       160         *       180
TrCHId : AATCTATTCCCTCCTACCGTCACACCACCGGGATCCACCAACAATTTCTTCCTCGGCGGT : 180

                    *       200         *       220         *       240
TrCHId : GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGCTATTGGTGTT : 240

                    *       260         *       280         *       300
TrCHId : TATCTACAGGACATTGCTGTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 300

                    *       320         *       340         *       360
TrCHId : GAGCTAACGGAAACTGTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 360

                    *       380         *       400         *       420
TrCHId : ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 420

                    *       440         *       460         *       480
TrCHId : AATTGTGTAGCTATTTGGAAGTCTCTTGGGATTTATACCGACGAAGAAGCCAAAGCAATT : 480

                    *       500         *       520         *       540
TrCHId : GAGAAGNNTGTTTCTGTCTTCAAAGANGAAACATTCCCACCAGGCTCCTCTATCCTTTTC : 540

                    *       560         *       580         *       600
TrCHId : ACAGNATTACCCAAAGGATTAGGATCACTAACGATAAGNTTCTCTAAAGATGGATCCATT : 600

                    *       620         *       640         *       660
TrCHId : CCAGAGACCGAGTCTGCAGTTATAGAGAATAAGCTACTCTCACAAGCTGTGCTNGAGTCG : 660

                    *       680         *       700         *       720
TrCHId : ATGATAGGGGCACACGGTGTCTCCCCTGCAGCAAAACAGAGTTTTGGCCACCAGGNTANC : 720

                    *       740         *       760         *       780
TrCHId : CGAGNTATTCAACGAGGNTGGCTGATGCCTAGCAACTTGATNATATCAACAAAACGAAAA : 780

                    *       800         *       820
TrCHId : TGAAAGNCCTTTTCTGCAATAAAGAACAAGCGGAAATTTTATTTT : 825
```

FIGURE 10

```
                   *         20          *         40          *         60
TrCHId : MALPSVTALNIENNLFPPTVTPPGSTNNFFLGGAGERGLQIQDKFVKFTAIGVYLQDIAV :  60

                   *         80          *        100          *        120
TrCHId : PYLATKWKGKTAQELTETVPFFRDIVTGPFEKFMQVTMILPLTGQQYSEKVSENCVAIWK : 120

                   *        140          *        160          *        180
TrCHId : SLGIYTDEEAKAIEKVSVFKETFPPGSSILFTLPKGLGSLTIXFSKDGSIPETESAVIEN : 180

                   *        200          *        220          *
TrCHId : KLLSQAVXESMIGAHGVSPAAKQSFGHQXXRXIQRXWLMPSNLXISTKRK : 230
```

FIGURE 11

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```
                   *        20         *        40         *        60
TrCHId1 : TTNANTNNNNTTNNCGGTTTNTNANAACTACACAACACCTTCT-TTTTTCCATTTATCTT :  59
TrCHId2 : -----------------GCAATTACAACCTNNCAACACCTTCTCC-TTA-CNTCTATCTT :  41
TrCHId3 : ---------------------TTAC-ACT-CACAACACCTTCTCCATTACCATCTATCTT :  37
TrCHId4 : --------------------------------TCACATTATTACAATTACAACTTAACAT :  28

                   *        80         *       100         *       120
TrCHId1 : CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTCNCCGCTTTGAATATCGAGAAC : 119
TrCHId2 : CTACTAAGTTNAACGAGATCAATGGCACTTCCTTCTGTGACCGCTTTGAATATCGAGAAC : 101
TrCHId3 : CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTCACCGCTTTGAATATCGAGAAC :  97
TrCHId4 : TNACT-CGTAAAAAGAGATNAATGGCACTTCCTTCTGTCACCGCTTTGGATATCGAGAAC :  87

                   *       140         *       160         *       180
TrCHId1 : AATCTATTCCCTCCTACCGTCACACCANCGGGATCCACCAACAATTTCTTCCTCGGCGGT : 179
TrCHId2 : AATCTATTCCCTCCTACCGTCACACCACCGGGATCCACCAACAATTTCTTCCTCGGCGGT : 161
TrCHId3 : AATCTATTCCCTCCTACCGTCACACCACCGGGATCCACCAACAATTTCTTCCTCGGCGGT : 157
TrCHId4 : AATCTATTCCCTCCCACCGTCACACCACCGGGATCCACTGACAACTTCTTCCTCGGCGGT : 147

                   *       200         *       220         *       240
TrCHId1 : GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGNTATTGGTGTT : 239
TrCHId2 : GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTNAAATTCACCGNTATTGGTGTT : 221
TrCHId3 : GCAGGAGAGCGGGGTCTTCAAATTCAAGACAAATTTGTCAAATTCACCGCTATTGGTGTT : 217
TrCHId4 : GCAGGAGAGAGGGGTCTTCAAATCCAAGACAAATTCGTCAAATTCACCGCTATTGGTGTT : 207

                   *       260         *       280         *       300
TrCHId1 : TATCTACAGGACATTGCTGTTCCTTACCTCGCCACTAAATGGAAGGGTNAGACTGCTCAA : 299
TrCHId2 : TATCTACNGGACATTGCTGNNCNTTNCCTCGCNCNTCCCTGGATN--------------- : 266
TrCHId3 : TATCTACAGGACATTGCTGTTCCTTACCTCGCCACTAAATGGAAGGGTAAGACTGCTCAA : 277
TrCHId4 : TATCTCCAGGACATTGCTGTTCCTTACCTCGCACCTAAATGGAAGGGTAAGACTGCTCAA : 267

                   *       320         *       340         *       360
TrCHId1 : GAGCTAACGGAAACTGNNCCTTTCTTCAGGGACATNGNNACAGGTCCATTTGAGAAATTT : 359
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : GAGCTAACGGAAACTGTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 337
TrCHId4 : GAGCTAACNGAAACTGTTCCTTTCTTCAGGGACATCGTTACAGGTCCATTTGAGAAATTT : 327

                   *       380         *       400         *       420
TrCHId1 : ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCANAA : 419
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 397
TrCHId4 : ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 387

                   *       440         *       460         *       480
TrCHId1 : AATTGTGTACCTATNTGNAAGTCTCTTCGGATTTATACCGACCAAGAAGCCAAAGCAATT : 479
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : AATTGTGTAGCTATTTGGAAGTCTCTTGGGATTTATACCGACGAAGAAGCCAAAGCAATT : 457
TrCHId4 : AATTGTGTAGCTATTTGGAAGTCTCTTGGGATATATACGGACGAACAANCCAAANCAATT : 447
```

FIGURE 12

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```
                *        500         *        520         *        540
TrCHId1 : GAGAAGNNTGTTTCTGTCTTCAAAGANGAAACATTCCCACCAGGCTCCTCTATCCTTTTC : 539
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : GAGAAGTTTGTTTCTGTCTTCAAAGATGAAACATTCCCACCAGGCTCCTCTATCCTTTTC : 517
TrCHId4 : GANAANNNTGNTTCTGNTTNN--------------------------------------- : 468

                *        560         *        580         *        600
TrCHId1 : ACAGNATTACCCAAAGGATTANGATCACTAACGATAAGNTTCTCTAAAGATGGATCCATT : 599
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : ACAGTATTACCCAAAGGATTAGGATCACTAACGATAAGTTTCTCTAAAGATGGATCCATT : 577
TrCHId4 : ------------------------------------------------------------ :   -

                *        620         *        640         *        660
TrCHId1 : CCAGAGACCGAGTCTGCAGTTATAGNGAATAAGCTACTCTCACAAGCTGTGCTNGAGTCG : 659
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : CCAGAGACCGAGTCTGCAGTTATAGAGAATAAGCTACTCTCACAAGCTGTGCTTGAGTCG : 637
TrCHId4 : ------------------------------------------------------------ :   -

                *        680         *        700         *        720
TrCHId1 : ATGATAGGGGCANNCGGTGTCTNNCNTGCANCAAANCATAGTTTTGNNCACCAGGNTANC : 719
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : ATGATAGGGGCCCACGGTGTCTCCCCTGCAGCAAAACAGAG-TTTGGCCACCAGGTTATC : 696
TrCHId4 : ------------------------------------------------------------ :   -

                *        740         *        760         *        780
TrCHId1 : CNAGNTATTCAACGAGGNTGGCTGATGCCTAGCANCTTGATNNTNTNAACAAAACNAAAA : 779
TrCHId2 : ------------------------------------------------------------ :   -
TrCHId3 : CGAGATATTCAACGAGGATGG-TGATG-CTAGCAAC-TGATTATATCAACAAAACGAAAA : 753
TrCHId4 : ------------------------------------------------------------ :   -

                *        800         *        820
TrCHId1 : TGNANGNCCTTTTCTGCATTAAAGAACA----------------- : 807
TrCHId2 : --------------------------------------------- :   -
TrCHId3 : TGAAAGTCC-TTTCTGCAATAAAGACCAAGCGGAAATTTTATTTT : 797
TrCHId4 : --------------------------------------------- :   -
```

FIGURE 12 (cont)

```
                 *        20         *        40         *        60
TrCHSa: TATTNTNNGAAACCACTTGTGTTGAAGNCGTGAACTTNGCTACCCTCCATATNATACTAT :   60

                 *        80         *       100         *       120
TrCHSa: NACCTCTTCTGAGACCCTTCATCATAGAAANACAACACACNTCAGCNCTTTGCTNTTTCT :  120

                 *       140         *       160         *       180
TrCHSa: ACAACAACCTATAACTANACATATTATTTTATNTATTTAGTATATAATTGAAATAAACT :  180

                 *       200         *       220         *       240
TrCHSa: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :  240

                 *       260         *       280         *       300
TrCHSa: GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTGAGCAG :  300

                 *       320         *       340         *       360
TrCHSa: AGCACATATCCTGATTTCTACTTCAAAATCACAAACAGTGAGCACAAGACTGAGCTCAAA :  360

                 *       380         *       400         *       420
TrCHSa: GAGAAATTCCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTATCTAACA :  420

                 *       440         *       460         *       480
TrCHSa: GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :  480

                 *       500         *       520         *       540
TrCHSa: AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAGGCT :  540

                 *       560         *       580         *       600
TrCHSa: ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :  600

                 *       620         *       640         *       660
TrCHSa: GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :  660

                 *       680         *       700         *       720
TrCHSa: GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTGCTTCGTTTG :  720

                 *       740         *       760         *       780
TrCHSa: GCAAAAGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTTCTGAAGTA :  780

                 *       800         *       820         *       840
TrCHSa: ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCACTTGGACAGTCTTGTTGGACAAGCA :  840

                 *       860         *       880         *       900
TrCHSa: CTATTTGGAGATGGAGCTGCTGCACTCATTGTTGGCTCAGACCCAGTACCAGAAATTGAG :  900

                 *       920         *       940         *       960
TrCHSa: AAACCAATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCAGACAGTGAAGGTGCC :  960

                 *       980         *      1000         *      1020
TrCHSa: ATTGATGGTCACCTTCGTGAAGCTGGACTAACATTTCATCTTCTTAAAGATGTTCCTGGG : 1020

                 *      1040         *      1060         *      1080
TrCHSa: ATTGTATCAAAGAACATTAATAAAGCATTGGTCGAGGCTTTCCAACCATTAGGAATTTCT : 1080

                 *      1100         *      1120         *
TrCHSa: GATTACAACTCAATCTTTTGGATTGCACACCCGGGTGGACCTGCAATTCT : 1130
```

FIGURE 13

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```
                  *        20         *        40         *        60
TrCHSa : MVSVAEIRKAQRAEGPATILAIGTANPANRVEQSTYPDFYFKITNSEHKTELKEKFQRMC :  60

                  *        80         *       100         *       120
TrCHSa : DKSMIKSRYMYLTEEILKENPSLCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGQP : 120

                  *       140         *       160         *       180
TrCHSa : KSKITHLIFCTTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGCFAGGTVLRLAKDLAEN : 180

                  *       200         *       220         *       240
TrCHSa : NKGARVLVVCSEVTAVTFRGPSDTHLDSLVGQALFGDGAAALIVGSDPVPEIEKPIFEMV : 240

                  *       260         *       280         *       300
TrCHSa : WTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPGIVSKNINKALVEAFQPLGISDYNSIFW : 300

TrCHSa : IAHPGGPAI : 309
```

FIGURE 14

```
                      *        20         *        40         *        60
TrCHSa1  : TATTNTNNGAAACCACTTGTGTTGAAGNCGTGAACTTNGCTACCCTCCATATNATACTAT : 60
TrCHSa2  : ------------------------------------------------------------ :  -
TrCHSa3  : ------------------------------------------------------------ :  -
TrCHSa4  : ------------------------------------------------------------ :  -
TrCHSa5  : ------------------------------------------------------------ :  -
TrCHSa6  : ------------------------------------------------------------ :  -
TrCHSa7  : ------------------------------------------------------------ :  -
TrCHSa8  : ------------------------------------------------------------ :  -
TrCHSa9  : ------------------------------------------------------------ :  -
TrCHSa10 : ------------------------------------------------------------ :  -
TrCHSa11 : ------------------------------------------------------------ :  -
TrCHSa12 : ------------------------------------------------------------ :  -
TrCHSa13 : ------------------------------------------------------------ :  -
TrCHSa14 : ------------------------------------------------------------ :  -
TrCHSa15 : ------------------------------------------------------------ :  -
TrCHSa16 : ------------------------------------------------------------ :  -
TrCHSa17 : ------------------------------------------------------------ :  -
TrCHSa18 : ------------------------------------------------------------ :  -
TrCHSa19 : ------------------------------------------------------------ :  -
TrCHSa20 : ------------------------------------------------------------ :  -
TrCHSa21 : ------------------------------------------------------------ :  -
TrCHSa22 : ------------------------------------------------------------ :  -
TrCHSa23 : ------------------------------------------------------------ :  -
TrCHSa24 : ------------------------------------------------------------ :  -
TrCHSa25 : ------------------------------------------------------------ :  -
TrCHSa26 : ------------------------------------------------------------ :  -
TrCHSa27 : ------------------------------------------------------------ :  -
TrCHSa28 : ------------------------------------------------------------ :  -
TrCHSa29 : ------------------------------------------------------------ :  -
TrCHSa30 : ------------------------------------------------------------ :  -
TrCHSa31 : ------------------------------------------------------------ :  -
TrCHSa32 : ------------------------------------------------------------ :  -
TrCHSa33 : ------------------------------------------------------------ :  -
TrCHSa34 : ------------------------------------------------------------ :  -
TrCHSa35 : ------------------------------------------------------------ :  -
TrCHSa36 : ------------------------------------------------------------ :  -
TrCHSa37 : ------------------------------------------------------------ :  -
TrCHSa38 : ------------------------------------------------------------ :  -
TrCHSa39 : ------------------------------------------------------------ :  -
```

FIGURE 15

```
                    *       80        *      100         *      120
TrCHSa1 : NACCTCTTCTGAGACCCTTCATCATATATATATAACNCATCTCACCTCATACATATTTCC :120
TrCHSa2 : --------------------------GNANNACAACACACTTCNAC-CTTTGCT-TTTCT : 32
TrCHSa3 : -------------------------------------CACNTTAGCNCTTTGCTNTTTCT : 23
TrCHSa4 : -------------------------------------CACNTTAGC-CTTTGCT-TTTCT : 21
TrCHSa5 : ---------------------------------------------------GCANACACT :  9
TrCHSa6 : ---------------------------------------------------------ACN :  3
TrCHSa7 : ----------------------------------------------------------CC :  2
TrCHSa8 : ----------------------------------------------------------CN :  2
TrCHSa9 : ----------------------------------------------------------GC :  2
TrCHSa10: ------------------------------------------------------------ :  -
TrCHSa11: ------------------------------------------------------------ :  -
TrCHSa12: ------------------------------------------------------------ :  -
TrCHSa13: ------------------------------------------------------------ :  -
TrCHSa14: ------------------------------------------------------------ :  -
TrCHSa15: ------------------------------------------------------------ :  -
TrCHSa16: ------------------------------------------------------------ :  -
TrCHSa17: ------------------------------------------------------------ :  -
TrCHSa18: ------------------------------------------------------------ :  -
TrCHSa19: ------------------------------------------------------------ :  -
TrCHSa20: ------------------------------------------------------------ :  -
TrCHSa21: ------------------------------------------------------------ :  -
TrCHSa22: ------------------------------------------------------------ :  -
TrCHSa23: ------------------------------------------------------------ :  -
TrCHSa24: ------------------------------------------------------------ :  -
TrCHSa25: ------------------------------------------------------------ :  -
TrCHSa26: ------------------------------------------------------------ :  -
TrCHSa27: ------------------------------------------------------------ :  -
TrCHSa28: ------------------------------------------------------------ :  -
TrCHSa29: ------------------------------------------------------------ :  -
TrCHSa30: ------------------------------------------------------------ :  -
TrCHSa31: ------------------------------------------------------------ :  -
TrCHSa32: ------------------------------------------------------------ :  -
TrCHSa33: ------------------------------------------------------------ :  -
TrCHSa34: ------------------------------------------------------------ :  -
TrCHSa35: ------------------------------------------------------------ :  -
TrCHSa36: ------------------------------------------------------------ :  -
TrCHSa37: ------------------------------------------------------------ :  -
TrCHSa38: ------------------------------------------------------------ :  -
TrCHSa39: ------------------------------------------------------------ :  -
```

FIGURE 15 (cont)

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```
                        *        140         *         160         *        180
TrCHSa1  : ACAACAANCTATAACTTNNCCTGTTATNTANACCAATTGAGTNTCAAATTNACATACATA :180
TrCHSa2  : ACAACAACTTCTATNTAAACCTTTTTTTAGT-TNA--AACTTACACTACTG--CTA--AA : 85
TrCHSa3  : ACNACNNCTTCTGTCTAAACCTTTTTTGAGTNTNACTTGCATACATAGAAANNCTANNCT : 83
TrCHSa4  : AC-AC-TCTTCTGTCTAAACNTTTTTTGAGT-TNACTTGCATACATAGAAA--CTA--CT : 74
TrCHSa5  : CTATCCCTTTCTTTTCNTATAANNTACAGTACTNGCAATAAACNACTCAATTNAATTACA : 69
TrCHSa6  : AAAACAAC-TACGCATATT-ATATATATATA-TATAGTCTATA-ATTCAAACNAAA--CT : 57
TrCHSa7  : ANGGAAAACAACCTCCGNGCATANTNTATATATATATANNGTCTATAATTGAAACAAACT : 62
TrCHSa8  : ACAAAAACACTCCCATAANCATATATCTCTC-TCTNCTCTATA-ATTCAAAG-AAA--CT : 57
TrCHSa9  : ACAAAAACACTNCGCTANTTATANTATATATATNTATATNATATATAATTGAAACAAACT : 62
TrCHSa10 : GCNACAANCTNTAACTTNNCCTGTTATNTNNACNNATTGAGTNTNNAATTNACATACATA : 60
TrCHSa11 : AAAACAAC-CGCGCATATT-ATATATATATA-TA-NGTCTATA-ATTCAAAG-AAA--CT : 52
TrCHSa12 : -CAACAACCN-TAACTT--CCTGTTAT-TA-ACC-ATTGAGT-T-NAATT-ACATACATA : 50
TrCHSa13 : -CAACAACCTNTAACTTNNCCTGTTANNTNNACCNATTGAGTNTNNAATTNACATACATA : 59
TrCHSa14 : -GANAAAACAGTCCGC-ATATTATATATATATNTNTATAGTCTATAATTGAAACAAACT : 58
TrCHSa15 : --AACAACCNATAACTT--CCTGTTAT-TA-ACC-ATTGAGT-T-NAATT:ACATACATA : 50
TrCHSa16 : --AAAAAACAACCTACNNGCATATTATATATATATATANNGTCTATAATTGAAACAAACT : 58
TrCHSa17 : ---NNAACCTATAACTNNCCCTNTTATNTANACNCATTGAGTNTNAAATTNACATACATA : 57
TrCHSa18 : ----GGNTAACAACCNNANACTTNCCTCTTATNNCTTNNANATNNNTACATACATAGNCA : 56
TrCHSa19 : -----CAACAAAAACACNTCGCNATATNTTTATNATNTTNGTTTATAATTGAAACAAACT : 55
TrCHSa20 : --------AACAATNCGCNATATTNTATATATATATNTATANGTTTATAATTGAAACAAACT : 53
TrCHSa21 : ---------AAATAACCNNCCGCANTATNTTANNNNTATNNGTCATAATTGAAACAAACT : 52
TrCHSa22 : -----------AACNCNTCGCNNTATNNTNNNTNTNNNTNGTCTATAATTGAAACAAACT : 49
TrCHSa23 : -------------CCNATN-ACCTTCCTCTTATNNCTTACATATACTACATACATAC-CA : 45
TrCHSa24 : -------------ACGNNATNACNTACTCTTATNNCTTACATATACTACATAGCAGCACT : 47
TrCHSa25 : ------------ACNCNTCGCCTATNTATTTATATATNTAGTCTATAATTGAAACAAACT : 47
TrCHSa26 : --------------AC-TATNAC-TACTCTT-T-ACTTACATNTACT-CATAG-NCCACT : 40
TrCHSa27 : ----------------ACCTACCTTCCTCTTAT-NCTT--N-A-ATT-CATACATNG-CA : 37
TrCHSa28 : ------------------ACNACTTCCTCTTATCACTTNCANANATTACATACATAGNCA : 42
TrCHSa29 : --------------------------------------TNTNGTCNNATTG-AACAAACT : 21
TrCHSa30 : ----------------------------------------------------------GN :  2
TrCHSa31 : ----------------------------------------------------------GT :  2
TrCHSa32 : ------------------------------------------------------------ :  -
TrCHSa33 : ------------------------------------------------------------ :  -
TrCHSa34 : ------------------------------------------------------------ :  -
TrCHSa35 : ---------------------------------------------------------AAG :  3
TrCHSa36 : -----------------------------------------------------------G :  1
TrCHSa37 : ------------------------------------------------------------ :  -
TrCHSa38 : ------------------------------------------------------------ :  -
TrCHSa39 : ------------------------------------------------------------ :  -
```

FIGURE 15 (cont)

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```
                       *         200         *         220         *         240
TrCHSa1  : GCGGAACATACTAAATACAAGATGGTTAGTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :240
TrCHSa2  : G--ATATA----TATCAAC--ATGGTTAGTGTGTCTGAAATTCGCAAGGCTCAAAGGGCT :137
TrCHSa3  : GCTAAAGANNNNTATCAAGNNATGGTTAGTGTGTCTGAAATTCGCAAGGCTCAAAGGGCA :143
TrCHSa4  : GCTAAAGA----TATCAAG--ATGGTTAGTGTGTCTGAAATTCGCAAGGCTCAAAGGGCA :128
TrCHSa5  : TAAAAATCTTACTATTAAGATATGGTGAGTGTATCTGAAATTCGTAAGGCTCAAAGGGCA :129
TrCHSa6  : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :116
TrCHSa7  : ACTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :122
TrCHSa8  : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :116
TrCHSa9  : ACTAAAGATANTTATTAAGATATGGTGAGTGTAGCAGAAATTCGCAAGGCTCAGAGGGCT :122
TrCHSa10: GCGGAACATACTAAATACAACATGGTTAGTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :120
TrCHSa11: GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :111
TrCHSa12: GCGGAACATACTAAATACAACATGGTTAGTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :110
TrCHSa13: GCGGAACNTACTAAATACAACATGGTTAGTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :119
TrCHSa14: GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :117
TrCHSa15: GCGGAACATACTAAATACAACATGGTTAGTGTTTCTGAAATTCGCANGGCTCAAAGGGCT :110
TrCHSa16: ACTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :118
TrCHSa17: GCGGAACATACTAAATACAACATGGTTAGTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :117
TrCHSa18: GCNAAAAAAGATATCAACATATGGTTAGTGTTTCTGAAATTCGTAAGGCTCAAAGGGCA :116
TrCHSa19: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :115
TrCHSa20: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :113
TrCHSa21: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :112
TrCHSa22: NCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :109
TrCHSa23: G--CAGCAAAGATATCAACATATGGTTACTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :103
TrCHSa24: GCAAAATTCAAGTATCAACATATGGTTACTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT :107
TrCHSa25: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :107
TrCHSa26: GCAAG-TATNAGTAT-AACATATGGTTACTGTTTCTGAAATTCGCAAGGCTCAAAGGGCT : 98
TrCHSa27: GC-AAACAAAGATAT-AACATATGGTTAGTGTATCTGAAATTCGCAAGGCTCAAAGGGCA : 95
TrCHSa28: GCNAAACAAAGATATCAACATATGGTTAGTGTATCTGNNATTCGCAAGGCTCAAAGGGCA :102
TrCHSa29: GCTA---AGA-TTTTTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 77
TrCHSa30: GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 61
TrCHSa31: NCTAAA-NNN-TTNTTAAGNAATGGTGAGTGTAGCTG-AATTCGC-AGGCTCAGNAGGCT : 58
TrCHSa32: GATA-AGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 58
TrCHSa33: --TNAAGATANNTNNTNAGANNTGGTGAGTGTAGCAGAAATTCGCAAGGCTCAGAGGGCT : 58
TrCHSa34: GGNTCANA-----------------------------------------------GGGCT : 13
TrCHSa35: GCCCTCCA---------------------------------------------------- : 11
TrCHSa36: GCCCTCCA---------------------------------------------------- :  9
TrCHSa37: ---ATAAG---------------------------------------------------- :  5
TrCHSa38: ----ATCA---------------------------------------------------- :  4
TrCHSa39: ----GCTA---------------------------------------------------- :  4
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FIGURE 15 (cont)

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```
                      *        260         *        280         *        300
TrCHSa1  : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAATCGTGTTGACCAG :300
TrCHSa2  : GAAGGCCCTGCAACTATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTGATCAG :197
TrCHSa3  : GAAGGCCCTGCAACAATCTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTGATCAG :203
TrCHSa4  : GAAGGCCCTGCAACAATCTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTGATCAG :188
TrCHSa5  : GAAGGCCCTGCAACCATTTTAGCCATTGGTACTGCAAATCCAGCAAACCGTGTAGACCAG :189
TrCHSa6  : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :176
TrCHSa7  : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :182
TrCHSa8  : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :176
TrCHSa9  : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :182
TrCHSa10 : GAAGGCCCTGCAACTATTTTGGCCATTGGCACTGCAAATCCAGCAAACCGTGTTGATCAG :180
TrCHSa11 : GAAGGCCCTGCAACCATTTTGGCCATTGGTACTGCAAATCCACCAAACCGTGTTGAGCGG :171
TrCHSa12 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAATCGTGTTGACCAG :170
TrCHSa13 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAATCGTGTTGACCAG :179
TrCHSa14 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :177
TrCHSa15 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAATCGTGTTGACCAG :170
TrCHSa16 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :178
TrCHSa17 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAATCGTGTTGACCAG :177
TrCHSa18 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAACCGTGTTGATCAG :176
TrCHSa19 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :175
TrCHSa20 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :173
TrCHSa21 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGCGTTGAGCAG :172
TrCHSa22 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :169
TrCHSa23 : GAAGGCCCTGCAACCATTTTGGCCATTGGTACTGCAAATCCAGCAAACCGTGTTGATCAG :163
TrCHSa24 : GAAGGCCCTGCAACCATTTTGGCCATTGGTACTGCAAATCCAGCAAACCGTGTTGATCAG :167
TrCHSa25 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :167
TrCHSa26 : GAAGGCCCTGCAACCATTTTGGCCATTGGTACTGCAAATCCAGCAAACCGTGTTGATCAG :158
TrCHSa27 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAACCGTGTTGATCAA :155
TrCHSa28 : GAAGGCCCTGCAACTATTTTGGCCATTGGTACTGCAAATCCAGCAAACCGTGTTGATCAA :162
TrCHSa29 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :137
TrCHSa30 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :121
TrCHSa31 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :118
TrCHSa32 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :118
TrCHSa33 : GAAGGCCCTGCAACCATTTTGGCCATTGGCACTGCAAATCCACCAAACCGTGTTGAGCAG :118
TrCHSa34 : GAAGGCCCTGCAACC-TTTTGGCCGTTGGCACTGCAAATCC-GCAAACCGTGTTGAGCAG : 71
TrCHSa35 : ------------ANCNTTTTTGCCCTTGGTACTGCAAATCCNGCAAATCGTGTTGACCNG : 59
TrCHSa36 : ------------ACCNNTTTTGCCCTTGGTACTGCAAATCCNGCAAATCGTGTTGACCAG : 57
TrCHSa37 : ------------------------------------------------------------ :  -
TrCHSa38 : ------------------------------------------------------------ :  -
TrCHSa39 : ------------------------------------------------------------ :  -
```

FIGURE 15 (cont)

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```
                   *       320         *       340         *       360
TrCHSa1  : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :360
TrCHSa2  : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAAGTTGAGCTCAAA :257
TrCHSa3  : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAACATAAAGTTGAGCTCAAA :263
TrCHSa4  : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAACATAAAGTTGAGCTCAAA :248
TrCHSa5  : AGCACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :249
TrCHSa6  : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :236
TrCHSa7  : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :242
TrCHSa8  : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :236
TrCHSa9  : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :242
TrCHSa10 : AGCACATATCCTGATTTTTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :240
TrCHSa11 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :231
TrCHSa12 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :230
TrCHSa13 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :239
TrCHSa14 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :237
TrCHSa15 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :230
TrCHSa16 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :238
TrCHSa17 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :237
TrCHSa18 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAAGTTGAGCTCAAA :236
TrCHSa19 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :235
TrCHSa20 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :233
TrCHSa21 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :232
TrCHSa22 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :229
TrCHSa23 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAG :223
TrCHSa24 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAG :227
TrCHSa25 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :227
TrCHSa26 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAG :218
TrCHSa27 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA :215
TrCHSa28 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTCAAA :222
TrCHSa29 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :197
TrCHSa30 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :181
TrCHSa31 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :178
TrCHSa32 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :178
TrCHSa33 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :178
TrCHSa34 : AGCACATATCCTGATTTCTACTTCAAAATTACAAACAGTGAGCACAAGACTGAGCTCAAA :131
TrCHSa35 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGATTGAGCTTAAA :119
TrCHSa36 : AGTACATATCCTGATTTCTACTTCAAAATCACTAACAGTGAGCATAAGGTTGAGCTTAAA :117
TrCHSa37 : ------------------------------------------------GCTGAGCTTAAA :  17
TrCHSa38 : ------------------------------------------------------------ :   -
TrCHSa39 : ------------------------------------------------------------ :   -
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FIGURE 15 (cont)

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```
                   *       380         *       400         *       420
TrCHSa1  : GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :420
TrCHSa2  : GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :317
TrCHSa3  : GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :323
TrCHSa4  : GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :308
TrCHSa5  : GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :309
TrCHSa6  : GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :296
TrCHSa7  : GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :302
TrCHSa8  : GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :296
TrCHSa9  : GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :302
TrCHSa10: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :300
TrCHSa11: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :291
TrCHSa12: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :290
TrCHSa13: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :299
TrCHSa14: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :297
TrCHSa15: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :290
TrCHSa16: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :298
TrCHSa17: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :297
TrCHSa18: GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :296
TrCHSa19: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :295
TrCHSa20: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :293
TrCHSa21: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :292
TrCHSa22: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :289
TrCHSa23: GAGAAATTCCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTATCTAACA :283
TrCHSa24: GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :287
TrCHSa25: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :287
TrCHSa26: GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :278
TrCHSa27: GAGAAATTCCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCCAACA :275
TrCHSa28: GAGAAATTCCAGCGCNNGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :282
TrCHSa29: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :257
TrCHSa30: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :241
TrCHSa31: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :238
TrCHSa32: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :238
TrCHSa33: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :238
TrCHSa34: GAGAAGTTCCAACGCATGTGTGACAAATCCATGATCAAGAGCAGATACATGTATCTAACA :191
TrCHSa35: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :179
TrCHSa36: GAGAAATTTCAGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :177
TrCHSa37: GAGAAATTTNNGCGCATGTGTGATAAATCTATGATCAAGAGCAGATACATGTATCTAACA :  77
TrCHSa38: -------------------------------------AGAGCAGATACATGTATCTAACA :  27
TrCHSa39: ------------------------------------------------------------ :   -
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FIGURE 15 (cont)

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```
                     *       440        *       460        *       480
TrCHSa1  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :480
TrCHSa2  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :377
TrCHSa3  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAGCACATGGCACCTTCATTGGATGCT :383
TrCHSa4  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAGCACATGGCACCTTCATTGGATGCT :368
TrCHSa5  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :369
TrCHSa6  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :356
TrCHSa7  : GAAGAGATTTTGAAAGAAAATCCTAGNCTTTGTGAATACATGNCACCTTCATTGGATGCT :362
TrCHSa8  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :356
TrCHSa9  : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :362
TrCHSa10 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :360
TrCHSa11 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :351
TrCHSa12 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :350
TrCHSa13 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :359
TrCHSa14 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :357
TrCHSa15 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGNACCTTCATTGNATGNT :350
TrCHSa16 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :358
TrCHSa17 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :357
TrCHSa18 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :356
TrCHSa19 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :355
TrCHSa20 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :353
TrCHSa21 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :352
TrCHSa22 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :349
TrCHSa23 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :343
TrCHSa24 : GAAGAGATTTTGAAAGAAAATCCTAGTCTCTGTGACTACATGGCACCTTCATTGGATGCT :347
TrCHSa25 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :347
TrCHSa26 : GAAGAGATTTTGAAAGAAAATCCTAGTCTCTGTGACTACATGGCACCTTCATTGGATGCT :338
TrCHSa27 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :335
TrCHSa28 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :342
TrCHSa29 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :317
TrCHSa30 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :301
TrCHSa31 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :298
TrCHSa32 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :298
TrCHSa33 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :298
TrCHSa34 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :251
TrCHSa35 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :239
TrCHSa36 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :237
TrCHSa37 : GAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTGAATACATGGCACCTTCATTGGATGCT :137
TrCHSa38 : GAAGAGATTTTGAAAGAAAATCCTAGTCTCTGTGACTACATGGCACCTTCATTGGATGCT : 87
TrCHSa39 : ------------------------------------------------------------ :
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FIGURE 15 (cont)

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```
                   *       500         *       520         *       540
TrCHSa1  : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :540
TrCHSa2  : AGGCAAGATATGGTGGTGGTTGAGGTACCTAGACTTGGAAAGGAGGCTGCAGTGAAGGCT :437
TrCHSa3  : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :443
TrCHSa4  : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :428
TrCHSa5  : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTAGGAAAGGAGGCTGCAGTCAAGGCC :429
TrCHSa6  : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCC :416
TrCHSa7  : AGNCAAGACATGGTGNCGCCNNANNNNCCCACCCTCCCCNCGCCN--------------- :407
TrCHSa8  : AGGCAAGACATGGTGGTGGTTGAGGTACCTANACTTGGGAAGGAGGCTGCANNCAAGGCC :416
TrCHSa9  : AGACAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCT :422
TrCHSa10 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :420
TrCHSa11 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :411
TrCHSa12 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :410
TrCHSa13 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :419
TrCHSa14 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCC :417
TrCHSa15 : AGNCAAGACATGNTGNTGNCNGAGGNACCNAGACTTGCCN-------------------- :390
TrCHSa16 : AGACAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCT :418
TrCHSa17 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :417
TrCHSa18 : AGGCAAGATATGGTGGNTGTTGAGGTACCTANACTTGNAAAGGAGGCTGCNNTGAAGGCT :416
TrCHSa19 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :415
TrCHSa20 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCC :413
TrCHSa21 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCT :412
TrCHSa22 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAAGCTGCAGTCAAGGCC :409
TrCHSa23 : AGGCAAGATATGGTGGTTGTTGAGGTACCTAGACTGGGAAAGGAAGCTGCAGTGAAGGCT :403
TrCHSa24 : AGGCAAGACATGGTTGTGGTTGAGGTACCTAGACTTGGAAAGGAGGCTGCAGTCAAGGCC :407
TrCHSa25 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCC :407
TrCHSa26 : AGGCAAGACATGGTTGTGGTTGAGGTACCTAGACTTGGAAAGGAGGCTGCAGTCAAGGCC :398
TrCHSa27 : AGACAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGAAAGGAGGCTGCAGTGAAGGCC :395
TrCHSa28 : AGACAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGAAAGGAGGCTGCAGTGAAGGCC :402
TrCHSa29 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :377
TrCHSa30 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGNCNAGGCC :361
TrCHSa31 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCC :358
TrCHSa32 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :358
TrCHSa33 : AGACAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTCAAGGCT :358
TrCHSa34 : AGACAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCCGCAGTCAAGGCT :311
TrCHSa35 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :299
TrCHSa36 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :297
TrCHSa37 : AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCTGCAGTGAAAGCT :197
TrCHSa38 : AGGCAAGACATGGTTGTGGTTGAGGTACCTAGACTTGGAAAGGAGGCTGCAGTCAAGGCC :147
TrCHSa39 : ------------------------------------------------------------ :  -
```

FIGURE 15 (cont)

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```
                 *         560          *         580          *         600
TrCHSa1  : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :600
TrCHSa2  : ATTAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :497
TrCHSa3  : ATAAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :503
TrCHSa4  : ATAAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :488
TrCHSa5  : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :489
TrCHSa6  : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :476
TrCHSa7  : ------------------------------------------------------------ :  -
TrCHSa8  : ATTAAAGAATGGGGTCAACCAAAGTCANAGATNACTNACTTAATCTTTTGCACCACAAGN :476
TrCHSa9  : ATCAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :482
TrCHSa10 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :480
TrCHSa11 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :471
TrCHSa12 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :470
TrCHSa13 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :479
TrCHSa14 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :477
TrCHSa15 : ------------------------------------------------------------ :  -
TrCHSa16 : ATCAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :478
TrCHSa17 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :477
TrCHSa18 : ATTAAAGAATGGGGCCANCCN--------------------------------------- :437
TrCHSa19 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :475
TrCHSa20 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :473
TrCHSa21 : ATCAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :472
TrCHSa22 : ATTAAAGAATGGGGTCATCCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :469
TrCHSa23 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACTACAAGT :463
TrCHSa24 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :467
TrCHSa25 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :467
TrCHSa26 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :458
TrCHSa27 : ATTAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :455
TrCHSa28 : ATTAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :462
TrCHSa29 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :437
TrCHSa30 : ATTAAANAATGGGGNCNACCAAAGNCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :421
TrCHSa31 : ATTAAAGAATGGGGTNAACCAAAGTCAAAGATTACTNACTTAATCTTTTGCACCACAAGT :418
TrCHSa32 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :418
TrCHSa33 : ATCAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :418
TrCHSa34 : ATCAAAGAATGGGGTCAACCAAAATCTAAGATTACACATTTGATCTTTTGCACCACAAGT :371
TrCHSa35 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :359
TrCHSa36 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :357
TrCHSa37 : ATCAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :257
TrCHSa38 : ATTAAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCACCACAAGT :207
TrCHSa39 : ---NAAGAATGGGGACNACCNAAATCTAAGANTNCACATTTGATCTTTTGCACCACAAGT : 61
```

FIGURE 15 (cont)

```
                     *       620         *       640         *       660
TrCHSa1  : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :660
TrCHSa2  : GGTGTAGACATGCCTGGTGCTGATTACCAGCCCACAAAACTTTTAGGACTTCGTCCATAT :557
TrCHSa3  : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :563
TrCHSa4  : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :548
TrCHSa5  : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTGGGACTTCGTCCATAT :549
TrCHSa6  : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :536
TrCHSa7  : ------------------------------------------------------------ :   -
TrCHSa8  : GGNGCCN----------------------------------------------------- :483
TrCHSa9  : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGACTTCGTCCATAT :542
TrCHSa10 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :540
TrCHSa11 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :531
TrCHSa12 : GGTGTTGACATGCCTGGTGCCGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :530
TrCHSa13 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :539
TrCHSa14 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :537
TrCHSa15 : ------------------------------------------------------------ :   -
TrCHSa16 : GGTGTANACATGCCTGGTGCTGATTACCNACTNGCAAAACTNTTAGGACTTNGCCCATAT :538
TrCHSa17 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :537
TrCHSa18 : ------------------------------------------------------------ :   -
TrCHSa19 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :535
TrCHSa20 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :533
TrCHSa21 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTGGGACTTCGTCCATAT :532
TrCHSa22 : GGTGTTGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :529
TrCHSa23 : GGTGTAGACATGCCTGGTGCTGATTACCAGCTCACAAAACTCTTAGGTCTTCGCCCATAT :523
TrCHSa24 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTANGTCTTCGTCCATAC :527
TrCHSa25 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :527
TrCHSa26 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGTCCATAC :518
TrCHSa27 : GGTGTAGACATGCCTGGTGCTGATTACCAGCTCACAAAACTCTTAGGTCTTCGTCCATAT :515
TrCHSa28 : GGTGTANACATGCCTGGTGCTGATTACCAGCTCACAAAACTCTTAGGTCTTCGTCCATAT :522
TrCHSa29 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :497
TrCHSa30 : GGTGCTGACATGNCTGGTGCTGATTACCAACTCACAAAACTCTTAGGNCTTCCCCCATAT :481
TrCHSa31 : GGTGTTGACATGNCTGGTGCTGATTACCAACTCACAAAACTCTTAGGNNTTGGCNCATAT :478
TrCHSa32 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :478
TrCHSa33 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGACTTCGTCCATAT :478
TrCHSa34 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGACTTCGTCCATAT :431
TrCHSa35 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :419
TrCHSa36 : GGTGTTGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :417
TrCHSa37 : GGTGTAGACATGCCTGGAGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGCCCATAT :317
TrCHSa38 : GGTGTAGACATGCCTGGTGCTGATTACCAACTCACAAAACTCTTAGGTCTTCGTCCATAC :267
TrCHSa39 : GGTGTAGACATGCCTGGTGCTGATTACCAGCTCACAAAACTCTTAGGTCTTCGCCCATAT :121
```

FIGURE 15 (cont)

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```
                          *        680         *        700         *        720
TrCHSa1  : GTG--------------------------------------------------------- :663
TrCHSa2  : GTGAAGAGGTACATGATG------------------------------------------ :575
TrCHSa3  : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGG---------------- :607
TrCHSa4  : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCTTCGTT-- :606
TrCHSa5  : GTGAAGAGGTTCATGATGTACCAACAAGGTTGTTTTGCAGGAGGC--------------- :594
TrCHSa6  : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACGGTGCTTCGTTTG :596
TrCHSa7  : ------------------------------------------------------------ :  -
TrCHSa8  : ------------------------------------------------------------ :  -
TrCHSa9  : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGG---------------- :586
TrCHSa10 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCT-------------------------- :574
TrCHSa11 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACGGTGCTTCGTTTG :591
TrCHSa12 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAG-------------------- :570
TrCHSa13 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCTTCGTTT- :598
TrCHSa14 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACGGTGCTTCGTTTG :597
TrCHSa15 : ------------------------------------------------------------ :  -
TrCHSa16 : GTGANGAGGCGCCTGNTGNNCCN------------------------------------- :561
TrCHSa17 : GTGAAG------------------------------------------------------ :543
TrCHSa18 : ------------------------------------------------------------ :  -
TrCHSa19 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACGGTGCTTCGTTTG :595
TrCHSa20 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACG------------ :581
TrCHSa21 : GTGAAGAGATTCATGATGTACCAACAAGGCTGCTTTGCAGGTGGGACGGTTCTTCG---- :588
TrCHSa22 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACGGTGCTTCGTTTG :589
TrCHSa23 : GTGAAGAGGTATATGATGTAT--------------------------------------- :544
TrCHSa24 : GTGAAGAGGCACATGATGTACCAACAAG-------------------------------- :555
TrCHSa25 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAG----------------- :570
TrCHSa26 : GTGAAGAGGTACATGATGTACCAACAAG-------------------------------- :546
TrCHSa27 : GTGAAAAGGTATATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTGCTTCGTTTG :575
TrCHSa28 : GTGAAAAGGCATATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACCGTGCTTCNTTTG :582
TrCHSa29 : GTGAAAAGGTATATGATGTACCAA------------------------------------ :521
TrCHSa30 : GTNAAAAGGNATATGATGCCCNCAN----------------------------------- :506
TrCHSa31 : GTGAAAAGGTCTATGATGCACCAACN---------------------------------- :504
TrCHSa32 : GTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTGCAGGAGGCACGGTGCTTCGTTTG :538
TrCHSa33 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGCCGGTTCTTCGTTTG :538
TrCHSa34 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCTTCGTTTG :491
TrCHSa35 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCTTCGTTTG :479
TrCHSa36 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCTTCGTTTG :477
TrCHSa37 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTTCTTCGTTTG :377
TrCHSa38 : GTGAAGAGGTACATGATGTACCAACAAGGGTGCTTTGCAGGTGGGACGGTGCTTCGTTTG :327
TrCHSa39 : GTGAAGAGGTATATGATGTATCAACAAGGTTGCTTTGCAGGAGGCACGGTGCTTCGTTTG :181
```

FIGURE 15 (cont)

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```
                     *       740         *       760         *       780
TrCHSa1  : ------------------------------------------------------------ :   -
TrCHSa2  : ------------------------------------------------------------ :   -
TrCHSa3  : ------------------------------------------------------------ :   -
TrCHSa4  : ------------------------------------------------------------ :   -
TrCHSa5  : ------------------------------------------------------------ :   -
TrCHSa6  : GCAAAAGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGcTAGTTGTTTGTTCTGAAGTc : 656
TrCHSa7  : ------------------------------------------------------------ :   -
TrCHSa8  : ------------------------------------------------------------ :   -
TrCHSa9  : ------------------------------------------------------------ :   -
TrCHSa10 : ------------------------------------------------------------ :   -
TrCHSa11 : GCAAAAGATTTGG----------------------------------------------- : 604
TrCHSa12 : ------------------------------------------------------------ :   -
TrCHSa13 : ------------------------------------------------------------ :   -
TrCHSa14 : GCAAAAGATTTG------------------------------------------------ : 609
TrCHSa15 : ------------------------------------------------------------ :   -
TrCHSa16 : ------------------------------------------------------------ :   -
TrCHSa17 : ------------------------------------------------------------ :   -
TrCHSa18 : ------------------------------------------------------------ :   -
TrCHSa19 : GCAAAAGATTTG------------------------------------------------ : 607
TrCHSa20 : ------------------------------------------------------------ :   -
TrCHSa21 : ------------------------------------------------------------ :   -
TrCHSa22 : GCAAAAGATTTGGCCGAGAACAAC------------------------------------ : 613
TrCHSa23 : ------------------------------------------------------------ :   -
TrCHSa24 : ------------------------------------------------------------ :   -
TrCHSa25 : ------------------------------------------------------------ :   -
TrCHSa26 : ------------------------------------------------------------ :   -
TrCHSa27 : GCcAAcG----------------------------------------------------- : 582
TrCHSa28 : GCcAANGATTTGGCCcANAACAACAAANGNGCTCGNGNGTTGGNTGcTTGGTCTNAANTc : 642
TrCHSa29 : ------------------------------------------------------------ :   -
TrCHSa30 : ------------------------------------------------------------ :   -
TrCHSa31 : ------------------------------------------------------------ :   -
TrCHSa32 : GCAAAAGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTTCTGAAGTc : 598
TrCHSa33 : GCTAAAGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTTCTGAAGT- : 597
TrCHSa34 : GCTAAAGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTTCTGAAGTA : 551
TrCHSa35 : GCcAAcGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGcTCTGAAGTA : 539
TrCHSa36 : GCcAAcGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGcTCTGAAGTA : 537
TrCHSa37 : GCcAAcGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGcTCTGAAGTA : 437
TrCHSa38 : GCcAAcGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGTTGGTTGTTTGTTCTGAAGTc : 387
TrCHSa39 : GCTAAAGATTTGGCCGAGAACAACAAAGGTGCTCGTGTGcTAGTTGTTTGTTCTGAAGTA : 241
```

FIGURE 15 (cont)

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```
                       *        800         *        820         *        840
TrCHSa1  : ------------------------------------------------------------ :   -
TrCHSa2  : ------------------------------------------------------------ :   -
TrCHSa3  : ------------------------------------------------------------ :   -
TrCHSa4  : ------------------------------------------------------------ :   -
TrCHSa5  : ------------------------------------------------------------ :   -
TrCHSa6  : ACCGCAGTCACATTTCGCGGCCCCAGTGATACTCACTTGGACAGTCTTGNTG-------- : 708
TrCHSa7  : ------------------------------------------------------------ :   -
TrCHSa8  : ------------------------------------------------------------ :   -
TrCHSa9  : ------------------------------------------------------------ :   -
TrCHSa10 : ------------------------------------------------------------ :   -
TrCHSa11 : ------------------------------------------------------------ :   -
TrCHSa12 : ------------------------------------------------------------ :   -
TrCHSa13 : ------------------------------------------------------------ :   -
TrCHSa14 : ------------------------------------------------------------ :   -
TrCHSa15 : ------------------------------------------------------------ :   -
TrCHSa16 : ------------------------------------------------------------ :   -
TrCHSa17 : ------------------------------------------------------------ :   -
TrCHSa18 : ------------------------------------------------------------ :   -
TrCHSa19 : ------------------------------------------------------------ :   -
TrCHSa20 : ------------------------------------------------------------ :   -
TrCHSa21 : ------------------------------------------------------------ :   -
TrCHSa22 : ------------------------------------------------------------ :   -
TrCHSa23 : ------------------------------------------------------------ :   -
TrCHSa24 : ------------------------------------------------------------ :   -
TrCHSa25 : ------------------------------------------------------------ :   -
TrCHSa26 : ------------------------------------------------------------ :   -
TrCHSa27 : ------------------------------------------------------------ :   -
TrCHSa28 : ACCGCAN----------------------------------------------------- : 649
TrCHSa29 : ------------------------------------------------------------ :   -
TrCHSa30 : ------------------------------------------------------------ :   -
TrCHSa31 : ------------------------------------------------------------ :   -
TrCHSa32 : ACTGCAGTTACATTCCGTGGCCCCAGTGACACTCACTTGGACAGTCTTGTTGGACAAGCA : 658
TrCHSa33 : ------------------------------------------------------------ :   -
TrCHSa34 : ACTGCAGTCACATTCCGTGGCCCCAGTGACACTCACTTG--------------------- : 590
TrCHSa35 : ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCATTTGGACAGCCTTGTTGGACAAGCA : 599
TrCHSa36 : ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCATTTGGACAGCCTTGTTGGACAAGCA : 597
TrCHSa37 : ACCGCAGTCACATTCCGCGGCCCCAGTGACACTCATTTGGACAGTCTTGTTGGACAAGCA : 497
TrCHSa38 : ACCGCAGTCACATTCCGTGGCCCTAGTGACACTCATTTGGACAGTCTTGTTGGACAAGCA : 447
TrCHSa39 : ACAGCAGTCACATTCCGCGGTCCAAGTGACACTCACTTGGACAGTCTTGTTGGACAAGCA : 301
```

FIGURE 15 (cont)

```
                     *       860         *       880         *       900
TrCHSa1  : ------------------------------------------------------------ :   -
TrCHSa2  : ------------------------------------------------------------ :   -
TrCHSa3  : ------------------------------------------------------------ :   -
TrCHSa4  : ------------------------------------------------------------ :   -
TrCHSa5  : ------------------------------------------------------------ :   -
TrCHSa6  : ------------------------------------------------------------ :   -
TrCHSa7  : ------------------------------------------------------------ :   -
TrCHSa8  : ------------------------------------------------------------ :   -
TrCHSa9  : ------------------------------------------------------------ :   -
TrCHSa10 : ------------------------------------------------------------ :   -
TrCHSa11 : ------------------------------------------------------------ :   -
TrCHSa12 : ------------------------------------------------------------ :   -
TrCHSa13 : ------------------------------------------------------------ :   -
TrCHSa14 : ------------------------------------------------------------ :   -
TrCHSa15 : ------------------------------------------------------------ :   -
TrCHSa16 : ------------------------------------------------------------ :   -
TrCHSa17 : ------------------------------------------------------------ :   -
TrCHSa18 : ------------------------------------------------------------ :   -
TrCHSa19 : ------------------------------------------------------------ :   -
TrCHSa20 : ------------------------------------------------------------ :   -
TrCHSa21 : ------------------------------------------------------------ :   -
TrCHSa22 : ------------------------------------------------------------ :   -
TrCHSa23 : ------------------------------------------------------------ :   -
TrCHSa24 : ------------------------------------------------------------ :   -
TrCHSa25 : ------------------------------------------------------------ :   -
TrCHSa26 : ------------------------------------------------------------ :   -
TrCHSa27 : ------------------------------------------------------------ :   -
TrCHSa28 : ------------------------------------------------------------ :   -
TrCHSa29 : ------------------------------------------------------------ :   -
TrCHSa30 : ------------------------------------------------------------ :   -
TrCHSa31 : ------------------------------------------------------------ :   -
TrCHSa32 : TTCTTTGGAGATGGAGCAGCTGCACTTATCGTTGGTTCTGATCCAGTCCCAGAAATTGAG : 718
TrCHSa33 : ------------------------------------------------------------ :   -
TrCHSa34 : ------------------------------------------------------------ :   -
TrCHSa35 : CTATTTGGAGATGGAGCTG----------------------------------------- : 618
TrCHSa36 : CTATTTGGAGATGGAGCTGCTG-------------------------------------- : 619
TrCHSa37 : CTATTCGGAGATGGAGCTGCTGCACTCATTGTTGGCTCAGACCCAGTACCAGAAATTGAG : 557
TrCHSa38 : CTATTTGGAGATGGAGCTGCTGCTCTCATTGTTGGTTCTGATCCAGTACCAGAAATTGAG : 507
TrCHSa39 : CTATTCGGAGATGGAGCTGCTGCTCTCATTGTTGGCTCAGACCCTGTACCAGAAATCGAG : 361
```

FIGURE 15 (cont)

```
                       *       920         *       940         *       960
TrCHSa1  : ------------------------------------------------------------ :  -
TrCHSa2  : ------------------------------------------------------------ :  -
TrCHSa3  : ------------------------------------------------------------ :  -
TrCHSa4  : ------------------------------------------------------------ :  -
TrCHSa5  : ------------------------------------------------------------ :  -
TrCHSa6  : ------------------------------------------------------------ :  -
TrCHSa7  : ------------------------------------------------------------ :  -
TrCHSa8  : ------------------------------------------------------------ :  -
TrCHSa9  : ------------------------------------------------------------ :  -
TrCHSa10 : ------------------------------------------------------------ :  -
TrCHSa11 : ------------------------------------------------------------ :  -
TrCHSa12 : ------------------------------------------------------------ :  -
TrCHSa13 : ------------------------------------------------------------ :  -
TrCHSa14 : ------------------------------------------------------------ :  -
TrCHSa15 : ------------------------------------------------------------ :  -
TrCHSa16 : ------------------------------------------------------------ :  -
TrCHSa17 : ------------------------------------------------------------ :  -
TrCHSa18 : ------------------------------------------------------------ :  -
TrCHSa19 : ------------------------------------------------------------ :  -
TrCHSa20 : ------------------------------------------------------------ :  -
TrCHSa21 : ------------------------------------------------------------ :  -
TrCHSa22 : ------------------------------------------------------------ :  -
TrCHSa23 : ------------------------------------------------------------ :  -
TrCHSa24 : ------------------------------------------------------------ :  -
TrCHSa25 : ------------------------------------------------------------ :  -
TrCHSa26 : ------------------------------------------------------------ :  -
TrCHSa27 : ------------------------------------------------------------ :  -
TrCHSa28 : ------------------------------------------------------------ :  -
TrCHSa29 : ------------------------------------------------------------ :  -
TrCHSa30 : ------------------------------------------------------------ :  -
TrCHSa31 : ------------------------------------------------------------ :  -
TrCHSa32 : AAACCAATATTTGAGATGGTTTGGACTGCACAAACAATTGCTCCAGACAGTGAAGGTGCC : 778
TrCHSa33 : ------------------------------------------------------------ :  -
TrCHSa34 : ------------------------------------------------------------ :  -
TrCHSa35 : ------------------------------------------------------------ :  -
TrCHSa36 : ------------------------------------------------------------ :  -
TrCHSa37 : AN---------------------------------------------------------- : 559
TrCHSa38 : AAGCCAATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCAG-------------- : 553
TrCHSa39 : AAACCTATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCGGACAGTGAAGGTGCC : 421
```

FIGURE 15 (cont)

```
                    *       980         *        1000         *        1020
TrCHSa1  : ------------------------------------------------------------ :   -
TrCHSa2  : ------------------------------------------------------------ :   -
TrCHSa3  : ------------------------------------------------------------ :   -
TrCHSa4  : ------------------------------------------------------------ :   -
TrCHSa5  : ------------------------------------------------------------ :   -
TrCHSa6  : ------------------------------------------------------------ :   -
TrCHSa7  : ------------------------------------------------------------ :   -
TrCHSa8  : ------------------------------------------------------------ :   -
TrCHSa9  : ------------------------------------------------------------ :   -
TrCHSa10 : ------------------------------------------------------------ :   -
TrCHSa11 : ------------------------------------------------------------ :   -
TrCHSa12 : ------------------------------------------------------------ :   -
TrCHSa13 : ------------------------------------------------------------ :   -
TrCHSa14 : ------------------------------------------------------------ :   -
TrCHSa15 : ------------------------------------------------------------ :   -
TrCHSa16 : ------------------------------------------------------------ :   -
TrCHSa17 : ------------------------------------------------------------ :   -
TrCHSa18 : ------------------------------------------------------------ :   -
TrCHSa19 : ------------------------------------------------------------ :   -
TrCHSa20 : ------------------------------------------------------------ :   -
TrCHSa21 : ------------------------------------------------------------ :   -
TrCHSa22 : ------------------------------------------------------------ :   -
TrCHSa23 : ------------------------------------------------------------ :   -
TrCHSa24 : ------------------------------------------------------------ :   -
TrCHSa25 : ------------------------------------------------------------ :   -
TrCHSa26 : ------------------------------------------------------------ :   -
TrCHSa27 : ------------------------------------------------------------ :   -
TrCHSa28 : ------------------------------------------------------------ :   -
TrCHSa29 : ------------------------------------------------------------ :   -
TrCHSa30 : ------------------------------------------------------------ :   -
TrCHSa31 : ------------------------------------------------------------ :   -
TrCHSa32 : ATTG-------------------------------------------------------- : 782
TrCHSa33 : ------------------------------------------------------------ :   -
TrCHSa34 : ------------------------------------------------------------ :   -
TrCHSa35 : ------------------------------------------------------------ :   -
TrCHSa36 : ------------------------------------------------------------ :   -
TrCHSa37 : ------------------------------------------------------------ :   -
TrCHSa38 : ------------------------------------------------------------ :   -
TrCHSa39 : ATTGATGGTCACCTTCGTGAAGCTGGACTAACATTTCATCTTCTTAAAGATGTTCCTGGG : 481
```

FIGURE 15 (cont)

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```
                       *      1040         *      1060         *      1080
TrCHSa1  : ------------------------------------------------------------ :   -
TrCHSa2  : ------------------------------------------------------------ :   -
TrCHSa3  : ------------------------------------------------------------ :   -
TrCHSa4  : ------------------------------------------------------------ :   -
TrCHSa5  : ------------------------------------------------------------ :   -
TrCHSa6  : ------------------------------------------------------------ :   -
TrCHSa7  : ------------------------------------------------------------ :   -
TrCHSa8  : ------------------------------------------------------------ :   -
TrCHSa9  : ------------------------------------------------------------ :   -
TrCHSa10 : ------------------------------------------------------------ :   -
TrCHSa11 : ------------------------------------------------------------ :   -
TrCHSa12 : ------------------------------------------------------------ :   -
TrCHSa13 : ------------------------------------------------------------ :   -
TrCHSa14 : ------------------------------------------------------------ :   -
TrCHSa15 : ------------------------------------------------------------ :   -
TrCHSa16 : ------------------------------------------------------------ :   -
TrCHSa17 : ------------------------------------------------------------ :   -
TrCHSa18 : ------------------------------------------------------------ :   -
TrCHSa19 : ------------------------------------------------------------ :   -
TrCHSa20 : ------------------------------------------------------------ :   -
TrCHSa21 : ------------------------------------------------------------ :   -
TrCHSa22 : ------------------------------------------------------------ :   -
TrCHSa23 : ------------------------------------------------------------ :   -
TrCHSa24 : ------------------------------------------------------------ :   -
TrCHSa25 : ------------------------------------------------------------ :   -
TrCHSa26 : ------------------------------------------------------------ :   -
TrCHSa27 : ------------------------------------------------------------ :   -
TrCHSa28 : ------------------------------------------------------------ :   -
TrCHSa29 : ------------------------------------------------------------ :   -
TrCHSa30 : ------------------------------------------------------------ :   -
TrCHSa31 : ------------------------------------------------------------ :   -
TrCHSa32 : ------------------------------------------------------------ :   -
TrCHSa33 : ------------------------------------------------------------ :   -
TrCHSa34 : ------------------------------------------------------------ :   -
TrCHSa35 : ------------------------------------------------------------ :   -
TrCHSa36 : ------------------------------------------------------------ :   -
TrCHSa37 : ------------------------------------------------------------ :   -
TrCHSa38 : ------------------------------------------------------------ :   -
TrCHSa39 : ATTGTATCAAAGAACATTAATAAAGCATTGGTCGAGGCTTTCCAACCATTAGGAATTTCT : 541
```

FIGURE 15 (cont)

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```
                    *        1100         *        1120         *
TrCHSa1  : -------------------------------------------------- :   -
TrCHSa2  : -------------------------------------------------- :   -
TrCHSa3  : -------------------------------------------------- :   -
TrCHSa4  : -------------------------------------------------- :   -
TrCHSa5  : -------------------------------------------------- :   -
TrCHSa6  : -------------------------------------------------- :   -
TrCHSa7  : -------------------------------------------------- :   -
TrCHSa8  : -------------------------------------------------- :   -
TrCHSa9  : -------------------------------------------------- :   -
TrCHSa10 : -------------------------------------------------- :   -
TrCHSa11 : -------------------------------------------------- :   -
TrCHSa12 : -------------------------------------------------- :   -
TrCHSa13 : -------------------------------------------------- :   -
TrCHSa14 : -------------------------------------------------- :   -
TrCHSa15 : -------------------------------------------------- :   -
TrCHSa16 : -------------------------------------------------- :   -
TrCHSa17 : -------------------------------------------------- :   -
TrCHSa18 : -------------------------------------------------- :   -
TrCHSa19 : -------------------------------------------------- :   -
TrCHSa20 : -------------------------------------------------- :   -
TrCHSa21 : -------------------------------------------------- :   -
TrCHSa22 : -------------------------------------------------- :   -
TrCHSa23 : -------------------------------------------------- :   -
TrCHSa24 : -------------------------------------------------- :   -
TrCHSa25 : -------------------------------------------------- :   -
TrCHSa26 : -------------------------------------------------- :   -
TrCHSa27 : -------------------------------------------------- :   -
TrCHSa28 : -------------------------------------------------- :   -
TrCHSa29 : -------------------------------------------------- :   -
TrCHSa30 : -------------------------------------------------- :   -
TrCHSa31 : -------------------------------------------------- :   -
TrCHSa32 : -------------------------------------------------- :   -
TrCHSa33 : -------------------------------------------------- :   -
TrCHSa34 : -------------------------------------------------- :   -
TrCHSa35 : -------------------------------------------------- :   -
TrCHSa36 : -------------------------------------------------- :   -
TrCHSa37 : -------------------------------------------------- :   -
TrCHSa38 : -------------------------------------------------- :   -
TrCHSa39 : GATTACAACTCAATCTTTTGGATTGCACACCCGGGTGGACCTGCAATTCT : 591
```

FIGURE 15 (cont)

```
                     *        20         *        40         *        60
TrCHSb : TCTTCGNCNAGCTGGACNAACATTTNTGCTTCTTAAAGATGTTCCTGAGATTGTCTCAAA :  60

                     *        80         *       100         *       120
TrCHSb : GAACATTGATAAGGCATTGGTTGAGGCATTCCAACCATTAAACATCTCTGATTACAATTC : 120

                     *       140         *       160         *       180
TrCHSb : AATCTTTTGGATTGCTCATCCAGGTGGTCCTGCAATTCTAGACCAAGTTGAGATAAAGTT : 180

                     *       200         *       220         *       240
TrCHSb : GGGCTTAAAACCTGAAAAAATGAAGGCCACCAGAGATGTACTTAGTGAATATGGTAACAT : 240

                     *       260         *       280         *       300
TrCHSb : GTCAAGTGCATGTGTATTGTTCATCTTAGATGAGATGCAAAAGAAATCGGCTGAAAATGG : 300

                     *       320         *       340         *       360
TrCHSb : ACTGAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTTGGACCAGGACT : 360

                     *       380         *       400         *       420
TrCHSb : TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGCGAGACTTGATTGTT : 420

                     *       440         *       460         *       480
TrCHSb : TTGTATTGTATTGTATTGTATTGTATTACTTTTAATCTTGCTTGAATTTCCATTTAACAA : 480

                     *       500         *       520         *       540
TrCHSb : TAAATATGGAGTTCAATAAGTACCATCAGTGTTAAAATAATATATCGTTAATAGCTATTA : 540

                     *       560         *       580         *       600
TrCHSb : TTTTAGTGTCTGTTTCTTTTTACTAAACTATATTTTATTTTAGTATTTGCTATTGATTTG : 600

                     *       620         *
TrCHSb : AAATAAATATTGTCCTCTTAACTGAAAAAAAAAA : 634
```

FIGURE 16

```
                   *        20         *        40         *        60
TrCHSb : LRXAGXTFXLLKDVPEIVSKNIDKALVEAFQPLNISDYNSIFWIAHPGGPAILDQVEIKL :  60

                   *        80         *       100         *       120
TrCHSb : GLKPEKMKATRDVLSEYGNMSSACVLFILDEMQKKSAENGLKTTGEGLDWGVLFGFGPGL : 120

                   *
TrCHSb : TIETVVLHSVAI : 132
```

FIGURE 17

```
                   *        20         *        40         *        60
TrCHSb1 : TCTTCGNCNAGCTGGACNAACATTTNTGCTTCTTAAAGATGTTCCTGAGATTGTCTCAAA :  60
TrCHSb2 : ------------------------------------------------------------ :   -
TrCHSb3 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
TrCHSb1 : GAACATTGATAAGGCATTGGTTGAGGCATTCCAACCATTAAACATCTCTGATTACAATTC : 120
TrCHSb2 : ------------------------------------------------------------ :   -
TrCHSb3 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
TrCHSb1 : AATCTTTTGGATTGCTCATCCAGGTGGTCCTGCAATTCTAGACCAAGTTGAGATAAAGTT : 180
TrCHSb2 : ------------------------------------------------------------ :   -
TrCHSb3 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
TrCHSb1 : GGGCTTAAAACCTGAAAAAATGAAGGCCACCAGAGATGTACTTAGTGAATATGGTAACAT : 240
TrCHSb2 : ------------------------------------------------------------ :   -
TrCHSb3 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
TrCHSb1 : GTCAAGTGCATGTGTATTGTTCATCTTAGATGAGATGAGAAAGAAATCGGCTGAAAATGG : 300
TrCHSb2 : -------------------------------GAGATGCACAAGAAATCGGCTNAAAATGG :  29
TrCHSb3 : -------------------------------GAGATGCCAAAGAAATCGGCTCAAAATGG :  29

                   *       320         *       340         *       360
TrCHSb1 : ACTNAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTTGGCCCCGGACT : 360
TrCHSb2 : ACTGAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTTGGACCAGGACT :  89
TrCHSb3 : ACTGAAAACCACAGGAGAAGGACTTGACTGGGGTGTGTTGTTTGGATTTGGACCAGGACT :  89

                   *       380         *       400         *       420
TrCHSb1 : TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGAGAGACTTGATTTCT : 420
TrCHSb2 : TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGCGAGACTTGATTGTT : 149
TrCHSb3 : TACCATTGAAACTGTTGTTCTACATAGTGTGGCTATATGAGAATGCGAGACTTGATTGTT : 149

                   *       440         *       460         *       480
TrCHSb1 : T--T--T---T---ATTGNATTGTATTACTTTAAATCTTGCNTGAACTTCCATTTAANAA : 470
TrCHSb2 : TTGTATTGTATTGTATTGTATTGTATTACTTTTAATCTTGCTTGAATTTCCATTTAACAA : 209
TrCHSb3 : TTGTATTGTATTGTATTGTATTGTATTACTTTTAATCTTGCTTGAATTTCCATTTAACAA : 209

                   *       500         *       520         *       540
TrCHSb1 : TAAGTATGGNGNTCANTNGGN--------------------------------------- : 491
TrCHSb2 : TAAATATGGAGTTCAATAAGTACCATCAGTGTTAAAATAATATATCGTTAATAGCTATTA : 269
TrCHSb3 : TAAATATGGAGTTCAATAAGTACCATCAGTGTTAAAATAATATATCGTTAATAGCTATTA : 269

                   *       560         *       580         *       600
TrCHSb1 : ------------------------------------------------------------ :   -
TrCHSb2 : TTTTAGTGTCTGTTTCTTTTTACTAAACTATATTTTATTTTAGTATTTGCTATTGATTTG : 329
TrCHSb3 : TTTTAGTGTCTGTTTCTTTTTACTAAACTATATTTTATTTTAGTATTTGCTATTGATTTG : 329

                    *       620         *
TrCHSb1  : ---------------------------------- :   -
TrCHSb2  : AAATAAATATTGTCCTCTTAACTGAAAAAAAAAA : 363
TrCHSb3  : AAATAAATATTGTCCTCTTAACTGAAAAAAAAAA : 363
```

FIGURE 18

```
                    *        20         *        40         *        60
TrCHSc : GNTTCAATCTGTTGTGCATAAAATTNCTTTGCNATAGAAAACCATACACATTTGATCTTG :  60

                    *        80         *       100         *       120
TrCHSc : CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 120

                    *       140         *       160         *       180
TrCHSc : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 180

                    *       200         *       220         *       240
TrCHSc : TATTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 240

                    *       260         *       280         *       300
TrCHSc : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 300

                    *       320         *       340         *       360
TrCHSc : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 360

                    *       380         *       400         *       420
TrCHSc : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 420

                    *       440         *       460         *       480
TrCHSc : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 480

                    *       500         *       520         *       540
TrCHSc : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 540

                    *       560         *       580         *       600
TrCHSc : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA : 600

                    *       620         *       640         *       660
TrCHSc : GACATAGCTGAGAACAACCCTGGAAGTAGAGTTTTGCTTGCTACTTCTGAAACTACAATT : 660

                    *       680         *       700         *       720
TrCHSc : ATTGGATTCAAGCCACCAAGTGTTGATAGACCTTATGATCTTGTTGGTGTGGCACTCTTT : 720

                    *       740         *       760         *       780
TrCHSc : GGAGATGGTGCTGGTGCTATGATAATTGGCTCAGACCCAATACTTGAAACTGAGACTCCA : 780

                    *       800         *       820         *       840
TrCHSc : TTGTTTGAGCTTCATACTTCAGCTCAGGAGTTTATACCAGACACAGAGAAGAAAATAGAT : 840

                    *       860         *       880         *
TrCHSc : GGGCGGCTGACGGAGGAGGGCATAAGTTTCACGCTAGCGAGGGAACTGCCGCAGATA : 897
```

FIGURE 19

```
                        *        20         *        40         *        60
TrCHSc : MGDEGIVRGVTKQTTPGKATILALGKAFPHQLVMQEYLVDGYFRDTNCDNPELKQKLARL :  60

                        *        80         *       100         *       120
TrCHSc : CKTTTVKTRYVVMNEEILKKYPELVVEGASTVKQRLEICNEAVTQMAIEASQVCLKNWGR : 120

                        *       140         *       160         *       180
TrCHSc : SLSDITHVVYVSSSEARLPGGDLYLSKGLGLNPKIQRTMLYFSGCSGGVAGLRVAKDIAE : 180

                        *       200         *       220         *       240
TrCHSc : NNPGSRVLLATSETTIIGFKPPSVDRPYDLVGVALFGDGAGAMIIGSDPILETETPLFEL : 240

                        *       260         *
TrCHSc : HTSAQEFIPDTEKKIDGRLTEEGISFTLARELPQI : 275
```

FIGURE 20

```
                   *        20         *        40         *        60
TrCHSc1 : GNTTCAATCTGTTGTGCATAAAATTNCTTTGCNATAGAAAACNCTACACATTTGATCTTG :  60
TrCHSc2 : ---TCAATCTGTTGNGCATTTTNTTNCTTTGCNATAGAAAACCATACACATTTGATCTTG :  57
TrCHSc3 : -------TCTGTTGTGNNTAACATTNCTTTCCNTTAGAAAACTATACACATTTGATCTTG :  53
TrCHSc4 : -------TCTGTTGTGCNTNAAATTACTTTGNNNTAGAAAACNCTACACATTTGATCTTG :  53
TrCHSc5 : --------------------TTAACATTTTTTTATTGTAGAAAATATACATTTGATCTAG :  40
TrCHSc6 : ------------------------------GCANTAGAAAACCCTACACATTTGATCTTG :  30
TrCHSc7 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
TrCHSc1 : CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 120
TrCHSc2 : CTTAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 117
TrCHSc3 : CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 113
TrCHSc4 : CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT : 113
TrCHSc5 : CAAAGAAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAGGCAGCCAACCCCT : 100
TrCHSc6 : CAAAGAAGAAATATGGGAGACGAANGTATAGTGAGAGGTGTCACAAAGCAGACAACCCCT :  90
TrCHSc7 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
TrCHSc1 : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 180
TrCHSc2 : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 177
TrCHSc3 : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 173
TrCHSc4 : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 173
TrCHSc5 : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 160
TrCHSc6 : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGATGCAAGAG : 150
TrCHSc7 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
TrCHSc1 : TGTTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 240
TrCHSc2 : TGTTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 237
TrCHSc3 : TATTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 233
TrCHSc4 : TGTTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 233
TrCHSc5 : TATTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTAAGCTTAAGCAGAAA : 220
TrCHSc6 : TATTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGACCTTAAGCAGAAA : 210
TrCHSc7 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
TrCHSc1 : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 300
TrCHSc2 : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 297
TrCHSc3 : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 293
TrCHSc4 : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 293
TrCHSc5 : CTTGCTAGACTTTGCAAGACAACCACAGTCAAAACAAGGTATGTTGTTATGAATGAAGAG : 280
TrCHSc6 : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 270
TrCHSc7 : ------------------------------------------------------------ :   -

                   *       320         *       340         *       360
TrCHSc1 : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 360
TrCHSc2 : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 357
TrCHSc3 : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 353
TrCHSc4 : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 353
TrCHSc5 : ATACTAAAGAAATATCCAGAACTTAGTATCGGAGGCACCTCGACGGTAAAACAACATTTA : 340
TrCHSc6 : ATACTAAAGAAATATCCAGAACTTGTTGTCGAAGGCGCCTCAACTGTAAAACAACGTTTA : 330
TrCHSc7 : -------------NTCCNGAACTTACTGTGGAAGGCGCCTCGACTGTAAAACNACGTTTA :  47
```

FIGURE 21

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```
                   *       380         *       400         *       420
TrCHSc1 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 420
TrCHSc2 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 417
TrCHSc3 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 413
TrCHSc4 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 413
TrCHSc5 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 400
TrCHSc6 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 390
TrCHSc7 : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 107

                   *       440         *       460         *       480
TrCHSc1 : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 480
TrCHSc2 : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 477
TrCHSc3 : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 473
TrCHSc4 : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 473
TrCHSc5 : AATTGGGGTAGACCCATATCAGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 460
TrCHSc6 : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 450
TrCHSc7 : AATTGGGGTAGACCCTTATCAGACATAACTCATGTGGTTTATGTTTCGTCTAGTGAAGCT : 167

                   *       500         *       520         *       540
TrCHSc1 : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 540
TrCHSc2 : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 537
TrCHSc3 : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 533
TrCHSc4 : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 533
TrCHSc5 : AGATTACCTGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 520
TrCHSc6 : AGATTACCCGGTGGTGACCTATACTTGTCAAAAGGACTAGGACTAAACCCTAAAATTCAA : 510
TrCHSc7 : AGATTACCCGGTGGTGACCTATATTTGTCAAAAGGACTAGGACTAAATCCTAAAATTCAA : 227

                   *       560         *       580         *       600
TrCHSc1 : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCG----------------------- : 577
TrCHSc2 : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA : 597
TrCHSc3 : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTT------------ : 581
TrCHSc4 : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTG----- : 588
TrCHSc5 : AGAACCATGCTCTATTTCTCCGGATGCTCGGGAGGCGTAGCCG----------------- : 563
TrCHSc6 : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA : 570
TrCHSc7 : AGAACCATGCTCTATTTCTCTGGATGCTCAGGAGGCGTAGCCGGCCTTCGCGTTGCGAAA : 287

                   *       620         *       640         *       660
TrCHSc1 : ------------------------------------------------------------ :   -
TrCHSc2 : GA---------------------------------------------------------- : 599
TrCHSc3 : ------------------------------------------------------------ :   -
TrCHSc4 : ------------------------------------------------------------ :   -
TrCHSc5 : ------------------------------------------------------------ :   -
TrCHSc6 : GACATAGCTGAGAACAACCCTGGAAGTAGAGTT--------------------------- : 603
TrCHSc7 : GACATAGCTGAGAACAACCCTGGAAGTAGAGTTTTGCTTGCTACTTCTGAAACTACAATT : 347

                   *       680         *       700         *       720
TrCHSc1 : ------------------------------------------------------------ :   -
TrCHSc2 : ------------------------------------------------------------ :   -
TrCHSc3 : ------------------------------------------------------------ :   -
TrCHSc4 : ------------------------------------------------------------ :   -
TrCHSc5 : ------------------------------------------------------------ :   -
TrCHSc6 : ------------------------------------------------------------ :   -
TrCHSc7 : ATTGGATTCAAGCCACCAAGTGTTGATAGACCTTATGATCTTGTTGGTGTGGCACTCTTT : 407
```

FIGURE 21 (cont)

```
                   *       740         *       760         *       780
TrCHSc1 : ------------------------------------------------------------ :   -
TrCHSc2 : ------------------------------------------------------------ :   -
TrCHSc3 : ------------------------------------------------------------ :   -
TrCHSc4 : ------------------------------------------------------------ :   -
TrCHSc5 : ------------------------------------------------------------ :   -
TrCHSc6 : ------------------------------------------------------------ :   -
TrCHSc7 : GGAGATGGTGCTGGTGCTATGATAATTGGCTCAGACCCAATACTTGAAACTGAGACTCCA : 467

                   *       800         *       820         *       840
TrCHSc1 : ------------------------------------------------------------ :   -
TrCHSc2 : ------------------------------------------------------------ :   -
TrCHSc3 : ------------------------------------------------------------ :   -
TrCHSc4 : ------------------------------------------------------------ :   -
TrCHSc5 : ------------------------------------------------------------ :   -
TrCHSc6 : ------------------------------------------------------------ :   -
TrCHSc7 : TTGTTTGAGCTTCATACTTCAGCTCAGGAGTTTATACCAGACACAGAGAAGAAAATAGAT : 527

                   *       860         *       880         *
TrCHSc1 : --------------------------------------------------------- :   -
TrCHSc2 : --------------------------------------------------------- :   -
TrCHSc3 : --------------------------------------------------------- :   -
TrCHSc4 : --------------------------------------------------------- :   -
TrCHSc5 : --------------------------------------------------------- :   -
TrCHSc6 : --------------------------------------------------------- :   -
TrCHSc7 : GGGCGGCTGACGGAGGAGGGCATAAGTTTCACGCTAGCGAGGGAACTGCCGCAGATA : 584
```

FIGURE 21 (cont)

```
                          *        20         *        40         *        60
TrCHSd : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCNTTACCAAAAAACG :  60

                          *        80         *       100         *       120
TrCHSd : TTGCTAAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT : 120

                          *       140         *       160         *       180
TrCHSd : CTTCCTCCCTGCTAACTTTATACTTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG : 180

                          *       200         *       220         *       240
TrCHSd : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240

                          *       260         *       280         *       300
TrCHSd : GTGTTGATCAGAGTACATACCCCGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA : 300

                          *       320         *       340         *       360
TrCHSd : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA : 360

                          *       380         *       400         *       420
TrCHSd : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT : 420

                          *       440         *       460         *       480
TrCHSd : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG : 480

                          *       500         *       520         *       540
TrCHSd : CAACAAAGGCAATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 540

                          *       560         *       580         *       600
TrCHSd : GCACCACAAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC : 600

                          *       620         *       640         *       660
TrCHSd : TTCGTCCGCATGTGAAGCGTTACATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG : 660

                          *       680         *       700         *       720
TrCHSd : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTATTGGTGGTTT : 720

                          *
TrCHSd : GTTCAGAGATAACTG : 735
```

FIGURE 22

```
                     *        20         *        40         *        60
TrCHSd : MVKVNEIRQAQRAEGPATVLAIGTATPPNCVDQSTYPDYYFRITNSEHKTELKEKFQRMC :  60

                     *        80         *       100         *       120
TrCHSd : DKSMIKKRYMHLTEEILKENPSLCEYMAPSLDARQDMVVVEVPRLGKEAATKAIKEWGQP : 120

                     *       140         *       160         *       180
TrCHSd : KSKITHLIFCTTSGVDMPGADYQLTKLLGLRPHVKRYMMYQQGCFAGGTVLRLAKDLAEN : 180

                     *
TrCHSd : NKGARVLVVCSEIT : 194
```

FIGURE 23

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```
                     *        20         *        40         *        60
TrCHSd1  : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCNTTACCAAAAAACG :  60
TrCHSd2  : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCTTTACCAAAAAACG :  60
TrCHSd3  : GTAGCAACACACACTTTGATTTCTTTTTGAGTCCTTGCTACGTGGCTTTACCAAAAAACG :  60
TrCHSd4  : ----------NNNCACNCACACTTTTTTGNATCCCTGCTACGTGGCNTTACCAAAAAACG :  50
TrCHSd5  : ------------------------------------------------------------ :   -
TrCHSd6  : ------------------------------------------------------------ :   -
TrCHSd7  : ------------------------------------------------------------ :   -
TrCHSd8  : ------------------------------------------------------------ :   -
TrCHSd9  : ------------------------------------------------------------ :   -
TrCHSd10 : ------------------------------------------------------------ :   -
TrCHSd11 : ------------------------------------------------------------ :   -

                     *        80         *       100         *       120
TrCHSd1  : TTGCTGAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTTACCATCTTTT : 120
TrCHSd2  : TTGCTAAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT : 120
TrCHSd3  : TTGCTAAGTNATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT : 120
TrCHSd4  : TTGCTAAGTCNTCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTT : 110
TrCHSd5  : --------------------------------------------------TTNATCGCCT :  10
TrCHSd6  : --------------------------------------------------TTNATNCCNT :  10
TrCHSd7  : ------------------------------------------------------TCCNAT :   6
TrCHSd8  : ------------------------------------------------------------ :   -
TrCHSd9  : ------------------------------------------------------------ :   -
TrCHSd10 : ------------------------------------------------------------ :   -
TrCHSd11 : ------------------------------------------------------------ :   -

                     *       140         *       160         *       180
TrCHSd1  : CTTCCTCCCTGCTAACTTTACAATCAGAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 180
TrCHSd2  : CTTCCTCCCTGCTAACTTTACACTCAGAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 180
TrCHSd3  : CTTCCTCCCTGCTAACTTTACACTCAGAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 180
TrCHSd4  : CTTCCTCCCTGCTAACTTTANACTCAGAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 170
TrCHSd5  : AATNTACTTTTCTTCTTCTTACTTANAGAATTATGGTTACAGTTAATGAGATCCGCCAGG :  70
TrCHSd6  : AATNTACTTTTCTTCTTCTTACTTANAGAATTATGGTTACAGTTAATGAGATCCGCCAGG :  70
TrCHSd7  : AATNTACTTTTCTTCTTCTTACTTNNAGAATTATGGTTACAGTTAATGAGATCCGCCAGG :  66
TrCHSd8  : -------GCNNTTAACTTTANAATNNGANAAGATGGTGAAAGTTAATGAGATCCGCCAGG :  53
TrCHSd9  : ------------TNNNTTTANAATNNGAGAAGATGGTGAAAGTNAATGAGATCCGCCAGG :  48
TrCHSd10 : ---------------TTCTTNATTGNAGAATTATGGTTACAGTTAATGAGATCCGCCNGG :  45
TrCHSd11 : ------------------------------------------------------------ :   -

                     *       200         *       220         *       240
TrCHSd1  : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240
TrCHSd2  : CACAGAGAGCTGAAGGCCCTGCCACCGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240
TrCHSd3  : CACAGAGAGCTGAAGGCCCTGCCACCGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240
TrCHSd4  : CACAGAGAGCTGAAGGCCCTGCCACCGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 230
TrCHSd5  : CACAGAGAGCTGAAGGCCCTGCAACTGTGTTTGCAATCGGCACTGCAACTCCTAAAAACT : 130
TrCHSd6  : CACAGAGAGCTGAAGGCCCTGCAACTGTGTTTGCAATCGGCACTGCAACTCCTAAAAACT : 130
TrCHSd7  : CACAGAGAGCTGAAGGCCCTGCAACTGTGTTTGCAATCGGCACTGCAACTCCTAAAAACT : 126
TrCHSd8  : CACAGANAGCTGAAGGCCCTGCCACTGTGTTGGNANTNGGCACTGCAACTCCTCCAAACT : 113
TrCHSd9  : CACAGAGAGCTGAAGGCCCTGCCACTGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 108
TrCHSd10 : CACAAAGAGCCGAAGGCCCTGCNCCTGTGTTTGCAATCGGCACTGCAACTCCTAAAAACT : 105
TrCHSd11 : -----------------------------------------------------TAAAACT :   7
```

FIGURE 24

```
                          *        260         *        280         *        300
TrCHSd1  : GTGTCGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :300
TrCHSd2  : GTGTCGATCAGAGTACATACCCAGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :300
TrCHSd3  : GTGTCGATCAGAGTACATACCCAGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :300
TrCHSd4  : GTGTTGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :290
TrCHSd5  : GTGTTGATCAGAGTACTTACCCCGACTACTATTTCCGAATCACAAACAGCGAACACAAGA :190
TrCHSd6  : GTGTTGATCAGAGTACTTACCCCGACTACTATTTCCGAATCACAAACAGCGAACACAAGA :190
TrCHSd7  : GTGTTGATCAGAGTACTTACCCCGACTACTATTTCCGAATCACAAACAGCGAACACAAGA :186
TrCHSd8  : GTGTCGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :173
TrCHSd9  : GTGTCGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA :168
TrCHSd10 : GTGTTGATCAGAGTACTTACCCCGACTACTATTTCCGAATCACAAACAGCGAACACAAGA :165
TrCHSd11 : GTGTTGATCNGAGTACTTACCCCGACTNCTATTTCCGAATNNCAAACAGCGAACACAAGA : 67

                          *        320         *        340         *        360
TrCHSd1  : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :360
TrCHSd2  : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :360
TrCHSd3  : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :360
TrCHSd4  : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :350
TrCHSd5  : CTGAACTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :250
TrCHSd6  : CTGAACTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :250
TrCHSd7  : CTGAACTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :246
TrCHSd8  : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :233
TrCHSd9  : CAGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :228
TrCHSd10 : CTGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :225
TrCHSd11 : CTGAGCTCAAAGAAAAATTCCAGCGCATGTGTGACAAATCTATGATTAAGAAGAGATACA :127

                          *        380         *        400         *        420
TrCHSd1  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :420
TrCHSd2  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :420
TrCHSd3  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :420
TrCHSd4  : TGCATTTAACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :410
TrCHSd5  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATTCAAGTTTATGTGAGTACATGGCACCTT :310
TrCHSd6  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATTCAAGTTTATGTGAGTACATGGCACCTT :310
TrCHSd7  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATTCAAGTTTATGTGAGTACATGGCACCTT :306
TrCHSd8  : TGCATTTGACAGANGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :293
TrCHSd9  : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :288
TrCHSd10 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT :285
TrCHSd11 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGNTTATGTGAGTACATGGCACCTT :187

                          *        440         *        460         *        480
TrCHSd1  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :480
TrCHSd2  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCTG :480
TrCHSd3  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCTG :480
TrCHSd4  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCNAGGCTAGGAAAAGAGGCAG :470
TrCHSd5  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCTG :370
TrCHSd6  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCTG :370
TrCHSd7  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCTG :366
TrCHSd8  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :353
TrCHSd9  : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :348
TrCHSd10 : CATTGGATGCAAGACAAGACATGGTGGTAGTGGAAGTACCAAGGCTAGGAAAAGAGGCAG :345
TrCHSd11 : NATTGGATGCAAGACAAGACATGGNGGCCGCCCACCNNCCNTCCNCCNCACCNCAACCCN :247
```

FIGURE 24 (cont)

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```
                     *       500         *       520         *       540
TrCHSd1  : CAACAAAGGCAATTAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT :540
TrCHSd2  : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT :540
TrCHSd3  : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT :540
TrCHSd4  : TAACAAAGGCAATTAGGGAATGGGGTCAACCTAAGTNCAAGATTACCCACCTCATCTTTT :530
TrCHSd5  : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT :430
TrCHSd6  : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT :430
TrCHSd7  : CAACAAAGGCTATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACTCACCTCATCTTTT :426
TrCHSd8  : CAACAAAGGCAATTAAGGAATGGGGCCAACCTAAGTCCAAGATTACCCACCTCATCTTTT :413
TrCHSd9  : CAACAAAGGCAATTAAGGAATGGGGCCAACCTAAGTCCAAGATTACCCACCTCATCTTTT :408
TrCHSd10 : CAACAAAGGCAATTAAAGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT :405
TrCHSd11 : CCN--------------------------------------------------------- :250

                     *       560         *       580         *       600
TrCHSd1  : GCACCACGAGTGGTGTCGACATGCCCGGTGCCGC-------------------------- :574
TrCHSd2  : GCACCACAAGTGGTGTGGACATGCCTGGCGCCGACTATCAGCTTACAAAGCTTTTAG--- :597
TrCHSd3  : GCACCACAAGTGGTGTGGACATGCCTGGCGCCGACTATCAGCTTACAAAGCTTTTAGGCC :600
TrCHSd4  : GCACCACGAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTCACAAAGCTCTT----- :585
TrCHSd5  : GCACCACAAGTGGTGTGGACATGCCTGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC :490
TrCHSd6  : GCACCACAAGTGGTGTGGACATGCCTGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC :490
TrCHSd7  : GCACCACAAGTGGTGTGGACATGCCTGGTGCCGACTATCAGCTTACAAAGCTTTTAGGCC :486
TrCHSd8  : GCACCACGAGTGGTGTCGACATGCCCGGTGCCGACTATCAGCTCACAAAGCTCTTAGGCC :473
TrCHSd9  : GCACCACGAGTGGTGTCGACATGCCCGGTGCCGACTATCAGCTCACAAAGCTCTTAGGCC :468
TrCHSd10 : GCACCACGAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTCACAAAGCTCTTAGGCC :465
TrCHSd11 : ------------------------------------------------------------ :  -

                     *       620         *       640         *       660
TrCHSd1  : ------------------------------------------------------------ :  -
TrCHSd2  : ------------------------------------------------------------ :  -
TrCHSd3  : TTCGTCCGCATGTGAN-------------------------------------------- :616
TrCHSd4  : ------------------------------------------------------------ :  -
TrCHSd5  : TTCGTCCGCATGTGAAGCGTTAGATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG :550
TrCHSd6  : TTCGTCCGCATGTGAAGCGTTAGATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG :550
TrCHSd7  : TTCGTCCGCATGTGAAGCGTTATATGATGTACCAACAAGGTTGTTTTGCTGGTGGCACGG :546
TrCHSd8  : TGCGTCCATATGTGAAGCGTTACATGATGTATCAACAAGGTTGTTTTGCTGGTGGCACGG :533
TrCHSd9  : TGCGTCCATATGTGAAGCGTTACATGATGTATCAACAAGGTTGTTTTGCTGGTGGCACGG :528
TrCHSd10 : TGCGTCCATATGTGAAGCGTTACATGATGTATCAACAAGGTTGTTTTGCTGGTGGCACGG :525
TrCHSd11 : ------------------------------------------------------------ :  -

                     *       680         *       700         *       720
TrCHSd1  : ------------------------------------------------------------ :  -
TrCHSd2  : ------------------------------------------------------------ :  -
TrCHSd3  : ------------------------------------------------------------ :  -
TrCHSd4  : ------------------------------------------------------------ :  -
TrCHSd5  : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCG-------------- :596
TrCHSd6  : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTATTGGTGGTTT :610
TrCHSd7  : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTATTGGTGGTTT :606
TrCHSd8  : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAN---------------------- :571
TrCHSd9  : TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAANGTGCCCGTGTGTTGGTGGGTT :588
TrCHSd10 : TACTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAAGGTGCCCGTGTGTTGGTGGTTT :585
TrCHSd11 : ------------------------------------------------------------ :  -
```

FIGURE 24 (cont)

```
                        *
TrCHSd1   : --------------- :    -
TrCHSd2   : --------------- :    -
TrCHSd3   : --------------- :    -
TrCHSd4   : --------------- :    -
TrCHSd5   : --------------- :    -
TrCHSd6   : GTTCAGAG------- :  618
TrCHSd7   : GTT------------ :  609
TrCHSd8   : --------------- :    -
TrCHSd9   : GTTCANAGATAACTG :  603
TrCHSd10  : GTT------------ :  588
TrCHSd11  : --------------- :    -
```

FIGURE 24 (cont)

```
                    *        20         *        40         *        60
TrCHSe : GNAGCAACACACACTTTGATTTCTTTTTGAATCCCTGCTACGTGGCNCACCAAAAAACGT :  60

                    *        80         *       100         *       120
TrCHSe : TGCTAAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATCTTTTC : 120

                    *       140         *       160         *       180
TrCHSe : TTCCTCCCTGCTAACTTTAGACTCAGTAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 180

                    *       200         *       220         *       240
TrCHSe : CACAGAGAGCTGAAGGCCCTGCCACCGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 240

                    *       260         *       280         *       300
TrCHSe : GTGTTGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA : 300

                    *       320         *       340         *       360
TrCHSe : CAGAGCTCAAAGAAAAATTCCAGCGCACGTGTAAGATATTTATCTTATACTCCATGCATG : 360

                    *       380         *       400         *       420
TrCHSe : TCTTTTTCTGCTGACTGCCGTGTTTATATATTGTTTTGTTTTGTTCCTTAAATTTGTTAT : 420

                    *       440         *       460         *       480
TrCHSe : GTCACTCTCACATGTACAAAACACTTAAGACTAAACTGCATATCATTTTTTTCAGGGACA : 480

                    *       500         *       520         *       540
TrCHSe : AATCTATGATTAAGAAGAGATACATGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAA : 540

                    *       560         *       580
TrCHSe : GTTTATGTGAGNACATGGCACCTTCTTGGGATGCAAGACAAGT : 583
```

FIGURE 25

```
                    *         20          *         40          *         60
TrCHSe : MVNVNEIRQAQRAEGPATVLAIGTATPPNCVDQSTYPDYYFRITNSEHKTELKEKFQRTR : 60

                    *         80          *
TrCHSe : DKSMIKKRYMHLTEEILKENPSLCEXMAPSWDARQ : 95
```

FIGURE 26

```
                  *        20         *        40         *        60
TrCHSe1 : GNAGCAACACACACTTTGATTTCTTTTTGAATCCCTGCTACGTGGCTTACCAAAAAACGT :  60
TrCHSe2 : ------------------------------GTCCCTGCTGCGTGGCNCACC-AAAAACGT :  29

                  *        80         *       100         *       120
TrCHSe1 : TGCTAAGTCATCAACCATTCCAATTCCTTAATATAACCTATCAGTACTCACCATTTTTTC : 120
TrCHSe2 : TGCTNAGT-NTGAACC-TTCC-ATTCCTTAATATAACCTATCAGTACTCACCATCTTTTC :  86

                  *       140         *       160         *       180
TrCHSe1 : TTCCTCCCTGCTAACTTTAGACTCAG-AGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 179
TrCHSe2 : TTCCTCCCTGCTAACTTTAGACTCAGTAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 146

                  *       200         *       220         *       240
TrCHSe1 : CACAGAGAGCTGAAGGCCCTGCCACCGTGTTGGCAATCGGCACTGCAACTCCTCCAAACT : 239
TrCHSe2 : CACAGAGAGCTGAAGGCCCTG--------------------------------------- : 167

                  *       260         *       280         *       300
TrCHSe1 : GTGTTGATCAGAGTACATACCCGGACTACTACTTCCGCATCACAAACAGTGAGCACAAGA : 299
TrCHSe2 : ------------------------------------------------------------ :   -

                  *       320         *       340         *       360
TrCHSe1 : CAGAGCTCAAAGAAAAATTCCAGCGCACGTGTAAGATATTTATCTTATACTCCATGCATG : 359
TrCHSe2 : ------------------------------------------------------------ :   -

                  *       380         *       400         *       420
TrCHSe1 : TCTTTTTCTGCTGACTGCCGTGTTTATATATTGTTTTGTTTTGTTCCTTAAATTTGTTAT : 419
TrCHSe2 : ------------------------------------------------------------ :   -

                  *       440         *       460         *       480
TrCHSe1 : GTCACTCTCACATGTACAAAACACTTAAGACTAAACTGCATATCATTTTTTTCAGGGACA : 479
TrCHSe2 : ------------------------------------------------------------ :   -

                  *       500         *       520         *       540
TrCHSe1 : AATCTATGATTAAGAAGAGATACATGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAA : 539
TrCHSe2 : ------------------------------------------------------------ :   -

                  *       560         *       580
TrCHSe1 : GTTTATGTGAGNACATGGCACCTTCTTGGGATGCAAGACAAGT : 582
TrCHSe2 : ------------------------------------------- :   -
```

FIGURE 27

```
                    *        20         *        40         *        60
TrCHSf : GCNTAAGCCTTGATTNTTGTTTGTTTCCTAACACAAGAACTAGTGTTTGCTTGAATCTTA :  60

                    *        80         *       100         *       120
TrCHSf : AGAAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCCTCGGTGAATGGAGCACGTGCTAG : 120

                    *       140         *       160         *       180
TrCHSf : ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCCGCCCA : 180

                    *       200         *       220         *       240
TrCHSf : AGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTCGCGACACTAAGTGTGACGATAC : 240

                    *       260         *       280         *       300
TrCHSf : TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAACTGTAAAAACAAGATACAC : 300

                    *       320         *       340         *       360
TrCHSf : AGTAATGTCAAAGGAGATCTTAGACAACTATCCAGAGCTAGCCATAGATGGAACACCAAC : 360

                    *       380         *       400         *       420
TrCHSf : AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG : 420

                    *       440         *       460         *       480
TrCHSf : CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT : 480

                    *       500         *       520         *       540
TrCHSf : TTCCTCGAGCGAAATTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 540

                    *       560         *       580         *       600
TrCHSf : AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCTCGGTTGCTACGGCGGTGTCACTGG : 600

                    *
TrCHSf : CTTACGTGTCGCC : 613
```

FIGURE 28

```
                         *        20         *        40         *        60
TrCHSf : MPQGDLNGSSSVNGARARRAPTQGKATILALGKAFPAQVLPQECLVEGFIRDTKCDDTYI :  60

                         *        80         *       100         *       120
TrCHSf : KEKLERLCKNTTVKTRYTVMSKEILDNYPELAIDGTPTIRQKLEIANPAVVEMATRASKD : 120

                         *       140         *       160         *       180
TrCHSf : CIKEWGRSPQDITHIVYVSSSEIRLPGGDLYLANELGLNSDVNRVMLYFLGCYGGVTGLR : 180

TrCHSf : VA : 182
```

FIGURE 29

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```
                   *        20         *        40         *        60
TrCHSf1: GCNTAAGCCTTGATTNTTGTTTGTTTCCTAACACAAGAACTAGTGTTTGCTTGAATCTTA :  60
TrCHSf2: ---TAAGCCTTGATTNTTGTTTGTTTCCTAACACAAGAACTAGTGTTTGCTTGAATCTTA :  57
TrCHSf3: ---------TTGATTGTTGTTTGTTTCCTAACACAAGAACTNGTGTTTGCTTGAATCTTA :  51
TrCHSf4: ------------------GTTTGTTTCCTAACACAAGAACTAGTGTTTGCTTGAATCTTA :  42

                   *        80         *       100         *       120
TrCHSf1: AGAAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCCTCGGTGAATGGAGCACGTGCTAG : 120
TrCHSf2: AGAAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCCTCGGTGAATGGAGCACGTGCTAG : 117
TrCHSf3: AGAAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCCTCGGTGAATGGAGCACGTGCTAG : 111
TrCHSf4: AGAAAAAATGCCTCAAGGTGATTTGAATGGAAGTTCCTCGGTGAATGGAGCACGTGCTAG : 102

                   *       140         *       160         *       180
TrCHSf1: ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCCGCCCA : 180
TrCHSf2: ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCCGCCCA : 177
TrCHSf3: ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCCGCCCA : 171
TrCHSf4: ACGTGCTCCTACTCAGGGAAAGGCAACGATACTTGCATTAGGAAAGGCTTTCCCCGCCCA : 162

                   *       200         *       220         *       240
TrCHSf1: AGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTCGCGACACTAAGTGTGACGATAC : 240
TrCHSf2: GGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTCGCGACACTAAGTGTGACGATAC : 237
TrCHSf3: GGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTCGCGACACTAAGTGTGACGATAC : 231
TrCHSf4: AGTCCTCCCTCAAGAGTGCTTGGTGGAAGGATTCATTCGCGACACTAAGTGTGACGATAC : 222

                   *       260         *       280         *       300
TrCHSf1: TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAACTGTAAAAACAAGATACAC : 300
TrCHSf2: TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAACTGTGAAAACAAGATACAC : 297
TrCHSf3: TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAACTGTGAAAACAAGATACAC : 291
TrCHSf4: TTATATTAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAACTGTAAAAACAAGATACAC : 282

                   *       320         *       340         *       360
TrCHSf1: AGTAATGTCAAAGGAGATCTTAGACAACTATCCAGAGCTAGCCATAGATGGAACACCAAC : 360
TrCHSf2: AGTAATGTCAAAGGAGATCTTAGACAACTATCCAGAGCTAGCCATAGATGGAACACCAAC : 357
TrCHSf3: AGTAATGTCAAAGGAGATCTTAGACAACTATCCAGAGCTAGCCATAGATGGAACACCAAC : 351
TrCHSf4: AGTAATGTCAAAGGAGATCTTAGACAACTATCCAGAGCTAGCCATAGATGGAACACCAAC : 342

                   *       380         *       400         *       420
TrCHSf1: AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG : 420
TrCHSf2: AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG : 417
TrCHSf3: AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG : 411
TrCHSf4: AATAAGGCAAAAGCTTGAAATAGCAAATCCAGCAGTAGTTGAAATGGCAACAAGAGCAAG : 402

                   *       440         *       460         *       480
TrCHSf1: CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT : 480
TrCHSf2: CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT : 477
TrCHSf3: CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT : 471
TrCHSf4: CAAAGATTGCATCAAAGAATGGGGAAGGTCACCTCAAGATATCACACACATAGTCTATGT : 462
```

FIGURE 30

```
                  *       500         *       520         *       540
TrCHSf1: TTCCTCGAGCGAAATTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 540
TrCHSf2: TTCCTCGAGCGAAATTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 537
TrCHSf3: TTCCTCGAGCGAAATTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 531
TrCHSf4: TTCCTCGAGCGAAATTCGTCTACCCGGTGGTGACCTTTATCTTGCAAATGAACTCGGCTT : 522

                  *       560         *       580         *       600
TrCHSf1: AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCTCGGTTGCTACGGCGGTGTCACTGG : 600
TrCHSf2: AAACAGCGATGTTAATCGCGTAATGCTCTATTT--------------------------- : 570
TrCHSf3: AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCTCGGTTGCT---------------- : 575
TrCHSf4: AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCTCGGTTGCTACGGCGG--------- : 573

                   *
TrCHSf1 : CTTACGTGTCGCC : 613
TrCHSf2 : ------------- :   -
TrCHSf3 : ------------- :   -
TrCHSf4 : ------------- :   -
```

FIGURE 30 (cont)

```
                        *        20         *        40         *        60
TrCHSg : GTATACCAAGGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA :  60

                        *        80         *       100         *       120
TrCHSg : AACAACAAAGGTGCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT : 120

                        *       140         *       160         *       180
TrCHSg : GGACCCAGTGACACTCACCTTGATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA : 180

                        *       200         *       220         *       240
TrCHSg : GCAGCTGTGATTGTTGGTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 240

                        *       260         *       280         *       300
TrCHSg : GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 300

                        *       320         *       340         *       360
TrCHSg : GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCTAGCCTTGTCTCAAATAACATT : 360

                        *       380         *       400         *       420
TrCHSg : GAGAAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT : 420

                        *       440         *       460         *       480
TrCHSg : TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA : 480

                        *       500         *       520         *       540
TrCHSg : AAGCCAGAGAAAATGCAAGCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT : 540

                        *       560         *       580         *       600
TrCHSg : GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGCC : 600

TrCHSg : ACAACAG : 607
```

FIGURE 31

```
                        *        20         *        40         *        60
TrCHSg : VYQGCFAGGTVLRLAKDLAENNKGARVLVVCSEITAVTFRGPSDTHLDSLVGQALFGDGA :  60

                        *        80         *       100         *       120
TrCHSg : AAVIVGSDPLPEVEKPLFELVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPSLVSNNI : 120

                        *       140         *       160         *       180
TrCHSg : EKALVDAFQPLNISDYNSIFWIAHPGGPAILDQVEAKLGLKPEKMQATRHVLSEYGNMSS : 180

                        *       200
TrCHSg : ACVLFILDEMRRKSKEDGLATT : 202
```

FIGURE 32

```
                   *        20         *        40         *        60
TrCHSg1 : GTATACCAAGGNTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTNAAGACTTGGCTGAA :  60
TrCHSg2 : -----CCAAGGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA :  55
TrCHSg3 : ---------GGTTGTTTTGCTGGTGGCACGGTACTTCGTTTGGCTAAAGACTTGGCTGAA :  51

                   *        80         *       100         *       120
TrCHSg1 : AACAACAAAGGTGCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT : 120
TrCHSg2 : AACAACAAAGGTGCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT : 115
TrCHSg3 : AACNACAAAGGTGCCCGTGTGTTGGTGGTTTGTTCAGAGATAACTGCAGTTACTTTCCGT : 111

                   *       140         *       160         *       180
TrCHSg1 : GGACCCAGTGACACTCATCTTGATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA : 180
TrCHSg2 : GGACCCAGTGACACTCACCTTGATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA : 175
TrCHSg3 : GGACCCAGTGACACTCACCTTGATAGCCTTGTGGGGCAAGCATTGTTTGGAGATGGTGCA : 171

                   *       200         *       220         *       240
TrCHSg1 : GCAGCTGTGATTGTTGGTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 240
TrCHSg2 : GCAGCTGTGATTGTTGGTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 235
TrCHSg3 : GCAGCTGTGATTGTTGGTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 231

                   *       260         *       280         *       300
TrCHSg1 : GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 300
TrCHSg2 : GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 295
TrCHSg3 : GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 291

                   *       320         *       340         *       360
TrCHSg1 : GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCTAGCCTTGTCTCAAATAACATT : 360
TrCHSg2 : GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCTAGCCTTGTCTCAAATAACATT : 355
TrCHSg3 : GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTTCCTAGCCTTGTCTCAAATAACATT : 351

                   *       380         *       400         *       420
TrCHSg1 : GAGAAAGCTCTTGTTGATGCCTTTCAACCTTTGAATATCTCCGATTACAATTCCATCTTT : 420
TrCHSg2 : GAGAAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT : 415
TrCHSg3 : GAGAAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCCATCTTT : 411

                   *       440         *       460         *       480
TrCHSg1 : TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA : 480
TrCHSg2 : TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA : 475
TrCHSg3 : TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA : 471

                   *       500         *       520         *       540
TrCHSg1 : AAGCCAGAGAAAATGCAATCCACTCGACATGTACTTAGCGAATATGGTAACATGTCCAGT : 540
TrCHSg2 : AAGCCAGAGAAAATGCAAGCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT : 535
TrCHSg3 : AAGCCAGAGAAAATGCAAGCCACTCGACATGTACTTAGCGAATATGGTAACATGTCAAGT : 531
```

FIGURE 33

```
                 *        560         *        580         *        600
TrCHSg1: GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGCC : 600
TrCHSg2: GCGTGTGTGTTATTTATCTTGGATGANATGAGGAGGAAGTCAAAAGAACACNGNCT---- : 591
TrCHSg3: GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAGAAGACGGACTTGC- : 590


TrCHSg1  : ACAACAG : 607
TrCHSg2  : ------- :   -
TrCHSg3  : ------- :   -
```

FIGURE 33 (cont)

```
                    *        20         *        40         *        60
TrCHSh : AATNACACCNTNANACCTTCCAATTCTCGTACCTCACCAATCTCATTTTTATTATATATC :  60

                    *        80         *       100         *       120
TrCHSh : TTGGTACATCTTTTGTTACCTCCAACAAAAAAATGGTGACCGTAGAAGAGATTCGTAACG : 120

                    *       140         *       160         *       180
TrCHSh : CCCAACGTTCAAATGGCCCTGCCACTATCTTAGCTTTTGGCACAGCCACTCCTTCTAACT : 180

                    *       200         *       220         *       240
TrCHSh : GTGTCACTCAAGCTGATTATCCTGATTACTACTTTCGTATCACCAACAGCGAACATATGA : 240

                    *       260         *       280         *       300
TrCHSh : CTGATCTTAAGGAAAAATTCAAGCGGATGTGTGATAGATCAATGATAAAGAAACGTTACA : 300

                    *       320         *       340         *       360
TrCHSh : TGCACCTAACAGAAGACTTTCTGAAGGAGAATCCAAATATGTGTGAATACATGGCACCAT : 360

                    *       380         *       400         *       420
TrCHSh : CACTAGATGTAAGACGAGACATAGTGGTTGTTGAAGNACCAAAGCTAGGTAAAGAANCAC : 420

                    *       440         *       460         *       480
TrCHSh : CAAAAAAAGCCATATGNGAATGGGGACAACCAAAATCNAAAATCACACATGCTTGGTTTC : 480

                    *       500         *
TrCHSh : TGACCACTTCCGGTGNTGACATGCCCGGGG : 510
```

FIGURE 34

```
                    *        20         *        40         *        60
TrCHSh : MVTVEEIRNAQRSNGPATILAFGTATPSNCVTQADYPDYYFRITNSEHMTDLKEKFKRMC :  60

                    *        80         *       100         *       120
TrCHSh : DRSMIKKRYMHLTEDFLKENPNMCEYMAPSLDVRRDIVVVEXPKLGKEPKKAIXEWGQPK : 120

                    *
TrCHSh : XKITHAWFLTTSGDMPG : 137
```

FIGURE 35

```
                  *        20         *        40         *        60
TrCHRa : GACAAATGCNTGTGGTTGGAATGGGATCCGCACCTGATTTTACATGTAAGAAAGACACAA :  60

                  *        80         *       100         *       120
TrCHRa : AAGATGCAATCGTTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGCTT : 120

                  *       140         *       160         *       180
TrCHRa : ATGGCTCANAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCANTTGAACTTGGTCTTGTCA : 180

                  *       200         *       220         *       240
TrCHRa : CTANAGAAGAGCTNTTTGTTACTTCTAAACTTTGGGNNACTGAAAATCATNCTAACCTTG : 240
```

FIGURE 36

```
                      *        20         *        40         *        60
TrCHRa : QMXVVGMGSAPDFTCKKDTKDAIVEAIKQGYRHFDTAAAYGSXQALGEGLKEAXELGLVT : 60

                      *
TrCHRa : XEEXFVTSKLWXTENHXNL : 79
```

FIGURE 37

```
                      *        20         *        40         *        60
TrCHRb : GTGTAGCAGAGTNAGAAAAAGAGAGAAAAAAAAAACATGGCAGGAAAGAAAATCCCAGAAG :  60

                      *        80         *       100         *       120
TrCHRb : TGTTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 120

                      *       140         *       160         *       180
TrCHRb : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 180

                      *       200         *       220         *       240
TrCHRb : ATTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAG : 240

                      *       260         *       280         *       300
TrCHRb : CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAAGCCATGGA : 300

                      *       320         *       340         *       360
TrCHRb : ATACTGATGCAGATTATGAACTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 360

                      *       380         *       400         *       420
TrCHRb : GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 420

                      *       440         *       460         *       480
TrCHRb : AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA : 480

                      *       500         *       520         *       540
TrCHRb : AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG : 540

                      *       560         *       580         *       600
TrCHRb : GTACCAAAAAACTCACCAAACTCTTGGAAACAGCCACCATTACCCCTGCAGTCAATCAGG : 600

TrCHRb : TGGA : 604
```

FIGURE 38

```
                         *        20         *        40         *        60
TrCHRb : MAGKKIPEVLLNSGHKMPVIGMGTSVDNRPSNDVLASIFVDAIEVGYRHFDSASVYGTEE :  60

                         *        80         *       100         *       120
TrCHRb : AIGIALAKALEKGLIKSRDEVFITSKPWNTDADYELIVPALKTTLKKLGTEYVDLYLIHW : 120

                         *       140         *       160         *       180
TrCHRb : PVRLRHDLENPVVFTKEDLLPFDIEGTWKAMEECYKLGLAKSIGICNYGTKKLTKLLETA : 180

TrCHRb : TITPAVNQV : 189
```

FIGURE 39

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```
                  *        20         *        40         *        60
TrCHRb1 : GTGTAGCAGNATTAGANAAANATAAAAAAAAAACATGGCAGGAAAGAAAATCCCAGAAG :  60
TrCHRb2 : --GTAGCAGNGTTAGNANAAGNGNGAAAAAAAAACATGGCAGGAAAGAAAATCCCAGAAG :  58
TrCHRb3 : ---------AGTNNGAAAAAGAGAGAAAAAAAAACNTGGCAGGAAAGAAAATCCCAGAAG :  51
TrCHRb4 : ---------AGTNNGAAAAAGAGAGAAAAAAAAACNTGGCAGGAAAGAAAATCCCAGAAG :  51
TrCHRb5 : --------------------------------ACATGGCAGGAAAGAAAATCCCAGAAG :  27

                  *        80         *       100         *       120
TrCHRb1 : TGTTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 120
TrCHRb2 : TGTTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 118
TrCHRb3 : TGTTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 111
TrCHRb4 : TGTTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC : 111
TrCHRb5 : TGTTATTGAATTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAATC :  87

                  *       140         *       160         *       180
TrCHRb1 : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 180
TrCHRb2 : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 178
TrCHRb3 : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 171
TrCHRb4 : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGCC : 171
TrCHRb5 : GTCCATCAAATGATGTTCTTGCTTCAATCTTTGTTGATGCAATTGAAGTTGGTTATCGTC : 147

                  *       200         *       220         *       240
TrCHRb1 : ATTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAG : 240
TrCHRb2 : ATTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAG : 238
TrCHRb3 : ATTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAG : 231
TrCHRb4 : ATTTCGATTCTGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCTTTAGCAAAAG : 231
TrCHRb5 : ATTTCGATTCTGCTTCTGTNTATGGAACAGAGGAAGCNATAGGAATTGCTTTAGCAAAAG : 207

                  *       260         *       280         *       300
TrCHRb1 : CTTTANAAAAAGGGCTTATTAAGAGTANAGATGAAGNTTTNATCACTTGCAAGNCATGGA : 300
TrCHRb2 : CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAAGCCATGGA : 298
TrCHRb3 : CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAAGCCATGGA : 291
TrCHRb4 : CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAAGCCATGGA : 291
TrCHRb5 : CTTTAGAAAAAGGGCTTATTAAGAGTAGAGATGAAGTTTTCATCACTTCAAAGCCATGGA : 267

                  *       320         *       340         *       360
TrCHRb1 : ATACTGATGCACATTATGAACTTATTGNTNCAAN-------------------------- : 334
TrCHRb2 : ATACTGATGCAGATTATGAACTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 358
TrCHRb3 : ATACTGATGCAGATTATGAACTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 351
TrCHRb4 : ATACTGATGCAGATTATGAACTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 351
TrCHRb5 : ATACTGATGCAGATTATGATCTTATTGNTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 327

                  *       380         *       400         *       420
TrCHRb1 : ------------------------------------------------------------ :   -
TrCHRb2 : GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 418
TrCHRb3 : GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 411
TrCHRb4 : GGACGGAGTATGTGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTG : 411
TrCHRb5 : GGACAGA----------------------------------------------------- : 334
```

FIGURE 40

```
                    *        440          *        460          *        480
TrCHRb1 : ------------------------------------------------------------ :   -
TrCHRb2 : AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA : 478
TrCHRb3 : AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA : 471
TrCHRb4 : AAAACCCTGTTGTTTTCACCAAAGAAGATTTACTTCCCTTTGATATAGAAGGGACATGGA : 471
TrCHRb5 : ------------------------------------------------------------ :   -

                    *        500          *        520          *        540
TrCHRb1 : ------------------------------------------------------------ :   -
TrCHRb2 : AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG : 538
TrCHRb3 : AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG : 531
TrCHRb4 : AAGCTATGGAAGAATGTTATAAGTTAGGCTTAGCAAAGTCTATTGGTATATGCAATTATG : 531
TrCHRb5 : ------------------------------------------------------------ :   -

                    *        560          *        580          *        600
TrCHRb1 : ------------------------------------------------------------ :   -
TrCHRb2 : GTACCAAAAAACTCACCAAACTCTTGGAAACAGCCACCATTACCCCTGCAGTCAATCAGG : 598
TrCHRb3 : GTACCAAAAAACTCACCAAACTCTTGGAAACAGCCACCATTACCCCTGCAGTC------- : 584
TrCHRb4 : GTACCAAAAAACTCAC-------------------------------------------- : 547
TrCHRb5 : ------------------------------------------------------------ :   -

TrCHRb1  : ---- :   -
TrCHRb2  : TGGA : 602
TrCHRb3  : ---- :   -
TrCHRb4  : ---- :   -
TrCHRb5  : ---- :   -
```

FIGURE 40 (cont)

```
                    *        20         *        40         *        60
TrCHRc : TAAGAATGAANCAATTTTATCTNANAAAAGGNNCANGCAAGTNAGTTNNATTCAAACATA :  60

                    *        80         *       100         *       120
TrCHRc : GNCTTAAAGTGTGTAACATATTCTTAACTTAAANNNTTTTNACCCNACAAAAAAAAAACAA : 120

                    *       140         *       160         *       180
TrCHRc : AGACAATAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA : 180

                    *       200         *       220         *       240
TrCHRc : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC : 240

                    *       260         *       280         *       300
TrCHRc : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC : 300

                    *       320         *       340         *       360
TrCHRc : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT : 360

                    *       380         *       400         *       420
TrCHRc : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT : 420

                    *       440         *       460         *       480
TrCHRc : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA : 480

                    *       500         *       520         *       540
TrCHRc : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC : 540

                    *       560         *       580         *       600
TrCHRc : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT : 600

                    *       620         *       640         *       660
TrCHRc : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCAAGAAACTTCAAAATCTTGT : 660

                    *       680         *
TrCHRc : CTCAGTTGCCACCGTTCTTCCTGCGGTCAATCAG : 694
```

FIGURE 41

```
                      *        20         *        40         *        60
TrCHRc : MGSVEIPTKVLTNTSSQVKMPVVGMGSAPDFTCKKDTKDAIIEAIKQGYRHFDTAAAYGS :  60

                      *        80         *       100         *       120
TrCHRc : EQALGEGLKEAIELGLVTREELFVTSKLWVTENHPHLVVPALQKSLKTLQLEYLDLYLIH : 120

                      *       140         *       160         *       180
TrCHRc : WPLSSQPGKFSFPIDVADLLPFDVKGVWESMEEGLKLGLTKAIGVSNFSVKKLQNLVSVA : 180

TrCHRc : TVLPAVNQ : 188
```

FIGURE 42

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```
                  *        20         *        40         *        60
TrCHRc1  : TAAGAATGAANCAATTTTATCTTATAAAAGGTNCANGCAAGTTAGTTNCTATTAAACATA : 60
TrCHRc2  : -------------------TCTNNNAAAAGGNNCANGCAAGTNAGTTNNTANTTNAACTA : 41
TrCHRc3  : -----------------------------------------------GNATTCAAACATA : 13
TrCHRc4  : -------------------------------------------------ATTCAAACATA : 11
TrCHRc5  : --------------------------------------------------TTCAAACATA : 10
TrCHRc6  : --------------------------------------------------TTCNAACATA : 10
TrCHRc7  : ------------------------------------------------------AACATA :  6
TrCHRc8  : ---------------------------------------------------------ACA :  3
TrCHRc9  : ----------------------------------------------------------CA :  2
TrCHRc10 : ----------------------------------------------------------CA :  2
TrCHRc11 : ----------------------------------------------------------CA :  2
TrCHRc12 : ----------------------------------------------------------CA :  2
TrCHRc13 : ------------------------------------------------------------ :  -
TrCHRc14 : ------------------------------------------------------------ :  -
TrCHRc15 : ------------------------------------------------------------ :  -
TrCHRc16 : ------------------------------------------------------------ :  -

                  *        80         *       100         *       120
TrCHRc1  : GNCTNAAAGTGTGTAACATATTCTTAACTTAAACNATTTTCACCCAACAAAAAAAAACAA :120
TrCHRc2  : GNCTNAAAGTGTGNAACATATTCTTAACTTAAACNATTTTCACCCAACAAAAAAAAACAA :101
TrCHRc3  : GNCTNAAAGTGTGTAACATATTCTTAACTTAAAACATTTTNACCCAACAAAAAAAAACAA : 73
TrCHRc4  : GNCTNAAAGTGTGTAACNTATTCTTAACTTAAAACNTTTTNACCCNACAAAAAAAAACAA : 71
TrCHRc5  : GCCTCCNAGTGTGTAACATATTCTTAACTTAAAANATTTTNACCCAACNATAAAAAACAA : 70
TrCHRc6  : GNCTCAAAGTGTGTAACATATTCTTAACTTAAAAGATTTTCACCCAACAAAAAAAAACAA : 70
TrCHRc7  : GNCTNAAAGTGTGTNANANATTCTTAACTTAAAANNTTTTCACCCAACNAAAAAAAAACAA : 66
TrCHRc8  : TNNNTNAAGTGTGNNAANNATTCNTAACNTAAACNATTTTNACCCNNNANAAAAAAACNA : 63
TrCHRc9  : NACNTNAAGTGTGNAANAANTTCTTAACTNAAANNNTTTTNACCCNACAAAAAAAAACNA : 62
TrCHRc10 : NNCCTAAAGTGTGNNANNTATTCNTAACNTAAANNNTTTTNACCCNACAAAAAAAAACNA : 62
TrCHRc11 : NNCNTNAAGTGTGNANCANATTNCTAACTNAAANNNTTTTNACCCNACAAAAAAAAACNA : 62
TrCHRc12 : NNNNTAAAGTGTGNNANAANTTCTTNACTNAAANNNTTTTNACCCNACAAAANAAAACNA : 62
TrCHRc13 : --------GNGTGTAACATATTCTTAACTTAAANNNTTTTNACCCNACAAAAAAAAACNA : 52
TrCHRc14 : --------GNGTGTAACATATNCTTAACTTAAANNATTTTNACCNAACAAAAAAAAACAA : 52
TrCHRc15 : --------GTGTGNANNNNNTTNCTAACTNAAANNNTTTTNACCNNACAAAAAATNAANG : 52
TrCHRc16 : ----------------------NTTNNNACNAANNNTTTTNACCNNACNAAAAAAAACNA : 38

                  *       140         *       160         *       180
TrCHRc1  : AGACAATAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :180
TrCHRc2  : AGACAATAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :161
TrCHRc3  : AGACAACAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :133
TrCHRc4  : AGACAACAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :131
TrCHRc5  : AGACAACAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACAGTTCTAGTCA :130
TrCHRc6  : AGACAACAACATGGNAGGGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :130
TrCHRc7  : AGACAANAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :126
TrCHRc8  : AGACAATAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :123
TrCHRc9  : AGACAANAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACAGTTCTAGTCA :122
TrCHRc10 : AGACAATAACATGGGTNGNGNNGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :122
TrCHRc11 : AGACNANAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACAGTTCTAGTCA :122
TrCHRc12 : AGACAANAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :122
TrCHRc13 : AGACNATAACATGGGTAGTGTTGAAATTCCNACAAAGGTTCTTACTAACACTTCTAGTCA :112
TrCHRc14 : AGACAATAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACACTTCTAGTCA :112
TrCHRc15 : ANACNNNAACATGGGTAGTGTTGAAATTCCAACAAAGGTTCTTACTAACAGTTCTAGTCA :112
TrCHRc16 : AGACNATNACATGGGTAGTGTTGAAATTCCNACAAAGGTTCTTACTAACACTTCTAGTCA : 98
```

FIGURE 43

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```
                  *        200         *        220         *        240
TrCHRc1  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :240
TrCHRc2  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :221
TrCHRc3  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :193
TrCHRc4  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :191
TrCHRc5  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGACTTCACATGTAAGAAAGACAC :190
TrCHRc6  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTTACATGTAAAAAAGACAC :190
TrCHRc7  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCACCTGATTTCACATGTAAGAAAGACAC :186
TrCHRc8  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :183
TrCHRc9  : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCACCTGATTTCACATGTAAGAAAGACAC :182
TrCHRc10 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :182
TrCHRc11 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCACCTGATTTCACATGTAAGAAAGACAC :182
TrCHRc12 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCACCTGATTTCACATGTAAGAAAGACAC :182
TrCHRc13 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :172
TrCHRc14 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :172
TrCHRc15 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCACCTGATTTCACATGTAAGAAAGACAC :172
TrCHRc16 : AGTGAAAATGCCTGTGGTTGGAATGGGATCAGCTCCTGATTTCACATGTAAGAAAGATAC :158

                  *        260         *        280         *        300
TrCHRc1  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :300
TrCHRc2  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :281
TrCHRc3  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATATTGCTGCTGC :253
TrCHRc4  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATATTGCTGCTGC :251
TrCHRc5  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGNTATAGACACTTTGAAACTGCTGCTGN :250
TrCHRc6  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGNTGCTGC :250
TrCHRc7  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :246
TrCHRc8  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :243
TrCHRc9  : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRc10 : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGNTGC :242
TrCHRc11 : AAAAGATGCAATCATTGAAGCCATCAAACACGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRc12 : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :242
TrCHRc13 : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :232
TrCHRc14 : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :232
TrCHRc15 : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :232
TrCHRc16 : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTTATAGACACTTTGATACTGCTGCTGC :218

                  *        320         *        340         *        360
TrCHRc1  : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGTCTTGT :360
TrCHRc2  : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGTCTTGT :341
TrCHRc3  : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGTCTTGT :313
TrCHRc4  : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGTCTTGT :311
TrCHRc5  : TTATGCNTCACAACAAGCTCTTGNNNNANNCTTCNATGCCCN------------------ :293
TrCHRc6  : TTATGGCTCANAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :310
TrCHRc7  : TTATGGCTCAGAACAAGCTCTTGGTGCAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :306
TrCHRc8  : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :303
TrCHRc9  : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :302
TrCHRc10 : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :302
TrCHRc11 : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGTCTTGT :302
TrCHRc12 : TTATGGCTCAGAACAAGCTCTTGGTGCAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :302
TrCHRc13 : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :292
TrCHRc14 : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :292
TrCHRc15 : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :292
TrCHRc16 : TTATGGCTCAGAACAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT :278
```

FIGURE 43 (cont)

```
                   *       380         *       400         *       420
TrCHRc1  : CACTAGAGAAGAGCTTTTTGTTGCTTCTAAACTTTGGGTCACTGAAAATCATCCTCATCT :420
TrCHRc2  : CACTAGAGAAGAGCTTTTTGTTGCTTCTAAACTTTGGGTCACTGAAAATCATCCTCATCT :401
TrCHRc3  : CACTAGAGAAGACCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :373
TrCHRc4  : CACTAGAGAAGACCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :371
TrCHRc5  : ------------------------------------------------------------ :  -
TrCHRc6  : CACTAGAAAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :370
TrCHRc7  : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :366
TrCHRc8  : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCATCT :363
TrCHRc9  : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :362
TrCHRc10 : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :362
TrCHRc11 : CACTAGAGAAGACCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCATCT :362
TrCHRc12 : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :362
TrCHRc13 : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :352
TrCHRc14 : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :352
TrCHRc15 : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :352
TrCHRc16 : CACTAGAGAAGAGCTTTTTGTTACTTCTAAACTTTGGGTCACTGAAAATCATCCTCACCT :338

                   *       440         *       460         *       480
TrCHRc1  : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :480
TrCHRc2  : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :461
TrCHRc3  : TGTTATTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :433
TrCHRc4  : TGTTATTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :431
TrCHRc5  : ------------------------------------------------------------ :  -
TrCHRc6  : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :430
TrCHRc7  : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :426
TrCHRc8  : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :423
TrCHRc9  : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :422
TrCHRc10 : TGTTATTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :422
TrCHRc11 : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :422
TrCHRc12 : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :422
TrCHRc13 : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :412
TrCHRc14 : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :412
TrCHRc15 : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :412
TrCHRc16 : TGTTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCAATTGGAGTACTTGGACTTGTA :398

                   *       500         *       520         *       540
TrCHRc1  : TTTGATTCAGTGGCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC :540
TrCHRc2  : TTTGATTCAGTGGCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC :521
TrCHRc3  : TTTGATCCAGTGGCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC :493
TrCHRc4  : TTTGATCCAGTGGCCACTTAGTTCTCAGCCCGGAAAGTTTTCATTTCCAATTGAGGTGGC :491
TrCHRc5  : ------------------------------------------------------------ :  -
TrCHRc6  : TTTGATCCATTGGCCACTTAATTCTCANCCTGGAAAGTTTTCATTTCCGATTGANGTGGC :490
TrCHRc7  : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :486
TrCHRc8  : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :483
TrCHRc9  : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :482
TrCHRc10 : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :482
TrCHRc11 : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :482
TrCHRc12 : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :482
TrCHRc13 : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :472
TrCHRc14 : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :472
TrCHRc15 : TTTGATCCATTGGCCACTTAGTTCTCAGCCCGAAAAGTTTTCATTTCCAATTGATGTGGC :472
TrCHRc16 : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC :458
```

FIGURE 43 (cont)

```
                 *      560       *       580       *      600
TrCHRc1  : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGG------------------------ :576
TrCHRc2  : AGN--------------------------------------------------------- :524
TrCHRc3  : AGATCTCTTGCCATTTGATGTGAGGGGTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :553
TrCHRc4  : AGATCTCTTGCCATTTGATGTGAGGGGTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :551
TrCHRc5  : ------------------------------------------------------------ :  -
TrCHRc6  : AAATCTCTTGCCATTTNATGTGAANGGTGTTTGGGAATCCATGGAAAAANGCTTNAAACT :550
TrCHRc7  : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :546
TrCHRc8  : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :543
TrCHRc9  : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrCHRc10 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrCHRc11 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrCHRc12 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :542
TrCHRc13 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAANAAGGCTTGAAACT :532
TrCHRc14 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :532
TrCHRc15 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :532
TrCHRc16 : AGATCTCTTGCCATTTGATGTGAAGGGTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :518

                 *      620       *       640       *      660
TrCHRc1  : ------------------------------------------------------------ :  -
TrCHRc2  : ------------------------------------------------------------ :  -
TrCHRc3  : TGGACTCACTAAAGCTATTGGTGT------------------------------------ :577
TrCHRc4  : TGGACTCACTAAAGCTATTGGTGTCAGTAACTTCTCTGTCAAGAAN-------------- :597
TrCHRc5  : ------------------------------------------------------------ :  -
TrCHRc6  : TGGACTCACTAAAGCTATTGGTGNCANNAACTTCTCTNTCAANAAACTTCAAAATCTTNT :610
TrCHRc7  : TGGACTCACTAAAGCTATTGGTGT------------------------------------ :570
TrCHRc8  : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCAAGAAACTTCAAAATCTTGT :603
TrCHRc9  : TGGACTCACTAAAGCTATTGGTGTTAGTAAN----------------------------- :573
TrCHRc10 : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCC------------------- :583
TrCHRc11 : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCAAGAAACTTCAAAAT----- :597
TrCHRc12 : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCAAGAAACTTCAAAAT----- :597
TrCHRc13 : TGGACTCNCTAAAGCTATTGGTGTTANNNACTTCTNTGTNAN------------------ :574
TrCHRc14 : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCAAGAAN-------------- :578
TrCHRc15 : TGGACTCACTAAAGCTATTGGTGTCAGTAACTTCTCTGTCAAGAAACTTCAAAATCTTGT :592
TrCHRc16 : TGGACTCACTAAAGCTATTGGTGTTAGTAACTTCTCTGTCAAGAAACTTCAAAATCTTGT :578

                 *      680       *
TrCHRc1  : ---------------------------------- :   -
TrCHRc2  : ---------------------------------- :   -
TrCHRc3  : ---------------------------------- :   -
TrCHRc4  : ---------------------------------- :   -
TrCHRc5  : ---------------------------------- :   -
TrCHRc6  : CTCAATTGCCACCGTTCTTNCTGCGG-------- : 636
TrCHRc7  : ---------------------------------- :   -
TrCHRc8  : CTCAGTTGCCACCGTTCT---------------- : 621
TrCHRc9  : ---------------------------------- :   -
TrCHRc10 : ---------------------------------- :   -
TrCHRc11 : ---------------------------------- :   -
TrCHRc12 : ---------------------------------- :   -
TrCHRc13 : ---------------------------------- :   -
TrCHRc14 : ---------------------------------- :   -
TrCHRc15 : CTCAGTTG-------------------------- : 600
TrCHRc16 : CTCAGTTGCCACCGTTCTTCCTGCGGTCAATCAG : 612
```

FIGURE 43 (cont)

```
                        *        20         *        40         *        60
TrDFRa : GCACACNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT :  60

                        *        80         *       100         *       120
TrDFRa : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCGAACG : 120

                        *       140         *       160         *       180
TrDFRa : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 180

                        *       200         *       220         *       240
TrDFRa : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240

                        *       260         *       280         *       300
TrDFRa : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA : 300

                        *       320         *       340         *       360
TrDFRa : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC : 360

                        *       380         *       400         *       420
TrDFRa : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC : 420

                        *       440         *       460         *       480
TrDFRa : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG : 480

                        *       500         *       520         *       540
TrDFRa : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT : 540

                        *       560         *       580         *       600
TrDFRa : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTTATGATTAA : 600

                        *
TrDFRa : CCCTGGTACT : 610
```

FIGURE 44

```
                    *        20         *        40         *        60
TrDFRa : MSKTVCXTGASGAIGSWVVRLLLERGYIVHATIQDLEDENETKHLEAMEGAKGHLKFFEM :  60

                    *        80         *       100         *       120
TrDFRa : DLLNSDSIAAAVKGCAGVIHLACPNIIGEVKDPEKQILEPAIQGTVNVLKVAKEAGVERV : 120

                    *       140         *       160         *       180
TrDFRa : VATSSISAIIPSPNWPADKIKGEDCWTDLDYCKEKKLYYPIAKTLAEKAGWEFAKETGFD : 180

TrDFRa : VVMINPGT : 188
```

FIGURE 45

```
                     *        20         *        40         *        60
TrDFRa1  : GCACACCTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 60
TrDFRa2  : GCNCACNTTCTTGACTTACCAATTGTAATNCATAATATTTATAAACATGTCAAAGACAGT : 60
TrDFRa3  : GCACACNTTCTTGACTTACNAATTGTAATNCATAATAATTNTAAACATGTCAAAGGCAGT : 60
TrDFRa4  : GCACACNTTCTTGACTTACCAATTGTAATNCATAATAATTNTAAACATGTCAAAGACAGT : 60
TrDFRa5  : --GCCNCTTCTTGACNCACNAATTGTAATNCATAATAATTATAAACATGTNNAAGACAGT : 58
TrDFRa6  : --GCTNCTTCTTGACTTACNAATTGTAATNCATAATAATTNTAAACATGTNAAAGACAGT : 58
TrDFRa7  : -----CNTTCTTGACNTACCAATTGTAATNCATAATAATTNTAAACATGTCNAAGGCAGT : 55
TrDFRa8  : -----CNTTCTTGACTTACNAATTGTAATNCATAATATTTATAAACATGTCAAAGACAGT : 55
TrDFRa9  : ------TTTCTTGACNTACCCATTNTTATNCATAATNATTNNNAACNTGTNAAAGACAGT : 54
TrDFRa10 : -------------------------------------------------------NCNGT :  5

                     *        80         *       100         *       120
TrDFRa1  : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCGAACG :120
TrDFRa2  : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCGAACG :120
TrDFRa3  : TTGTGTNACCGGAGCCAGCGGAGCCATNGGTTCATGGGTGGTTCGCCTCCTCCTCNAACG :120
TrDFRa4  : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCGAACG :120
TrDFRa5  : TTGTGTNACNGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCNAACG :118
TrDFRa6  : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCGAACG :118
TrDFRa7  : TTGTGTNNCCGGAGCCNGCGGAGCCATNGGTTCATGGGTGGTTCGCCTCCTCCTCNAACG :115
TrDFRa8  : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTCATGGGTGGTTCGNCTCCTCCTCGAACG :115
TrDFRa9  : TTGTGTNACCGGAGCCNGCGGAGCCATCGGTTCATGGGTGGTTCGCCTCCTCCTCGAACG :114
TrDFRa10 : TTGTGTNANCNGAGCNNGCGGAGCCNTCGGTTANTGGGTGGTTCGCCTCCTCCTNCCACG : 65

                     *       140         *       160         *       180
TrDFRa1  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :180
TrDFRa2  : CGGCTACATNGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :180
TrDFRa3  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :180
TrDFRa4  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :180
TrDFRa5  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :178
TrDFRa6  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :178
TrDFRa7  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :175
TrDFRa8  : CGGCTACATNGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :175
TrDFRa9  : CGGCTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :174
TrDFRa10 : CGGNTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT :125

                     *       200         *       220         *       240
TrDFRa1  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG :240
TrDFRa2  : GGAAGCAATGGAAGGCGCAAAGGGTCATCTNAAATTTTTCGAAATGGATCTTCTTAACAG :240
TrDFRa3  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTNGAAATGGATCTTCTTAACAG :240
TrDFRa4  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTCAACAG :240
TrDFRa5  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG :238
TrDFRa6  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTCAACAG :238
TrDFRa7  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTNGAAATGGATCTTCTTAACAG :235
TrDFRa8  : GGAAGCAATGGAAGGCGCAAAGGGTNATCTNAAATTTTTCGAAATGGATCTTCTTAACAG :235
TrDFRa9  : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTTNGAAATGGATCTTCTTAACAG :234
TrDFRa10 : GGAAGCAATGGAAGGAGCAAAGGGTCATNTNAAATTTTTCGAAATGGATCTTNTTAACAG :185
```

FIGURE 46

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```
                        *        260         *        280         *        300
TrDFRa1  : CGACTCTATTGCGGNCGCCGTGAAAGGTTGNGCCGGAGTTATACATNTTGNCTGTCCTAC :300
TrDFRa2  : TGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATNTTGCATGTGCTAA :300
TrDFRa3  : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA :300
TrDFRa4  : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAG :300
TrDFRa5  : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA :298
TrDFRa6  : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAG :298
TrDFRa7  : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA :295
TrDFRa8  : TGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA :295
TrDFRa9  : CGACTCTATTGCGGNCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGNGCTAA :294
TrDFRa10 : NGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATN------------- :232

                        *        320         *        340         *        360
TrDFRa1  : CCCCCTTGGCGANGAGNNNGCACCCNN--------------------------------- :327
TrDFRa2  : CATCATTGCTGAANGNAAANACCNCGANAACGNGATTTTGNAACCNGNN----------- :349
TrDFRa3  : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC :360
TrDFRa4  : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC :360
TrDFRa5  : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC :358
TrDFRa6  : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC :358
TrDFRa7  : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCAATTCAAGGAAC :355
TrDFRa8  : CATCATTGGTGAAGTCAAAGACCCCGAGAAGCAAATTTTGGAACCGGCGATTCAAGGAAC :355
TrDFRa9  : CATCATTGGCGAAGCNAAAGNACTCNATAAGNAN-------------------------- :328
TrDFRa10 : ------------------------------------------------------------ :  -

                        *        380         *        400         *        420
TrDFRa1  : ------------------------------------------------------------ :  -
TrDFRa2  : ------------------------------------------------------------ :  -
TrDFRa3  : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :420
TrDFRa4  : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :420
TrDFRa5  : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :418
TrDFRa6  : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :418
TrDFRa7  : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :415
TrDFRa8  : GGTTAACGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACGTCATC :415
TrDFRa9  : ------------------------------------------------------------ :  -
TrDFRa10 : ------------------------------------------------------------ :  -

                        *        440         *        460         *        480
TrDFRa1  : ------------------------------------------------------------ :  -
TrDFRa2  : ------------------------------------------------------------ :  -
TrDFRa3  : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG :480
TrDFRa4  : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG :480
TrDFRa5  : GATCTCTGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG :478
TrDFRa6  : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG :478
TrDFRa7  : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG :475
TrDFRa8  : GATCTCCGCCATCATACCGAGTCCTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG :475
TrDFRa9  : ------------------------------------------------------------ :  -
TrDFRa10 : ------------------------------------------------------------ :  -
```

FIGURE 46 (cont)

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```
                   *       500         *       520         *       540
TrDFRa1  : ------------------------------------------------------------ :   -
TrDFRa2  : ------------------------------------------------------------ :   -
TrDFRa3  : NTGGACAGACCTTGATTATTGCAANGAAAAGAAGTTATACTACCCCATTGCAAAGACATT :540
TrDFRa4  : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT :540
TrDFRa5  : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT :538
TrDFRa6  : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT :538
TrDFRa7  : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACATT :535
TrDFRa8  : TTGGACGGACCTTGATTATTGCAAGGAAAAGAAGTTACACTACCCCATCGCAAAGACACT :535
TrDFRa9  : ------------------------------------------------------------ :   -
TrDFRa10 : ------------------------------------------------------------ :   -

                   *       560         *       580         *       600
TrDFRa1  : ------------------------------------------------------------ :   -
TrDFRa2  : ------------------------------------------------------------ :   -
TrDFRa3  : ANCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTT-------- :592
TrDFRa4  : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTTAT------ :594
TrDFRa5  : AGCAGAAAAAGCTGGTTGGGAATTTGCTAGAGAGACCGGTTTTGT--------------- :583
TrDFRa6  : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGTTATGATTAA :598
TrDFRa7  : ANCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGAC------------------------ :571
TrDFRa8  : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTGATGTTGT--------- :586
TrDFRa9  : ------------------------------------------------------------ :   -
TrDFRa10 : ------------------------------------------------------------ :   -

                      *
TrDFRa1  : ---------- :   -
TrDFRa2  : ---------- :   -
TrDFRa3  : ---------- :   -
TrDFRa4  : ---------- :   -
TrDFRa5  : ---------- :   -
TrDFRa6  : CCCTGGTACT : 608
TrDFRa7  : ---------- :   -
TrDFRa8  : ---------- :   -
TrDFRa9  : ---------- :   -
TrDFRa10 : ---------- :   -
```

FIGURE 46 (cont)

```
                  *        20         *        40         *        60
TrDFRb : ATAAAACCAANCTNCAAAACTGATTGGAACTCAGAAAAATAGAAGAAAAGAGATGCCTGA :  60

                  *        80         *       100         *       120
TrDFRb : GTTTTGTGTTACAGGGGGCACTGGCTTCATAGCAGCCTACCTAGTGAAAGCCTTATTAGA : 120

                  *       140         *       160         *       180
TrDFRb : AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA : 180

                  *       200         *       220         *       240
TrDFRb : TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT : 240

                  *       260         *       280         *       300
TrDFRb : GGAAGGGAGTTTTGATGAGGCAGTGAGTGGTGTTGATGGTGTGTTTCATACAGCTTCCCC : 300

                  *       320         *       340         *       360
TrDFRb : TGTTCTTGTTCCACATGATGACAACATTCAGGTTACTTTGATTGATCCATGTATAAAAGG : 360

                  *       380         *       400         *       420
TrDFRb : AACACAAAATGTGCTTAACTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC : 420

                  *       440         *       460         *       480
TrDFRb : TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC : 480

                  *       500         *       520         *       540
TrDFRb : TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 540

                  *       560         *       580         *       600
TrDFRb : TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGGAATTGATCTAGTTGTAGT : 600

                  *       620
TrDFRb : TAACCCCTCTTTTGTTGGTGGTC : 623
```

FIGURE 47

```
                    *        20         *        40         *        60
TrDFRb : MPEFCVTGGTGFIAAYLVKALLEKGHTVRTTVRNPDDLEKVGYLTELSEDKERLKILKAD :  60

                    *        80         *       100         *       120
TrDFRb : LLVEGSFDEAVSGVDGVFHTASPVLVPHDDNIQVTLIDPCIKGTQNVLNSCIKAKVKRVV : 120

                    *       140         *       160         *       180
TrDFRb : LTSSCSSIRYRDDVQQISPLNESHWSDSEYCKRYNLWYAYAKTLGEKEAWRIAKESGIDL : 180

                    *
TrDFRb : VVVNPSFVGG : 190
```

FIGURE 48

```
                   *        20         *        40         *        60
TrDFRb1 : ATAAAACCAANCTNCAAAACTGATTGGAACTNAGAAAAATAGAAGAAAAGAGATGCCTGA :  60
TrDFRb2 : -------------------------GNAGCTCNNAAAAATAGAAGAAAAGAGATGCCTGA :  35
TrDFRb3 : --------------------------------------------GGAAAGAGATGCCTGA :  16
TrDFRb4 : -------------------------------------------------GAGATGCCTGA :  11

                   *        80         *       100         *       120
TrDFRb1 : GTTTTGTGTTACAGGGGGCACTGGGTTCATAGCAGCCTACCTAGTGAAAGCCTTATTAGA : 120
TrDFRb2 : GTTTTGTGTTACAGGGGGCACTGGGTTCATAGCAGCCTACCTAGTGAAAGCCCTATTAGA :  95
TrDFRb3 : GTTTTGTGTTACAGGGGGCACTGGCTTCATAGCAGCTTACCTAGTGAAAGCCTTATTAGA :  76
TrDFRb4 : GTTTTGTGTTACAGGGGGCACTGGCTTCNTAGCAGCTTACCTAGTGAAAGCCTTATTAGA :  71

                   *       140         *       160         *       180
TrDFRb1 : AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA : 180
TrDFRb2 : AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA : 155
TrDFRb3 : AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTA : 136
TrDFRb4 : AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGGTTTGGAGAAGGTTGGTTA : 131

                   *       200         *       220         *       240
TrDFRb1 : TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT : 240
TrDFRb2 : TCTAACTGAACTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT : 215
TrDFRb3 : TCTAACTGAACTGAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT : 196
TrDFRb4 : TCTAACTGAACTGAGTGAAGACAAAGAGAGATTGAAGATTTTAAAAGCAGATCTATTGGT : 191

                   *       260         *       280         *       300
TrDFRb1 : GGAAGGGAGTTTTGATGAGGCAGTGAGTGGTGTTGATGGTGTGTTTCATACAGCTTCCCC : 300
TrDFRb2 : GGAAGGGAGTTTTGATGAGGCAGTGAGTGGTGTTGATGGTGTGTTTCATACAGCTTCCCC : 275
TrDFRb3 : GGAAGGGAGTTTTGATGAGGCAGTGAGTGGTGTTGATGGTGTGTTTCATACAGCTTCCCC : 256
TrDFRb4 : GGAAGGGAGTTTTGATGAGGCAGTGAGTGGTGTTGATGGTGTGTTTCATACAGCTTCCCC : 251

                   *       320         *       340         *       360
TrDFRb1 : TGTTCTTGTTCCACATGATGACAAGATTCAGGTTACTTTGATTGATCCATGTATAAAAGG : 360
TrDFRb2 : TGTTCTTGTTCCACATGATGACAAGATTCAGGTTACTTTGATTGATCCATGTATAAAAGG : 335
TrDFRb3 : TGTTCTTGTTCCACATGATGACAACATTCAGGTTACTTTGATTGATCCATGTATAAAAGG : 316
TrDFRb4 : TGTTCTTGTTCCACATGATGACAACATTCAGGTTACTTTGATTGATCCATGTATAAAAGG : 311

                   *       380         *       400         *       420
TrDFRb1 : AACACAAAATGTGCTTAGCTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC : 420
TrDFRb2 : AACACAGAATGTGCTTAACTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC : 395
TrDFRb3 : AACACAAAATGTGCTTAACTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTTAACATC : 376
TrDFRb4 : AACACAAAATGTGCTTAACTCATGCATCATAGCAAAGGTGAAACGTGTGGTGTTAACATC : 371

                   *       440         *       460         *       480
TrDFRb1 : TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCACCACTTAATGAATC : 480
TrDFRb2 : GTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC : 455
TrDFRb3 : TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC : 436
TrDFRb4 : TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCTCCTCTTAATGAATC : 431
```

FIGURE 49

```
                     *       500         *       520         *       540
TrDFRb1: TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 540
TrDFRb2: TCATTGGAGTGATTCTGATTACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 515
TrDFRb3: TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 496
TrDFRb4: TCATTGGAGTGATTCTGAATACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 491

                     *       560         *       580         *       600
TrDFRb1: ATTAGGAGAAAAAGAAGCATGGAGGATTGC------------------------------ : 570
TrDFRb2: TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGGGATTAATCTAGTTGT--- : 572
TrDFRb3: TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGGAATTGATCTAGTTGTAGT : 556
TrDFRb4: TTTAGGAGAAAAAGAAGCATGGAGGATTGCAAAGGAAAGTGGAATTGATCTAGTTGTAGT : 551

                     *       620
TrDFRb1 : ----------------------- :   -
TrDFRb2 : ----------------------- :   -
TrDFRb3 : TAACCCCTCTTTTGTT------- : 572
TrDFRb4 : TAACCCCTCTTTTGTTGGTGGTC : 574
```

FIGURE 49 (cont)

```
                    *        20         *        40         *        60
TrDFRc : GNGAAGANCTAGTTTGCGTAACCCGGANCAACGGTTTCATCGGAACATGGCTAGTTAAAA :  60

                    *        80         *       100         *       120
TrDFRc : CCCTACTCCAAAAACACTACAAAATTCACGCCACAATCTTCCCCAATTCCAACGCATCTC : 120

                    *       140         *       160         *       180
TrDFRc : ATCTCTTCACACTCCACCCGGAAGCTCAATCCCGGATCACAATTTTCCCTGTCGATATCC : 180

                    *       200         *       220         *       240
TrDFRc : TCGACTCCACCGCCGTCTTCTCCGCTATCAATAACTGCTCAGGTGTCTTTCATGCCGCTT : 240

                    *       260         *       280         *       300
TrDFRc : CTCCATGTACCCTCGAAGATCCAACTGATCCGCAAAAAGAGCTTCTAGAACCTGCTGTAC : 300

                    *       320         *       340         *       360
TrDFRc : AAGGAACCCTAAATGTTCTAGAAGCATCCAGCGCGCAGGTACCAAACCCTAATTGGCCGG : 360

                    *       380         *       400         *       420
TrDFRc : AGAAAAAGGCGATCGATGAGGCGTCGTGGACGGATGTTGAGTACTGTAAATTGAGAGGGA : 420

                    *       440         *       460         *       480
TrDFRc : AGTGGTATCTGGTGTCGAAAACGGAGGCGGAGAAGGCGGCTTGGGATTTTCGAGAGAAAA : 480

                    *       500         *       520         *       540
TrDFRc : ATGGTGGTGTTGATGTGGGGGCGGNTCATCCGGGGACTTGTTTGGGAGAGTTGATACAGA : 540

                    *       560         *       580         *       600
TrDFRc : AGGAGTTGAATGCGAGTTCAGCGGNTTTACAGAGGTTGATGATGGGGAGTGAGGATACTC : 600

                    *       620         *       640
TrDFRc : AAGAGTGNTATTGGNNGGGGGGCTGNNNATGNTAAAGATGN : 641
```

FIGURE 50

```
                    *        20          *        40          *        60
TrDFRc : EXLVCVTRXNGFIGTWLVKTLLQKHYKIHATIFPNSNASHLFTLHPEAQSRITIFPVDIL :  60

                    *        80          *       100          *       120
TrDFRc : DSTAVFSAINNCSGVFHAASPCTLEDPTDPQKELLEPAVQGTLNVLEASSAQVPNPNWPE : 120

                    *       140          *       160          *       180
TrDFRc : KKAIDEASWTDVEYCKLRGKWYLVSKTEAEKAAWDFREKNGGVDVGAXHPGTCLGELIQK : 180

                    *       200
TrDFRc : ELNASSALQRLMMGSEDTQEXYWXGG : 206
```

FIGURE 51

```
                              *        20          *        40          *        60
TrDFRd : GCNTTGATCAGCGTATNAACACACANGTCTTCCCTTGAGCTCTGTTTCTCCACATGTCGA :  60

                              *        80          *       100          *       120
TrDFRd : AGCTAGTTTGCGTCACCGGCGGCAGCGGATGCATCGGTTCATGGCTAGTCCATCTCCTTC : 120

                              *       140          *       160          *       180
TrDFRd : TCCTCCGCGGCTACACTGTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACGA : 180

                              *       200          *       220          *       240
TrDFRd : AGCATCTAGAAGCTCTCGAAGGAGCACAAACTAATCTCCGTCTCTTCCAGATCGATCTCC : 240

                              *       260          *       280          *       300
TrDFRd : TTAACTACGACACAATCCTCGCTGCTGTCCGCGGTTGCGTCGGAATTTTCCACCTCGCTT : 300

                              *       320          *       340          *       360
TrDFRd : CACCTTGCACTGTAGACAAAGTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATTA : 360

                              *       380          *       400          *       420
TrDFRd : AAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGTTA : 420

                              *       440          *       460          *       480
TrDFRd : CCTCGTCTGTCTCGGCGATTACTCCTAGTCCTGATTGGCCTTCTGATGTTGTTAAAAGAG : 480

                              *       500          *       520          *       540
TrDFRd : AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAAGAGTTGGGGTATCCGTTGTCCA : 540

                              *       560          *       580          *       600
TrDFRd : AAACATTGGCTGAAAAAGCTGCGTGGGATTTTTNCAAAGAAAATGGTTTGGATGTTGTTG : 600

                              *       620          *       640          *       660
TrDFRd : NGGTGAATCCCGGNACTGNGATGGGTCCTGTTTTTCCACCACGGCATAATGCAAGCATGC : 660

                              *       680          *       700          *       720
TrDFRd : TCATGCCTTGGGAAACTTTTTTGAAGGCTGGNNCTGAAACATTTGAAGACTATTTTATGG : 720

                              *       740          *       760          *       780
TrDFRd : GATTGGCCNNCTTTAAAGATGTNGCATTGGCNCATNNTTTGGGGTATGAGAACAAANANN : 780

                              *       800          *       820
TrDFRd : CTTTGGGANACATNGGNGGGTTGAAACTATCNNTCCTTACGG : 822
```

FIGURE 52

```
                         *        20         *        40         *        60
TrDFRd : MSKLVCVTGGSGCIGSWLVHLLLLRGYTVHATVQNLNDENETKHLEALEGAQTNLRLFQI :  60

                         *        80         *       100         *       120
TrDFRd : DLLNYDTILAAVRGCVGIFHLASPCTVDKVHDPQKELLDPAIKGTLNVLTAAKEVGVKRV : 120

                         *       140         *       160         *       180
TrDFRd : VVTSSVSAITPSPDWPSDVVKREDCWTDVEYCKKKELGYPLSKTLAEKAAWDFXKENGLD : 180

                         *       200         *       220         *       240
TrDFRd : VVXVNPXTXMGPVFPPRHNASMLMPWETFLKAXXETFEDYFMGLAXFKDXALXHXLGYEN : 240

                         *
TrDFRd : KXXLGXXXGLKLXXLT : 256
```

FIGURE 53

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```
                        *        20         *        40         *        60
TrDFRd1 : GCNTTGATCAGCGTATNAACACACANGTCTTCCCTTGAGCTCTGTTTCTCCNCATGTCGA :  60
TrDFRd2 : ---------------------NACANNTCTTCCCTTGAGCTCTGTTTCTCCACATGTCGA :  39

                        *        80         *       100         *       120
TrDFRd1 : AGCTAGTTTGCGTCACCGGCGGCAGCGGATGCATCGGTTCATGGCTAGTCCATCTCCTTC : 120
TrDFRd2 : AGCTAGTTTGCGTCACCGGCGGNGGCGGATGCATCGGTTCATGGCTAGTCCATCTCCTTC :  99

                        *       140         *       160         *       180
TrDFRd1 : TCCTCCGCGGCTACACTGTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACGA : 180
TrDFRd2 : TCCTCCGCGGCTACACTGTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACGA : 159

                        *       200         *       220         *       240
TrDFRd1 : AGCATCTAGAAGCTCTCGAAGGAGCACAAACTAATCTCCGTCTCTTCCAGATCGATCTCC : 240
TrDFRd2 : AGCATCTAGAAGCTCTCGAAGGAGCACAAACTAATCTCCGTCTCTTCCAGATCGATCTCC : 219

                        *       260         *       280         *       300
TrDFRd1 : TTAACTACGACACAATCCTCGCTGCTGTCCGCGGTTGCGTCGGAATTTTCCACCTCGCTT : 300
TrDFRd2 : TTAACTACGACACAATCCTCGCTGCTGTCCGCGGTTGCGTCGGAATTTTCCACCTCGCTT : 279

                        *       320         *       340         *       360
TrDFRd1 : CACCTTGCACTGTAGACAAAGTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATTA : 360
TrDFRd2 : CACCTTGCACTGTAGACAAAGTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATTA : 339

                        *       380         *       400         *       420
TrDFRd1 : AAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGTTA : 420
TrDFRd2 : GAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGTTA : 399

                        *       440         *       460         *       480
TrDFRd1 : CCTCGTCTGTCTCGGCGATTACTCCTAGTCCTGATTGGCCTTCTGATGTTGTTAAAAGAG : 480
TrDFRd2 : CCTCGTCTGTCTCGGCGATTACTCCTAGTCCTGATTGGCCTTCTGATGTTGTTAAAAGAG : 459

                        *       500         *       520         *       540
TrDFRd1 : AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAAGAGTTGAGGTATCCGTT----- : 535
TrDFRd2 : AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAAGAGTTGGGGTATCCGTTGTCCA : 519

                        *       560         *       580         *       600
TrDFRd1 : ------------------------------------------------------------ :   -
TrDFRd2 : AAACATTGGCTGAAAAAGCTGCGTGGGATTTTTNCAAAGAAAATGGTTTGGATGTTGTTG : 579

                        *       620         *       640         *       660
TrDFRd1 : ------------------------------------------------------------ :   -
TrDFRd2 : NGGTGAATCCCGGNACTGNGATGGGTCCTGTTTTTCCACCACGGCATAATGCAAGCATGC : 639
```

FIGURE 54

```
                 *       680        *       700        *       720
TrDFRd1: ------------------------------------------------------------ :   -
TrDFRd2: TCATGCCTTGGGAAACTTTTTTGAAGGCTGGNNCTGAAACATTTGAAGACTATTTTATGG : 699

                 *       740        *       760        *       780
TrDFRd1: ------------------------------------------------------------ :   -
TrDFRd2: GATTGGCCNNCTTTAAAGATGTNGCATTGGCNCATNNTTTGGGGTATGAGAACAAANANN : 759

                 *       800        *       820
TrDFRd1  : ------------------------------------------ :   -
TrDFRd2  : CTTTGGGANACATNGGNGGGTTGAAACTATCNNTCCTTACGG : 801
```

FIGURE 54 (cont)

```
                     *        20         *        40         *        60
TrDFRe : GTCACTTATGAAATGGAACACAAAGGTGGAGACAAAGTATGTGTGACAGGGGCATCAGGC :  60

                     *        80         *       100         *       120
TrDFRe : TTTTTAGCATCTTGGCTTATTAAGAAACTTCTTTTGTCTGGCTATCAAGTCATTGGAACA : 120

                     *       140         *       160         *       180
TrDFRe : GTTAGAGATTTAGGGAAGAAGAAGAAAGTTGAACATTTATGGAAATTGGAAGGAGCAACA : 180

                     *       200         *       220         *       240
TrDFRe : GAAAGACTAGAACTAATCCAAGCTGATTTAATGGAAGAAAATAGTTTCGACAAAGCGATC : 240

                     *       260         *       280         *       300
TrDFRe : ATGGGATGCAAAGGTGTCTTCCACATTGCCTCTCCAGTACTCAATCATATATCAGATAAT : 300

                     *       320         *       340         *       360
TrDFRe : CCTAAGGCGGAAATCTTGGAACCGGCAGTCCAAGGTACGCTAAATGTGTTGCGTTCTTGT : 360

                     *       380         *       400         *       420
TrDFRe : AAGAGGAACCCCGATCTTGTTCGAGTGGTGCTAGCCTCATCATCTTCGGCTGTTAGAGTA : 420

                     *       440         *       460         *       480
TrDFRe : AGAGCTGATTTTGATCCAAGCATACCAATTGATGAATCATCTTGGAGCTCCTTGGAATTG : 480

                     *       500         *       520         *       540
TrDFRe : TGCGAGAAACTCAAGGCATGGTACCCAATGTCAAAGACAATGGCAGAAAAAGCAGCTTGG : 540

                     *       560         *       580
TrDFRe : GAATATAGCAAAGAGAATGGAATAGACTTAGTGACTATTTTC : 582
```

FIGURE 55

```
                        *        20         *        40         *        60
TrDFRe : MEHKGGDKVCVTGASGFLASWLIKKLLLSGYQVIGTVRDLGKKKKVEHLWKLEGATERLE :  60

                        *        80         *       100         *       120
TrDFRe : LIQADLMEENSFDKAIMGCKGVFHIASPVLNHISDNPKAEILEPAVQGTLNVLRSCKRNP : 120

                        *       140         *       160         *       180
TrDFRe : DLVRVVLASSSSAVRVRADFDPSIPIDESSWSSLELCEKLKAWYPMSKTMAEKAAWEYSK : 180

                        *
TrDFRe : ENGIDLVTIF : 190
```

FIGURE 56

```
                     *        20          *        40          *        60
TrDFRf : TNCNNGCTNCNTNCGGGCAGAGANTTTCCCTGACCTATNTGTTACTNAAGAATATTTCTA :  60

                     *        80          *       100          *       120
TrDFRf : TATATATATTTGTGTTTCAAGAACCCAAAAAATAGAATAGTGATGGAAAGGAGTTGCAAG : 120

                     *       140          *       160          *       180
TrDFRf : GTTTGTGTCACCGGTGGTGCTGGTTATATTGGTTCTCTTTTAGTCAAAAAGCTTTTGGAA : 180

                     *       200          *       220          *       240
TrDFRf : AAGGGTTACACCGTTCATGCTACTCTTAGAAACTTGAAGGACGAATCCAAAGTAGATTTT : 240

                     *       260          *       280          *       300
TrDFRf : TTGAGAGGCTTTCCACATGCAGATACTAGACTTATGTTATTTGAAGCTGATATATACAAA : 300

                     *       320          *       340          *       360
TrDFRf : TCAGATGAATTTTGGCCCGCAATTCAAGGTTGTGAGTTTGTTTTTCACCTTGCTACTCCT : 360

                     *       380          *       400          *       420
TrDFRf : TTTCAACATCAAACTGATTCTCAGTTTAAGAGCATAGAGGAAGCTGCAATAGCAGGGGTA : 420

                     *       440          *       460          *       480
TrDFRf : AAAAGCATAGCTGAAAATTGCATAAAATCAGGAACAGTGAGAAAATTGATATACACTGGA : 480

                     *       500          *       520          *       540
TrDFRf : ACTGTAATTGCTTCTTCTTCTCTGAAAGATGATGGAAGTGGCTACAAAGACTTCATTGAT : 540

                     *       560          *
TrDFRf : GAAACTTGTTGGACACCTCTCCATCTTCCTCT : 572
```

FIGURE 57

```
                         *        20         *        40         *        60
TrDFRf : MERSCKVCVTGGAGYIGSLLVKKLLEKGYTVHATLRNLKDESKVDFLRGFPHADTRLMLF :  60

                         *        80         *       100         *       120
TrDFRf : EADIYKSDEFWPAIQGCEFVFHLATPFQHQTDSQFKSIEEAAIAGVKSIAENCIKSGTVR : 120

                         *       140         *
TrDFRf : KLIYTGTVIASSSLKDDGSGYKDFIDETCWTPLHLP : 156
```

FIGURE 58

```
                        *        20          *        40          *        60
TrDFRg : GCCNTTGCCTACTACTAAACTATATATTATTATTATATTATATGATGATACATAGTGACA :  60

                        *        80          *       100          *       120
TrDFRg : TTAATAATTGGAAGGGAGAATAAATAGTTGAAAAACACACAGTTGGAGTGTTTTTGTTGT : 120

                        *       140          *       160          *       180
TrDFRg : TAAAGAAGCTNGAAAATGGAGGAAGCNACAAAGATGGTGAAAAAGAGTGGACAAATTGTT : 180

                        *       200          *       220          *       240
TrDFRg : CCTACTGCCAAATACTGTGTTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTTGAA : 240

                        *       260          *       280          *       300
TrDFRg : GCTCTTCTTCAAAGAGGTTGCACTGTTCATGCTACTGTTAGAGATCCTGAAAAATCGTTA : 300

                        *       320          *       340          *       360
TrDFRg : CACCTCCTGTCGTTGTGGAAAGGTAGTGACCAATTGAGAATTTTCCGTGCGGATTTGCAA : 360

                        *       380          *       400          *       420
TrDFRg : GAAGAAGGAAGTTTCGATGATGCCGTAAAAGGATGTATTGGTGTGTTCCATGTTGCAGCT : 420

                        *       440          *       460          *       480
TrDFRg : TCAATGCAATTCAATATTAGTGACAAAGAAAACACTGAGGACTTTGTTGAAGCAAATATA : 480

                        *       500          *       520          *       540
TrDFRg : ATTGACCCTGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAAATCAAATTCA : 540

                        *       560          *       580          *       600
TrDFRg : GTGAAAAGGGTTGTTTTCACATCTTCCATAAGTACTATTACTGCTAAAGACAACGACGGA : 600

                        *       620          *       640          *       660
TrDFRg : AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAAACTGAGATTCTGTGGAATACA : 660

                        *       680          *       700          *
TrDFRg : CAACCAAGTGGATGGGTTTATGCACTTTCAAAGCTTCATGCAGAAGAAGCGGCT : 714
```

FIGURE 59

```
                      *        20         *        40         *        60
TrDFRg : MVKKSGQIVPTAKYCVTGATGYIGSWLVEALLQRGCTVHATVRDPEKSLHLLSLWKGSDQ :  60

                      *        80         *       100         *       120
TrDFRg : LRIFRADLQEEGSFDDAVKGCIGVFHVAASMQFNISDKENTEDFVEANIIDPAIKGTINL : 120

                      *       140         *       160         *       180
TrDFRg : LKSCLKSNSVKRVVFTSSISTITAKDNDGKWKPIVDESCQTKTEILWNTQPSGWVYALSK : 180

TrDFRg : LHAEEAA : 187
```

FIGURE 60

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```
                 *        20         *        40         *        60
TrDFRg1: GCCNTTGCCTACTACTAAACTATATATTATTATTATATTATATGATGATACATAGTGACA :  60
TrDFRg2: ------------------------------------------------------------ :   -
TrDFRg3: ------------------------------------------------------------ :   -

                 *        80         *       100         *       120
TrDFRg1: TTAATAATTGGAAGGGAGAATAAATAGTTGAAAAACACACAGTTGGAGTGTTTTTGTTGT : 120
TrDFRg2: ------------------------------------------------------------ :   -
TrDFRg3: ------------------------------------------------------------ :   -

                 *       140         *       160         *       180
TrDFRg1: TAAAGAAGCTATAAAATGGAGGAAACAACAAAGATGGTGAAAAATAGTGGACAAATTGTT : 180
TrDFRg2: ---AGAAGCTNGAAAATGGAGGAAGNNACAAAGATGGTGAAAAAGAGTGGACAAATTGTT :  57
TrDFRg3: --------CTNGAAAATGGAGGAAGCNACAAAGATGGTGAAAAAGAGTGGACAAATTGTT :  52

                 *       200         *       220         *       240
TrDFRg1: CCTATTGCCAAATACTGTGTTACAGGAGCCACAGGCTATATTGGTTCATGGCTTGTTGAA : 240
TrDFRg2: CCTACTGCCAAATACTGTGTTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTTGAA : 117
TrDFRg3: CCTACTGCCAAATACTGTGTTACAGGAGCAACAGGCTATATTGGTTCATGGCTTGTTGAA : 112

                 *       260         *       280         *       300
TrDFRg1: GCTCTTCTTCAAAGAGGTTGCACTGTTCATGCTACTGTTAGAGATCCTG----------- : 289
TrDFRg2: GCTCTTCTTCAAAGAGGTTGCACTGTTCATGCTACTGTTAGAGATCCTGAAAAATCGTTA : 177
TrDFRg3: GCTCTTCTTCAAAGAGGTTGCACTGTTCATGCTACTGTTAGAGATCCTGAAAAATCGTTA : 172

                 *       320         *       340         *       360
TrDFRg1: ------------------------------------------------------------ :   -
TrDFRg2: CACCTCCTGTCGTTGTGGAAAGGTAGTGACCAATTGAGAATTTTCCGTGCGGATTTGCAA : 237
TrDFRg3: CACCTCCTGTCGTTGTGGAAAGGTAGTGACCAATTGAGAATTTTCCGTGCGGATTTGCAA : 232

                 *       380         *       400         *       420
TrDFRg1: ------------------------------------------------------------ :   -
TrDFRg2: GAAGAAGGAAGTTTCGATGATGCCGTAAAAGGATGTATTGGTGTGTTCCATGTTGCAGCT : 297
TrDFRg3: GAAGAAGGAAGTTTCGATGATGCCGTAAAAGGATGTATTGGTGTGTTCCATGTTGCAGCT : 292

                 *       440         *       460         *       480
TrDFRg1: ------------------------------------------------------------ :   -
TrDFRg2: TCAATGCAATTCAATATTAGTGACAAAGAAAACACTGAGGACTTTGTTGAAGCAAATATA : 357
TrDFRg3: TCAATGCAATTCAATATTAGTGACAAAGAAAACACTGAGGACTTTGTTGAAGCAAATATA : 352

                 *       500         *       520         *       540
TrDFRg1: ------------------------------------------------------------ :   -
TrDFRg2: ATTGACCCTGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAAATCAAATTCA : 417
TrDFRg3: ATTGACCCTGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAAATCAAATTCA : 412
```

FIGURE 61

```
                     *       560         *       580         *       600
TrDFRg1: ------------------------------------------------------------ :   -
TrDFRg2: GTGAAAAGGGTTGTTTTCACATCTTCCATAAGTACTATTACTGCTAAAGACAACGACGGA : 477
TrDFRg3: GTGAAAAGGGTTGTTTTCACATCTTCCATAAGTACTATTACTGCTAAAGACAACGACGGA : 472

                     *       620         *       640         *       660
TrDFRg1: ------------------------------------------------------------ :   -
TrDFRg2: AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAAACTGAGATTCTGTGGAATACA : 537
TrDFRg3: AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAAACTGAGATTCTGTGGAATACA : 532

                      *       680         *       700         *
TrDFRg1  : ------------------------------------------------------ :   -
TrDFRg2  : CAACCAAGTGGATGGGTTTATGCACTTTCAAAGCTTCATGCAGAAGAAGCGGCT : 591
TrDFRg3  : CAACCAAGTGGATGGGTTTATGCACTTTCAAAGCTTCATG-------------- : 572
```

FIGURE 61 (cont)

```
                         *        20         *        40         *        60
TrDFRh : GNNGNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAGGAAAAAAAGAGTAGAGAAGTGA :  60

                         *        80         *       100         *       120
TrDFRh : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 120

                         *       140         *       160         *       180
TrDFRh : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 180

                         *       200         *       220         *       240
TrDFRh : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA : 240

                         *       260         *       280         *       300
TrDFRh : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA : 300

                         *       320         *       340         *       360
TrDFRh : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC : 360

                         *       380         *       400         *       420
TrDFRh : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC : 420

                         *       440         *       460         *       480
TrDFRh : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT : 480

                         *       500         *       520         *       540
TrDFRh : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 540

                         *       560         *       580         *       600
TrDFRh : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT : 600

                         *       620         *       640         *       660
TrDFRh : TGGAAGTATTCGAAAGAGCACAACATAGACTTTGTCTCCATCATTCCACCTCTTGTTGTT : 660

                         *       680         *       700         *       720
TrDFRh : GGCCCCTTTCTTATGGCCTCAATGCCACCTAGTCTAATCACTGCTCTTTCTCTTATCACA : 720

                         *       740         *       760         *       780
TrDFRh : GGAAATGAGGCCCATTACTCAATCATAAAGCAAGGGCAATACGTCCATTTAGATGACCTT : 780

                         *       800         *       820         *       840
TrDFRh : TGTCTTGCTCATATATTTCTGTATGAGAATCCAAAAGCTCAAGGGAGATACATTTGCTGT : 840
```

FIGURE 62

```
                       *        860         *        880         *        900
TrDFRh  : TCACATGAAGCAACCATTCATCAAGTTGCAAAACTTATTAAAGAAAAATACCCAGAGTTC : 900

                       *        920         *        940         *        960
TrDFRh  : AATGTCCCAACAAAATTCAATGATATCCCAGATGAATTGGAAATTATTAAATTTTCTAAA : 960

                       *
TrDFRh  : AAGAAGATCACAGACT : 976
```

FIGURE 62 (cont)

```
                     *        20         *        40         *        60
TrDFRh : MGSESEIVCVTGASGFIGSWLVMRLIERGYTVRATVRDPDNMKKVKHLVELPGAKSKLSL :  60

                     *        80         *       100         *       120
TrDFRh : WKADLDKEGSFDEAIKGCTGVFHVATPMDFESKDPENEVIKPTINGLIDILKACEKAKTV : 120

                     *       140         *       160         *       180
TrDFRh : RKLVFTSSAGTVDVTEHPKSIIDETCWSDVDFCRRVKMTGWMYFVSKTLAEQEAWKYSKE : 180

                     *       200         *       220         *       240
TrDFRh : HNIDFVSIIPPLVVGPFLMASMPPSLITALSLITGNEAHYSIIKQGQYVHLDDLCLAHIF : 240

                     *       260         *       280         *
TrDFRh : LYENPKAQGRYICCSHEATIHQVAKLIKEKYPEFNVPTKFNDIPDELEIIKFSKKKITD : 299
```

FIGURE 63

```
                     *        20         *        40         *        60
TrDFRh1  : GNNTTGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAAGAGTAGNNNANNGA :  60
TrDFRh2  : -TTTTGTCTTAAATCCAATTTCAGNCTAAATTGAAAAGGAAAAAAAGAGCAGAGAAGTCA :  59
TrDFRh3  : ---GNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAAGAGTAGNNNANNGA :  57
TrDFRh4  : ---GNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAAGAGTAGAGAANNGN :  57
TrDFRh5  : ---GNGTCTTCCGTTNAATTTAAGNCTATATTGAAAAGNAAAAAAAGAGTAGNNNANNGA :  57
TrDFRh6  : ---GNGTCTTCCGTTNAANTTAAGNCTATATTGAAAAGNAAAAAAAGAGTAGNNNANNGA :  57
TrDFRh7  : ---GNGTCTTCCGTTNAATTTNAGNCTATATTGAAAAAGAAAAAAAGAGTAGAGAAGTGA :  57
TrDFRh8  : ----CGTCTTCCNTTNAATTCNAGNCCAAATTGAAAAGGAAAAAAAGAGCAGAGAAGTGA :  56
TrDFRh9  : ----CGTCTTCCGTTNAATTTAAGNCTATATTGAAAAAGAAAAAAAGAGTAGAGAAGTGA :  56
TrDFRh10 : ----CGTCTTCCGTTNNATTTAAGNCTATATTGAAAAAGAAAAAAAGAGTAGAGAAGTGA :  56
TrDFRh11 : -----GTCTTCNNTTNAATTCNAGNCCAAATTGAAAAGGAAAAAAAGAGCAGAGAAGTGA :  55
TrDFRh12 : -----GTCTTCCGTTCNATTTNAGNCTATATTGAAAAGNAAAAAAAGAGTAGAGAANNGN :  55
TrDFRh13 : --------CCTCTTCTTNAATCCAGCTAAATTGAAAAGGAAAAAAAGAGCAGAGAAGTGA :  52
TrDFRh14 : ------------------------------------------------GNAGAGAAGTNA :  12
TrDFRh15 : ------------------------------------------------------------ :   -

                     *        80         *       100         *       120
TrDFRh1  : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 120
TrDFRh2  : ACTGCAGTGAAAATATACATGGGTTCTGAATCCGAAATAGTTTGTGTTACCGGAGCTTCA : 119
TrDFRh3  : AGTGAAGTGAANACATACATGGGTTCCGAATCAGAAATAGTTTGNGTTACCGGAGCTTCA : 117
TrDFRh4  : NNTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 117
TrDFRh5  : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 117
TrDFRh6  : AGTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 117
TrDFRh7  : AGTGAAGTGAAAACATACATGGGTTCTGAATCAGAAATAGTTTGTGTTACCGGAGCATCA : 117
TrDFRh8  : ACTGAAGTGAAAATATACATGGGTTCCGAATCCGAAATAGTTTGTGTTACCGGAGCTTCA : 116
TrDFRh9  : AGTGAAGTGAAAACATACATGGGTTCTGAATCAGAAATAGTTTGTGTTACCGGAGCATCA : 116
TrDFRh10 : AGTGAAGTGAAAACATACATGGGTTCTGAATCAGAAATAGTTTGTGTTACCGGAGCATCA : 116
TrDFRh11 : ACTGAAGTGAAAATATACATGGGTTCCGAATCCGAAATAGTTTGTGTTACCGGAGCTTCA : 115
TrDFRh12 : NNTGAAGTGAAAACATACATGGGTTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 115
TrDFRh13 : ACTGCAGTGAAAATATACATGGGTTCTGAATCCGAAATAGTTTGTGTTACCGGAGCTTCA : 112
TrDFRh14 : CCTGCAGTGAAAATATACATGGGTTCTGAATCCGAAATAGTTTGTGTTACCGGAGCTTCA :  72
TrDFRh15 : ------------------------------------------------------------ :   -

                     *       140         *       160         *       180
TrDFRh1  : TGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 180
TrDFRh2  : GGTTTCATCGGGTCGTGGCTTGTTATGAGACTTATCGAGCATGGCTACACTGTTCGAGCC : 179
TrDFRh3  : TGTTTNATCGGATCGTGGCTTGTTATGAGACTTATANAGCGTGNCTACACGGCTCGAGCC : 177
TrDFRh4  : TGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh5  : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh6  : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh7  : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh8  : GGTTTCATCGGGTCGTGGCTTGTTATGAGACTTATCGAGCGCGGCTACACGGTTCGAGCC : 176
TrDFRh9  : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 176
TrDFRh10 : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 176
TrDFRh11 : GGTTTCATCGGGTCGTGGCTTGTTATGAGACTTATCGAGCGCGGCTACACGGTTCGAGCC : 175
TrDFRh12 : GGTTTCATCGGATCGTGGCTTGTTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 175
TrDFRh13 : GGTTTCATCGGGTCGTGGCTTGTTATGAGACTTATCGAGCGTGGCTACACTGTTCGAGCC : 172
TrDFRh14 : GGTTTCATCGGGTCGTGGCTTGTTATGAGACTTATCGAGCGTGGCTACACTGTTCGAGCC : 132
TrDFRh15 : ------------------------------------------------------------ :   -
```

FIGURE 64

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```
                   *       200         *       220         *       240
TrDFRh1  : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :240
TrDFRh2  : ACCGTTCGTGACCCAGATAACATGAAGAANGTGAAGCATTTGCTGGAACTGCCAGGTGCA :239
TrDFRh3  : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRh4  : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRh5  : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRh6  : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRh7  : ACTGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRh8  : ACTGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGATGGAACTGCCGGGTGCA :236
TrDFRh9  : ACTGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :236
TrDFRh10 : ACTGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :236
TrDFRh11 : ACTGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGATGGAACTGCCGGGTGCA :235
TrDFRh12 : ACCGTTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :235
TrDFRh13 : ACCGTTCGTGACCCAGATAACATGAAGAAGGTGAAGCATTTGCTGGAACTGCCGGGTGCA :232
TrDFRh14 : ACCGTTCGTGACCCAGATAACATGAAGAAGGTGAAGCATTTGCTGGAACTGCCGGGTGCA :192
TrDFRh15 : ------------------------------------------------------------ :  -

                   *       260         *       280         *       300
TrDFRh1  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :300
TrDFRh2  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :299
TrDFRh3  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :297
TrDFRh4  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :297
TrDFRh5  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :297
TrDFRh6  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :297
TrDFRh7  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :297
TrDFRh8  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :296
TrDFRh9  : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :296
TrDFRh10 : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :296
TrDFRh11 : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :295
TrDFRh12 : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :295
TrDFRh13 : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :292
TrDFRh14 : AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTTGATGAAGCA :252
TrDFRh15 : ------------------------------------------------------------ :  -

                   *       320         *       340         *       360
TrDFRh1  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :360
TrDFRh2  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAGTCCAAGGAC :359
TrDFRh3  : ATTAAAGGGTGCACAGGAGTTTTTNATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRh4  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRh5  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRh6  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRh7  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRh8  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :356
TrDFRh9  : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :356
TrDFRh10 : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :356
TrDFRh11 : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :355
TrDFRh12 : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :355
TrDFRh13 : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :352
TrDFRh14 : ATTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAGTCCAAGGAC :312
TrDFRh15 : ------------------------------------------------------------ :  -
```

FIGURE 64 (cont)

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```
                      *       380         *       400         *       420
TrDFRh1  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :420
TrDFRh2  : CCTGAGAATGAAGTGATAAAGCCTACAATAAACGGATTAATAGACATACTGAAAGCATGC :419
TrDFRh3  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :417
TrDFRh4  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :417
TrDFRh5  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :417
TrDFRh6  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :417
TrDFRh7  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :417
TrDFRh8  : CCTGAGAACGAAGTGATAAAGCCTACAATAAATGGACTAATAGACATACTGAGAGCATGT :416
TrDFRh9  : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :416
TrDFRh10 : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :416
TrDFRh11 : CCTGAGAACGAAGTGATAAAGCCTACAATAAATGGACTAATAGACATACTGAGAGCATGT :415
TrDFRh12 : CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC :415
TrDFRh13 : CCTGAGAATGAAGTGATAAAGCCTACAATAAACGGATTAATAGACATACTGAAAGCATGC :412
TrDFRh14 : CCTGAGAATGAAGTGATAAAGCCTACAATAAACGGATTAATAGACATACTGAAAGCATGC :372
TrDFRh15 : ----------------------------------------------TACTGAAAGNNTGC : 14

                      *       440         *       460         *       480
TrDFRh1  : GAAAAGGCAAAAACAGTTAAAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :480
TrDFRh2  : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :479
TrDFRh3  : NAAAAGGCAAAAACAGTTAAAAAATTGGTTTTCACATCATCGGCTGNAACTGTGGACGTT :477
TrDFRh4  : GAAAAGGCAAAAACAGTTAAAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :477
TrDFRh5  : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :477
TrDFRh6  : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :477
TrDFRh7  : GAAAAGGCAAAAACAGTTAAAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :477
TrDFRh8  : GAAAAGGCAAAAACAATTAGAAGATTGGTTTTCACATCATCAGCTGGAACTGTGGACGTA :476
TrDFRh9  : GAAAAGGCAAAAACAGTTAAAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :476
TrDFRh10 : GAAAAGGCAAAAACAGTTAAAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :476
TrDFRh11 : GAAAAGGCAAAAACAATTAGAAGATTGGTTTTCACATCATCAGCTGGAACTGTGGACGTA :475
TrDFRh12 : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :475
TrDFRh13 : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :472
TrDFRh14 : GAAAAGGCAAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT :432
TrDFRh15 : GAAAAGGCNAAAACAGTTAGAAAATTGGTTTTCACATCATCGGCTGGAACTGTGGACGTT : 74

                      *       500         *       520         *       540
TrDFRh1  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :540
TrDFRh2  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :539
TrDFRh3  : ACTGAACATCCAAAGN-------------------------------------------- :493
TrDFRh4  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :537
TrDFRh5  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :537
TrDFRh6  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :537
TrDFRh7  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :537
TrDFRh8  : ACTGAACACTCAAAATCAATTGTTGATGAAACATGTTGGAGTGACGTTGACTTTTGCCGT :536
TrDFRh9  : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :536
TrDFRh10 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :536
TrDFRh11 : ACTGAACACTCAAAATCAATTGTTGATGAAACATGTTGGAGTGACGTTGACTTTTGCCGT :535
TrDFRh12 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :535
TrDFRh13 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :532
TrDFRh14 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :492
TrDFRh15 : ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT :134
```

FIGURE 64 (cont)

```
                     *       560         *       580         *       600
TrDFRh1  : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAG-------------- :586
TrDFRh2  : AGAGTCAAAATGACCGGTTGGATGTATTTT------------------------------ :569
TrDFRh3  : ------------------------------------------------------------ :  -
TrDFRh4  : ANAGTCAANATGACCGGCTGGATGTATTTTGTTTCAAANACCC----------------- :580
TrDFRh5  : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCT---------------- :581
TrDFRh6  : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAG----- :592
TrDFRh7  : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT :597
TrDFRh8  : AGAGTCAAAATGACCGGTTGGATGTATTTTGTTTCAAAGA-------------------- :576
TrDFRh9  : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAG--------- :587
TrDFRh10 : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT :596
TrDFRh11 : AGAGTCAAAATGACCGGTTGGATGTATTTTGTTTCAAAGACCCT---------------- :579
TrDFRh12 : AGAGTCAAGATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT :595
TrDFRh13 : AGAGTCAAAATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAG------ :586
TrDFRh14 : AGAGTCAAAATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT :552
TrDFRh15 : AGAGTCAAAATGACCGGTTGGATGTATTTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT :194

                     *       620         *       640         *       660
TrDFRh1  : ------------------------------------------------------------ :  -
TrDFRh2  : ------------------------------------------------------------ :  -
TrDFRh3  : ------------------------------------------------------------ :  -
TrDFRh4  : ------------------------------------------------------------ :  -
TrDFRh5  : ------------------------------------------------------------ :  -
TrDFRh6  : ------------------------------------------------------------ :  -
TrDFRh7  : T----------------------------------------------------------- :598
TrDFRh8  : ------------------------------------------------------------ :  -
TrDFRh9  : ------------------------------------------------------------ :  -
TrDFRh10 : TGGAAGTATTCTAAAGAGCACAACATAGATTTTG-------------------------- :630
TrDFRh11 : ------------------------------------------------------------ :  -
TrDFRh12 : TGGAAGTAT--------------------------------------------------- :604
TrDFRh13 : ------------------------------------------------------------ :  -
TrDFRh14 : TGGAAGTATTCGAAAGAGCACAACATAGACTTTG-------------------------- :586
TrDFRh15 : TGGAAGTATTCGAAAGAGCACAACATAGACTTTGTCTCCATCATTCCACCTCTTGTTGTT :254

                     *       680         *       700         *       720
TrDFRh1  : ------------------------------------------------------------ :  -
TrDFRh2  : ------------------------------------------------------------ :  -
TrDFRh3  : ------------------------------------------------------------ :  -
TrDFRh4  : ------------------------------------------------------------ :  -
TrDFRh5  : ------------------------------------------------------------ :  -
TrDFRh6  : ------------------------------------------------------------ :  -
TrDFRh7  : ------------------------------------------------------------ :  -
TrDFRh8  : ------------------------------------------------------------ :  -
TrDFRh9  : ------------------------------------------------------------ :  -
TrDFRh10 : ------------------------------------------------------------ :  -
TrDFRh11 : ------------------------------------------------------------ :  -
TrDFRh12 : ------------------------------------------------------------ :  -
TrDFRh13 : ------------------------------------------------------------ :  -
TrDFRh14 : ------------------------------------------------------------ :  -
TrDFRh15 : GGCCCCTTTCTTATGGCCTCAATGCCACCTAGTCTAATCACTGCTCTTTCTCTTATCACA :314
```

FIGURE 64 (cont)

```
                    *        740         *        760         *        780
TrDFRh1  : ------------------------------------------------------------ :   -
TrDFRh2  : ------------------------------------------------------------ :   -
TrDFRh3  : ------------------------------------------------------------ :   -
TrDFRh4  : ------------------------------------------------------------ :   -
TrDFRh5  : ------------------------------------------------------------ :   -
TrDFRh6  : ------------------------------------------------------------ :   -
TrDFRh7  : ------------------------------------------------------------ :   -
TrDFRh8  : ------------------------------------------------------------ :   -
TrDFRh9  : ------------------------------------------------------------ :   -
TrDFRh10 : ------------------------------------------------------------ :   -
TrDFRh11 : ------------------------------------------------------------ :   -
TrDFRh12 : ------------------------------------------------------------ :   -
TrDFRh13 : ------------------------------------------------------------ :   -
TrDFRh14 : ------------------------------------------------------------ :   -
TrDFRh15 : GGAAATGAGGCCCATTACTCAATCATAAAGCAAGGGCAATACGTCCATTTAGATGACCTT : 374

                    *        800         *        820         *        840
TrDFRh1  : ------------------------------------------------------------ :   -
TrDFRh2  : ------------------------------------------------------------ :   -
TrDFRh3  : ------------------------------------------------------------ :   -
TrDFRh4  : ------------------------------------------------------------ :   -
TrDFRh5  : ------------------------------------------------------------ :   -
TrDFRh6  : ------------------------------------------------------------ :   -
TrDFRh7  : ------------------------------------------------------------ :   -
TrDFRh8  : ------------------------------------------------------------ :   -
TrDFRh9  : ------------------------------------------------------------ :   -
TrDFRh10 : ------------------------------------------------------------ :   -
TrDFRh11 : ------------------------------------------------------------ :   -
TrDFRh12 : ------------------------------------------------------------ :   -
TrDFRh13 : ------------------------------------------------------------ :   -
TrDFRh14 : ------------------------------------------------------------ :   -
TrDFRh15 : TGTCTTGCTCATATATTTCTGTATGAGAATCCAAAAGCTCAAGGGAGATACATTTGCTGT : 434

                    *        860         *        880         *        900
TrDFRh1  : ------------------------------------------------------------ :   -
TrDFRh2  : ------------------------------------------------------------ :   -
TrDFRh3  : ------------------------------------------------------------ :   -
TrDFRh4  : ------------------------------------------------------------ :   -
TrDFRh5  : ------------------------------------------------------------ :   -
TrDFRh6  : ------------------------------------------------------------ :   -
TrDFRh7  : ------------------------------------------------------------ :   -
TrDFRh8  : ------------------------------------------------------------ :   -
TrDFRh9  : ------------------------------------------------------------ :   -
TrDFRh10 : ------------------------------------------------------------ :   -
TrDFRh11 : ------------------------------------------------------------ :   -
TrDFRh12 : ------------------------------------------------------------ :   -
TrDFRh13 : ------------------------------------------------------------ :   -
TrDFRh14 : ------------------------------------------------------------ :   -
TrDFRh15 : TCACATGAAGCAACCATTCATCAAGTTGCAAAACTTATTAAAGAAAAATACCCAGAGTTC : 494
```

FIGURE 64 (cont)

```
                      *        920         *        940         *        960
TrDFRh1  : ------------------------------------------------------------ :   -
TrDFRh2  : ------------------------------------------------------------ :   -
TrDFRh3  : ------------------------------------------------------------ :   -
TrDFRh4  : ------------------------------------------------------------ :   -
TrDFRh5  : ------------------------------------------------------------ :   -
TrDFRh6  : ------------------------------------------------------------ :   -
TrDFRh7  : ------------------------------------------------------------ :   -
TrDFRh8  : ------------------------------------------------------------ :   -
TrDFRh9  : ------------------------------------------------------------ :   -
TrDFRh10 : ------------------------------------------------------------ :   -
TrDFRh11 : ------------------------------------------------------------ :   -
TrDFRh12 : ------------------------------------------------------------ :   -
TrDFRh13 : ------------------------------------------------------------ :   -
TrDFRh14 : ------------------------------------------------------------ :   -
TrDFRh15 : AATGTCCCAACAAAATTCAATGATATCCCAGATGAATTGGAAATTATTAAATTTTCTAAA : 554

                      *
TrDFRh1  : ---------------- :   -
TrDFRh2  : ---------------- :   -
TrDFRh3  : ---------------- :   -
TrDFRh4  : ---------------- :   -
TrDFRh5  : ---------------- :   -
TrDFRh6  : ---------------- :   -
TrDFRh7  : ---------------- :   -
TrDFRh8  : ---------------- :   -
TrDFRh9  : ---------------- :   -
TrDFRh10 : ---------------- :   -
TrDFRh11 : ---------------- :   -
TrDFRh12 : ---------------- :   -
TrDFRh13 : ---------------- :   -
TrDFRh14 : ---------------- :   -
TrDFRh15 : AAGAAGATCACAGACT : 570
```

FIGURE 64 (cont)

```
                      *        20         *        40         *        60
TrLCRa : GGNCATAAAAACTGCACTAGTGTGTATAAGTTTNTTAGTGAAAAAAGAGTGTGTAAATTA :  60

                      *        80         *       100         *       120
TrLCRa : ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 120

                      *       140         *       160         *       180
TrLCRa : GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 180

                      *       200         *       220         *       240
TrLCRa : CTGTTAGAGACCCAGATAGTCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 240

                      *       260         *       280         *       300
TrLCRa : GGGAACTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 300

                      *       320         *       340         *       360
TrLCRa : CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG : 360

                      *       380         *       400         *       420
TrLCRa : AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 420

                      *       440         *       460         *       480
TrLCRa : GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 480

                      *       500         *       520         *       540
TrLCRa : AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540

                      *       560         *       580         *       600
TrLCRa : ACACTGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAATGCTAGCTGAAAAGGCTG : 600

                      *       620         *       640         *       660
TrLCRa : CATGGAAATTTGCTGAAGAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 660

                      *       680         *       700         *       720
TrLCRa : CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTTGGCTTGGCAATGTCTCTAATAA : 720

                      *       740         *       760         *       780
TrLCRa : CAGGCAATGATTTCCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTCGTTAT : 780

                      *       800         *       820         *
TrLCRa : CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGGCAGAGAAG : 833
```

FIGURE 65

```
                        *        20         *        40         *        60
TrLCRa : MASIKQIGNKKACVIGGTGFVASMLIKQLLEKGYAVNTTVRDPDSPKKISHLVALQSLGE :  60

                        *        80         *       100         *       120
TrLCRa : LNLFRADLTVEEDFDAPIAGCELVFQLATPVNFASQDPENDMIKPAIKGVLNVLKASARA : 120

                        *       140         *       160         *       180
TrLCRa : KEVKRVILTSSAAAVTINELKGTGHVMDETNWSDVEFLNTAKPPTWGYPASKMLAEKAAW : 180

                        *       200         *       220         *       240
TrLCRa : KFAEENDIDLITVIPSLTTGPSLTPDIPSSVGLAMSLITGNDFLINALKGMQFLSGSLSI : 240

                        *
TrLCRa : THVEDICRAHIFLAEK : 256
```

FIGURE 66

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```
                     *        20         *        40         *        60
TrLCRa1: GGNCATAAAAACTGCACTAGTGTGTATAAGTTTNATAGTGAAAAAAGAGTGTGTAAATTA :  60
TrLCRa2: GGNCNTAAAAACTGCACTAGTGTGTATAAGTTTNNTAGTGAAAAAAGAGTGTGTAAATTA :  60
TrLCRa3: -----TAAAAACTGTACTNGTGTGTATAAGTTTNNTAGTGAAAAAAGAGTGTGTAAATTA :  55
TrLCRa4: -----TAAAAACTGCACTAGTGTGTATAAGTTTCTTGGTGAAAAAAGAGTTTGTAAATTA :  55
TrLCRa5: -------------GACCTCGTGTGNANTAGTTTCTTGGTGAAAAAAGAGTTTGTAAANTA :  47
TrLCRa6: ------------------------------------------------------------ :   -
TrLCRa7: ------------------------------------------------------------ :   -

                     *        80         *       100         *       120
TrLCRa1: ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 120
TrLCRa2: ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 120
TrLCRa3: ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 115
TrLCRa4: ACATCATGGCTAGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 115
TrLCRa5: ACATCNTGGCTNGTATCAAACAAATTGGAAACAAGAAAGCATGTGTGATTGGTGGCACTG : 107
TrLCRa6: ------------------------------------------------------------ :   -
TrLCRa7: ------------------------------------------------------------ :   -

                     *       140         *       160         *       180
TrLCRa1: GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 180
TrLCRa2: GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 180
TrLCRa3: GTTTTGTTGCATCTATGTTGATCAAACAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 175
TrLCRa4: GTTTTGTTGCATCTATGTTGATCAAGCAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 175
TrLCRa5: GTTTTGTTGCATCTATGTTGATCAAGCAGTTACTTGAAAAGGGTTATGCTGTTAATACTA : 167
TrLCRa6: ------------------------------------------------------------ :   -
TrLCRa7: ------------------------------------------------------------ :   -

                     *       200         *       220         *       240
TrLCRa1: CTGTTAGAGACCCAGATAGTCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 240
TrLCRa2: CTGTTAGAGACCCAGATAGTCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 240
TrLCRa3: CTGTTAGAGACCCAGATAGTCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 235
TrLCRa4: CCGTTAGAGACCCAGATAGCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 235
TrLCRa5: CCGTTAGAGACCCAGATAGCCCTAAGAAAATATCTCACCTAGTGGCACTGCAAAGTTTGG : 227
TrLCRa6: -----------------------------------------------------------G :   1
TrLCRa7: ------------------------------------------------------------ :   -

                     *       260         *       280         *       300
TrLCRa1: GGGAACTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 300
TrLCRa2: GGGAACTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 300
TrLCRa3: GGGAACTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 295
TrLCRa4: GGGAACTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 295
TrLCRa5: GGGAACTGAATCTATTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 287
TrLCRa6: NGNACCTGAATCTATTTAGAGNAGACTTAACAGTTGAAGAAGATTTTGATGCTCCTATAG :  61
TrLCRa7: --------------------------TTAACAGTTGAAGAAGATTTTGATGCTCCTATAG :  34

                     *       320         *       340         *       360
TrLCRa1: CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG : 360
TrLCRa2: CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG : 360
TrLCRa3: CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG : 355
TrLCRa4: CAGGATGTGAACTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG : 355
TrLCRa5: CAGGATGTGAACTTGTTTTTCAACTTGCTACACCTGTGAACTTTGCTTCTCAAGATCCTG : 347
TrLCRa6: CAGGATGTGAGCTTGTTTTTCAACTTGCTACACCTGTGACCTTTGCTTCTCAAGATCCTG : 121
TrLCRa7: CAGGATGTGAGCTTGTTTTTNAACTTGCTACACCTGTGACCTTTGCTTCTCAAGATCCTG :  94
```

FIGURE 67

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```
                  *       380         *       400         *       420
TrLCRa1: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 420
TrLCRa2: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 420
TrLCRa3: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 415
TrLCRa4: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAATTGCAA : 415
TrLCRa5: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAATTGCAA : 407
TrLCRa6: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 181
TrLCRa7: AGAATGACATGATAAAGCCAGCAATCAAAGGTGTGTTGAATGTGTTGAAAGCAAGTGCAA : 154

                  *       440         *       460         *       480
TrLCRa1: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 480
TrLCRa2: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 480
TrLCRa3: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 475
TrLCRa4: GAGCAAAAGAAGTTAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 475
TrLCRa5: GAGCAAAAGAAGTTAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 467
TrLCRa6: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 241
TrLCRa7: GAGCAAAAGAAGTCAAAAGAGTTATCTTAACATCTTCGGCAGCCGCGGTGACTATAAATG : 214

                  *       500         *       520         *       540
TrLCRa1: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540
TrLCRa2: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540
TrLCRa3: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 535
TrLCRa4: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCTGATGTTGAATTTCTCA : 535
TrLCRa5: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCTGATGTTGAATTTCTCA : 527
TrLCRa6: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGGTGTTGAATTTCTGA : 301
TrLCRa7: AACTCAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 274

                  *       560         *       580         *       600
TrLCRa1: ACACTGCAAAGCCACCCACTTGGGGTTATCCTGCTT------------------------ : 576
TrLCRa2: ACACTGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAN-------------------- : 580
TrLCRa3: ACACTGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAAT----------------- : 578
TrLCRa4: ACACTGCAAAACCACCCACTTGGGGTTATCCTGCCTCAAAAATGCTAGCTGAAAAGGCTG : 595
TrLCRa5: ACACTGCAAAACCACCCACTTGGGGTTATCCTGCCTCAAAAATGCTAGCTGAAAAGGCTG : 587
TrLCRa6: ACACTGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAATGCTAGCTGAAAAGGCTG : 361
TrLCRa7: ACACTGCAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAATGCTAGCTGAAAAGGCTG : 334

                  *       620         *       640         *       660
TrLCRa1: ------------------------------------------------------------ :   -
TrLCRa2: ------------------------------------------------------------ :   -
TrLCRa3: ------------------------------------------------------------ :   -
TrLCRa4: CATGGAAATTTGCTGAAGAAAATG------------------------------------ : 619
TrLCRa5: CATGGAAATTTGCTGAAGAAAATGACNTTGAT---------------------------- : 619
TrLCRa6: CATGGAAATTTGCTGAAGAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 421
TrLCRa7: CATGGAAATTTGCTGAAGAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 394

                  *       680         *       700         *       720
TrLCRa1: ------------------------------------------------------------ :   -
TrLCRa2: ------------------------------------------------------------ :   -
TrLCRa3: ------------------------------------------------------------ :   -
TrLCRa4: ------------------------------------------------------------ :   -
TrLCRa5: ------------------------------------------------------------ :   -
TrLCRa6: CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTTGGCTTGGCAATGTCTCTAATAA : 481
TrLCRa7: CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTTGGCTTGGCAATGTCTCTAATAA : 454
```

FIGURE 67 (cont)

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```
                  *        740         *        760         *        780
TrLCRa1 : ------------------------------------------------------------ :    -
TrLCRa2 : ------------------------------------------------------------ :    -
TrLCRa3 : ------------------------------------------------------------ :    -
TrLCRa4 : ------------------------------------------------------------ :    -
TrLCRa5 : ------------------------------------------------------------ :    -
TrLCRa6 : CAGGCAATGATTTCCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTCGTTAT :  541
TrLCRa7 : CAGGCAATGATTTCCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTCGTTAT :  514

                  *        800         *        820         *
TrLCRa1 : ----------------------------------------------------- :    -
TrLCRa2 : ----------------------------------------------------- :    -
TrLCRa3 : ----------------------------------------------------- :    -
TrLCRa4 : ----------------------------------------------------- :    -
TrLCRa5 : ----------------------------------------------------- :    -
TrLCRa6 : CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGG-------- :  586
TrLCRa7 : CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGGCAGAGAAG :  567
```

FIGURE 67 (cont)

```
                      *        20         *        40         *        60
TrF3'5'Ha: GGAACCAATTTGTCGGACTTTTTCCCGGGTTGGCCCGATTCGATTTGCAGGGTGTGGTG : 60

                      *        80         *       100         *       120
TrF3'5'Ha: AAAGAGATGGATGTCTTGGTTCCACGTTTTGATAGCATATTTGAAAAAATGATTGGTGAA :120

                      *       140         *       160         *       180
TrF3'5'Ha: CGTAAGAAGAAGGAAGTGGAGGGGAAAGAAAATGAAAGTAAGGATTTTCTGCAGTTTTTG :180

                      *       200         *       220         *       240
TrF3'5'Ha: TTGAATTTGAAGGATGAGGGTGATTCTAAGACTCCATTCACAATTACCCATGTTAAGGCT :240

                      *       260         *       280         *       300
TrF3'5'Ha: CTACTCATGGACATGGTTGTGGGTGGATCAGACACATCCTCCAACACAATTGAGTTTGCA :300

                      *       320         *       340         *       360
TrF3'5'Ha: TTGGCAGAAATGATGAACAACCCAGAAGTAATGAGGAAGGTTCAAGAGGAATTAGAAGAT :360

                      *       380         *       400         *       420
TrF3'5'Ha: GTAGTTGGGAAAGATAACTTAGTAGAAGAGTCTCACATTCATAAGCTACCCTACTTGCAT :420

                      *       440         *       460         *       480
TrF3'5'Ha: GCAGTGATGAAAGAAACACTTCGTTTACACCCAGCACTTCCACTTTTAGTCCCTCACTGT :480

                      *       500         *       520         *       540
TrF3'5'Ha: CCAAGTGAAACCACCAATGTTGGAGGCTACACAATTCCAAAGGGATCTCGTGTGTTTGTG :540

                      *       560         *       580         *
TrF3'5'Ha: AACGTTTGGGCTATTCATAGAGACCCTTCCATTTGGGAGAAACCACTAGAATTTGAT :597
```

FIGURE 68

```
                          *        20         *        40         *        60
TrF3'5'Ha: GTNLSDFFPGLARFDLQGVVKEMDVLVPRFDSIFEKMIGERKKKEVEGKENESKDFLQFL : 60

                          *        80         *       100         *       120
TrF3'5'Ha: LNLKDEGDSKTPFTITHVKALLMDMVVGGSDTSSNTIEFALAEMMNNPEVMRKVQEELED :120

                          *       140         *       160         *       180
TrF3'5'Ha: VVGKDNLVEESHIHKLPYLHAVMKETLRLHPALPLLVPHCPSETTNVGGYTIPKGSRVFV :180

                          *
TrF3'5'Ha: NVWAIHRDPSIWEKPLEFD :199
```

FIGURE 69

```
                      *        20          *        40          *        60
TrF3'5'Hb: GNAATCCACNAATCTCTTGAANTAATACCATTTCTTTACAAGAACTTAACCATGGTGATG : 60

                      *        80          *       100          *       120
TrF3'5'Hb: ATCACTCAATACCAAACCTTCCTTTACAAAGAACTTTCTATATCCTTTTTCATTTTCTTG :120

                      *       140          *       160          *       180
TrF3'5'Hb: ATAACCCATTTCATCATAAGTTTTCTCTTCAAAAAAAATCTCAAAAAACTTCCACCAGGC :180

                      *       200          *       220          *       240
TrF3'5'Hb: CCAAAAGGTTTTCCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCTCATGTTACC :240

                      *       260          *       280          *       300
TrF3'5'Hb: CTATTCAAAATGTCACAAAAATATGGTCCCATAATGTACCTAAAAATGGGATCAAATAAC :300

                      *       320          *       340          *       360
TrF3'5'Hb: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT :360

                      *       380          *       400          *       420
TrF3'5'Hb: TTCTCCAATAGACCGCCGAACGCTGGCGCAACTCACCTAGCTTATGATTCACAAGACTTG :420

                      *       440          *       460          *       480
TrF3'5'Hb: GTTTTCGCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACTTGCACATG :480

                      *       500          *       520          *       540
TrF3'5'Hb: CTCGGCGGAAAAGCCCTCGAAAATTGGTCGAAAGTTCGTGAGATTGAAATGGGTCACATG :540

                      *       560          *       580          *       600
TrF3'5'Hb: ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATCCGTTGTTGTGGCCGAAATGTTG :600

                      *       620          *       640          *       660
TrF3'5'Hb: ACATATGCTATGGCCAATATGATAGGTCAAGTTATATTGAGTCGTCGCGTGTTCGAGACA :660

                      *       680          *       700
TrF3'5'Hb: AAAGGTAGTGACTCAAATGAATTTAAGGATATGGTTGNTG :700
```

FIGURE 70

```
                       *        20         *        40         *        60
TrF3'5'Hb: MVMITQYQTFLYKELSISFFIFLITHFIISFLFKKNLKKLPPGPKGFPVVGALPLMGSMP : 60

                       *        80         *       100         *       120
TrF3'5'Hb: HVTLFKMSQKYGPIMYLKMGSNNMVVASTPSSAKAFLKTLDLNFSNRPPNAGATHLAYDS :120

                       *       140         *       160         *       180
TrF3'5'Hb: QDLVFADYGSRWKLLRKLSNLHMLGGKALENWSKVREIEMGHMIRTMYDCSKKDESVVVA :180

                       *       200         *
TrF3'5'Hb: EMLTYAMANMIGQVILSRRVFETKGSDSNEFKDMVX :216
```

FIGURE 71

```
                      *        20         *        40         *        60
TrF3'5'Hb1: GNAATCCACNAATCTCTTGAATTAATNCCATTTCTTTACAAGAACTTAACCATGGTGATG : 60
TrF3'5'Hb2: ------GNCAAATCTCTTGCANTAANNCCATTTCTTTACAAGAACTTAACCATGGTGATG : 54
TrF3'5'Hb3: --------CNAATCTCTTGAANTNATACCATTTCTTTACAAGAACTTAACCNTGGTGATG : 52
TrF3'5'Hb4: ------------TCTCTTGNAATNATACCATTTCTTTACAAGAACTTAACCNTGGTGATG : 48

                      *        80         *       100         *       120
TrF3'5'Hb1: ATCACTCAATACCAAACCTTCCTTTTCAAAGAACTTTCTATCTCCTTTTTCATTTTCTTG :120
TrF3'5'Hb2: ATCACTCAAGACCAAACCTTCCTTTACAAAGAACTTTCTATATCCTTTTTCATTTTCTTG :114
TrF3'5'Hb3: ATNNCTCAATACCAAACCTTCCTTTTCAAAGAACTTTCTATCTCCTTTTTCATTTTCTTG :112
TrF3'5'Hb4: ATNNCTCNATACCAAACCTTCCTTTACAAAGAACTTTCTATATCCTTTTTCATTTTCTTG :108

                      *       140         *       160         *       180
TrF3'5'Hb1: ATAACCCGTTTCATCATAAGTTTTCTCTTCAAAAAAAATCTCAAAAAACTTCCACCAGGC :180
TrF3'5'Hb2: ATAACCCATTTCATCATTAGTTTTCTCTTCAAAAAAAATCTCAAAAAACTTCCACCAGGC :174
TrF3'5'Hb3: ATAACCCGTTTCATCATAAGTCTTCTCTTCAAAAAAAATCTCAAAAAACTTCCACCAGGC :172
TrF3'5'Hb4: ATAACCCATTTCATCATTAGTTTTCTCTTCAAAAAAAATCTCAAAAAACTTCCACCAGGC :168

                      *       200         *       220         *       240
TrF3'5'Hb1: CCAAAGGGTTTTCCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCTCATGTTACC :240
TrF3'5'Hb2: CCAAAAGGTTTTCCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCTCATGTTACC :234
TrF3'5'Hb3: CCAAAGGGTTTTCCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCTCATGTTACC :232
TrF3'5'Hb4: CCAAAAGGTTTTCCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCTCATGTTACC :228

                      *       260         *       280         *       300
TrF3'5'Hb1: CTATTCAAAATGTCACAAAAATATGGTCCCATAATGTACCTAAAAATGGGATCAAATAGC :300
TrF3'5'Hb2: CTATTCAAAATGTCACAAAAATATGGTCCTATAATGTACCTAAAAATGGGATCAAATAAC :294
TrF3'5'Hb3: CTATTCAAAATGTCACAAAAATATGGTCCCATAATGTACCTAAAAATGGGATCAAATAAC :292
TrF3'5'Hb4: CTATTCAAAATGTCACAAAAATATGGTCCTATAATGTACCTAAAAATGGGATCAAATAAC :288

                      *       320         *       340         *       360
TrF3'5'Hb1: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT :360
TrF3'5'Hb2: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT :354
TrF3'5'Hb3: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT :352
TrF3'5'Hb4: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTTCTCAAAACACTTGACCTAAAT :348

                      *       380         *       400         *       420
TrF3'5'Hb1: TTCTCCAATAGACCGCCGAACGCTGGCGCGACTCACCTAGCTTATGATTCACAAGACTTG :420
TrF3'5'Hb2: TTCTCCAATAGGCCGTCGAACGCTGGCGCAACTCACCTAGCTTATGATCCACAAGACTTG :414
TrF3'5'Hb3: TTCTCCAATAGACCGCCGAACGCTGGCGCGACTCACCTAGCTTATGATTCACAAGACTTG :412
TrF3'5'Hb4: TTCTCCAATAGGCCGTCGAACGCTGGCGCAACTCACCTAGCTTATGATTCACAAGACTTG :408

                      *       440         *       460         *       480
TrF3'5'Hb1: GTTTTCGCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACTTGCACATG :480
TrF3'5'Hb2: GTTTTCGCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACTTGCACATG :474
TrF3'5'Hb3: GTTTTCGCCGACTATGGATCTAGGTGGAAATTGCTTAGGAAACTAAGTAACTTGCACATG :472
TrF3'5'Hb4: GTTTTCGCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAGTAACTTGCACATG :468

                      *       500         *       520         *       540
TrF3'5'Hb1: CTCGGCGGAAAAGCCCTCGAAGATTGGTCGAAAGTTCGTGAGATTGAAATGGGTCACATG :540
TrF3'5'Hb2: CTCGGCGGAAAAGCCCTTGAAAATTGGTCGAAAGTTCGTGAGATTGAAATGGGTCACATG :534
TrF3'5'Hb3: CTCGGCGGAAAAGCCCTCGAAGATTGGTCGAAAGTTCGCGAGATTGAGATGGGTCACATG :532
TrF3'5'Hb4: CTCGGCGGAAAAGCCCTTGAAAATTGGTCGAAAGTTCGTGAGATTGAAATGGGTCACATG :528
```

FIGURE 72

```
                       *       560         *       580         *       600
TrF3'5'Hb1: ATTCGTACAATGTATGATTGTAGCAAGAAAGACGAATCCGTTGT---------------- :584
TrF3'5'Hb2: ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATCCGTTGTTGTGGCCCGAAATGTTG :594
TrF3'5'Hb3: ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATATGTTGTTGTG------------ :580
TrF3'5'Hb4: ATTCGTACAATGTACGATTGTAGCAAGAAAGACGAATCCGNTGNTG-------------- : 74

                       *       620         *       640         *       660
TrF3'5'Hb1: ------------------------------------------------------------ :  -
TrF3'5'Hb2: ACATATGCTATGGCCAATATGATAGGTCAAGTTATATTGAGTCGTCGCGTGTTCGAGACA :654
TrF3'5'Hb3: ------------------------------------------------------------ :  -
TrF3'5'Hb4: ------------------------------------------------------------ :  -

                       *       680         *       700
TrF3'5'Hb1: ---------------------------------------- :  -
TrF3'5'Hb2: AAAGGTAGTGACTCAAATGAATTTAAGGATATGGTTGNTG :694
TrF3'5'Hb3: ---------------------------------------- :  -
TrF3'5'Hb4: ---------------------------------------- :  -
```

FIGURE 72 (cont)

```
                 *        20         *        40         *        60
TrF3Ha : GCACACNTCTATTTATTTCTACTTAAACCTNACAAAAAATAANACCCACAAAACACAAAC :  60

                 *        80         *       100         *       120
TrF3Ha : ACCACAAACACCAAAACCGAGTCCGTTTCCTNNTCNAACATGGCACCAAGCCAAACTCTA : 120

                 *       140         *       160         *       180
TrF3Ha : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT : 180

                 *       200         *       220         *       240
TrF3Ha : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 240

                 *       260         *       280         *       300
TrF3Ha : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT : 300

                 *       320         *       340         *       360
TrF3Ha : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 360

                 *       380         *       400         *       420
TrF3Ha : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC : 420

                 *       440         *       460         *       480
TrF3Ha : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 480

                 *       500         *       520         *       540
TrF3Ha : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG : 540

                 *       560         *       580         *       600
TrF3Ha : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT : 600

                 *       620         *       640         *       660
TrF3Ha : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 660

                 *       680         *       700         *       720
TrF3Ha : ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT : 720

                 *       740         *       760         *       780
TrF3Ha : GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAATTACTCTTTTG : 780
```

FIGURE 73

```
                      *        800         *        820         *        840
TrF3Ha : CTTCAAGATCAAGTTGGTGGCCTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA :  840

                      *        860         *        880         *        900
TrF3Ha : GTTCAACCAGTTGAAGGTGCTTTTGTTGTTAATCTTGGAGACCATGGTCACTATCTAAGT :  900

                      *        920         *        940         *        960
TrF3Ha : AATGGACGGTTCAAAAATGCTGACCACCAAGCAGTGGTGAATTCGAACTACAGCCGNTTA :  960

                      *        980         *       1000         *       1020
TrF3Ha : TCAATAGCAACATTTCAAAATCCAGCTCCCGATGCAACTGTATACCCTTTGAAGATTAGA : 1020

                      *       1040         *       1060         *       1080
TrF3Ha : GAGGGTGAAAAATCTGTGTTGGAAGAACCAATCACTTTTGCTGAAATGTATAGAAGGAAG : 1080

                      *       1100         *       1120         *       1140
TrF3Ha : ATGACCAAAGACCTTGAAATTGCTAGGATGAAGAAGTTGGCTAAGGAACAACAACTTAGG : 1140

                      *       1160         *       1180         *       1200
TrF3Ha : GACTTGGAGGAGAACAAGACTAAATATGAGGCCAAACCTTTGAATGAGATCTTTGCTTAA : 1200

                      *       1220         *       1240         *       1260
TrF3Ha : TTAATTAGTCTTAATTTAAATAATTAATAAATTTTAGACTTAATTTACATATAATAATTT : 1260

TrF3Ha : T : 1261
```

FIGURE 73 (cont)

```
                         *        20         *        40         *         6
TrF3Ha  :  MAPSQTLSYLSQQNTLESSFVREEDERPKVAYNNFSNEIPIISLAGIDEVDGRRTEICNK  :   59

                         *        80         *       100         *       120
TrF3Ha  :  IVEACENWGIFQVVDHGVDTKLVSEMTRFAREFFALPPEEKLRFDMSGGKKGGFIVSSHL  :  120

                         *       140         *       160         *       180
TrF3Ha  :  QGEAVKDWRELVTYFSYPIKQRDYSRWPDKPEGWKEVTEKYSENLMNLACKLLEVLSEAM  :  180

                         *       200         *       220         *       240
TrF3Ha  :  GLEKEALTKACVDMDQKVVINYYPKCPEPDLTLGLKRHTDPGTITLLLQDQVGGLQATKD  :  240

                         *       260         *       280         *       300
TrF3Ha  :  NGKTWITVQPVEGAFVVNLGDHGHYLSNGRFKNADHQAVVNSNYSXLSIATFQNPAPDAT  :  300

                         *       320         *       340         *       360
TrF3Ha  :  VYPLKIREGEKSVLEEPITFAEMYRRKMTKDLEIARMKKLAKEQQLRDLEENKTKYEAKP  :  360

TrF3Ha  :  LNEIFA  :  366
```

FIGURE 74

```
                     *        20         *        40         *        60
TrF3Ha1  : GCACACNTCTATTTATTTCTACTTAAACCTCACAAAAAATAA-ACCCACAACACACAAAC : 59
TrF3Ha2  : GCACNGNTCTATTTATTTCTACTTAAACCT---NAAAAATAA-ACCCACAA--CAC-AA- : 52
TrF3Ha3  : -CACACNTCTATTTATTTCTACTTAAACCTNACAAAAAATAANACCCACAACACACAAAC : 59
TrF3Ha4  : --TCCCCTCTANTTATTTCTNCTTAAACCTNNCAAAAATNANNACCCACAACACACNAAN : 58
TrF3Ha5  : -------------------------------------GTTAACACAC-NCCAACACAAAC : 22
TrF3Ha6  : ---------------------------------------GNA-ACCCACAACACACAAAC : 20
TrF3Ha7  : --------------------------------------------CACACNAACNCCAAAC : 16
TrF3Ha8  : --------------------------------------------CACNACNACCACAAAC : 16
TrF3Ha9  : ---------------------------------------------CCACANCACAC-AA- : 13
TrF3Ha10 : -----------------------------------------------GAANCCCACNAAC : 13
TrF3Ha11 : -----------------------------------------------GNACCACACAAAC : 13
TrF3Ha12 : -----------------------------------------------GGCA--CAC-AA- :  9
TrF3Ha13 : ------------------------------------------------TCTAACACAAAC : 12
TrF3Ha14 : ------------------------------------------------CNCAACACAAAC : 12
TrF3Ha15 : -------------------------------------------------GNNAATCCACA : 11
TrF3Ha16 : --------------------------------------------------GAACCCCACA : 10
TrF3Ha17 : ---------------------------------------------------AACCCCACG :  9
TrF3Ha18 : ----------------------------------------------------GCACNAAC :  8
TrF3Ha19 : ------------------------------------------------------AC-ANC :  5
TrF3Ha20 : ------------------------------------------------------GCNNCA :  6
TrF3Ha21 : ------------------------------------------------------GNACCC :  6
TrF3Ha22 : -------------------------------------------------------CTACA :  5
TrF3Ha23 : --------------------------------------------------------CACA :  4
TrF3Ha24 : ---------------------------------------------------------ACA :  3
TrF3Ha25 : ---------------------------------------------------------CCA :  3
TrF3Ha26 : ----------------------------------------------------------GC :  2
TrF3Ha27 : ----------------------------------------------------------CA :  2
TrF3Ha28 : ----------------------------------------------------------GC :  2
TrF3Ha29 : -----------------------------------------------------------A :  1
TrF3Ha30 : ------------------------------------------------------------ :  -
TrF3Ha31 : ------------------------------------------------------------ :  -
TrF3Ha32 : ------------------------------------------------------------ :  -
TrF3Ha33 : ------------------------------------------------------------ :  -
TrF3Ha34 : ------------------------------------------------------------ :  -
TrF3Ha35 : ------------------------------------------------------------ :  -
TrF3Ha36 : ------------------------------------------------------------ :  -
TrF3Ha37 : ------------------------------------------------------------ :  -
TrF3Ha38 : ------------------------------------------------------------ :  -
TrF3Ha39 : ------------------------------------------------------------ :  -
TrF3Ha40 : ------------------------------------------------------------ :  -
TrF3Ha41 : ------------------------------------------------------------ :  -
```

FIGURE 75

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```
                         *        80          *        100          *        120
TrF3Ha1  : ACCAAAAACAG-AGCACCGTTTCCATCATC---A--AACATGGCACCAAGCCAAACTCTA :113
TrF3Ha2  : ACCAAAAACAG-AGCACCGTTTCCATCATC---A--AACATGGCACCAAGCCAAACCCTA :106
TrF3Ha3  : ACCAAAAACAGNAGCACCGTTTCCATCATCNNNANNAACATGGCACCAAGCCAAACTCTA :119
TrF3Ha4  : ANCACCAAANANACAGNAGTAGCGTTTCCATCATCAAACATGGCACCAAGCCAAACTCTA :118
TrF3Ha5  : ACCAAAAACAGNANCACCGTTTCC-A-TNCA-T:CAAACATGGCACCAAGCCAAACTCTA :  78
TrF3Ha6  : A-CCAAAACAG-AG-NCCGTTTCN-TNATC---A--AACATGGCACCAAGCCAAACTCTA :  71
TrF3Ha7  : ACCAAAAACAGNANCACCGTTTCC-A-TNCA-TNCAAACATGGCACCAAGCCAAACTCTA :  73
TrF3Ha8  : ACCAAAAACAGNANCACCGTTTCC-A-TNCA-T:CAAACATGGCACCAAGCCAAACTCTA :  72
TrF3Ha9  : A-CACCAAA-A-ACAGAAGCACCGTTTCCATCATCAAACATGGCACCAAGCCAAACTCTA :  70
TrF3Ha10 : ANCAAACACNCAAAAANAGAGACCGTTTCCTNNTNNAACATGGCACCAAGCCAAACTCTA :  73
TrF3Ha11 : ACCCAAAACAG-AGCACCGTTTCC-TNATC---A--ACAATGGCACCAAGCCAAACTCTA :  66
TrF3Ha12 : ACC--AAAC-G-AGC-CCGTTTCC-T-NT----N--AACATGGCACCAAGCCAAACCCTA :  57
TrF3Ha13 : ACCAAAAACAG-AGNACCGTTTCC-TNTCC---A--A-CATGGCACCAAGCCAAACTCTA :  64
TrF3Ha14 : ACCAAAAACAGNANCACCGTTTCC-A-TNCA-TNCAAACATGGCACCAAGCCAAACTCTA :  69
TrF3Ha15 : AC-NCAAACNCCANAAACGAGCCCGTTTCCTNCTCNAACATGGCACCAAGCCAAACTCTA :  71
TrF3Ha16 : ACCCCAAACCCA-AAACGAGNCCGTTTCCT-NTC-AACATGGCACCAAGCCAAACTCTA :  67
TrF3Ha17 : ACACANAACCCANAAACGAGCCCGTTTCCTNNTCNAACATGGCACCAAGCCAAACTCTA :  69
TrF3Ha18 : ANCACAAACNCCAAAANGAGACCGTTTCCTNNTNAAACATGGCACCAAGCCAAACTCTA :  68
TrF3Ha19 : A-CNNNANN-C-CAAACGAGTCCGTTCCCT-NT-NAACATGGCACCAAGCCAAACTCTA :  60
TrF3Ha20 : ANCACAAACNCNAAAACGAGCACCGTTTCCTANTNNAACATGGCACCAAGCCAAACTCTA :  66
TrF3Ha21 : ACANCAAACNCCANAAACGAGCCCGTTTCCTNCTNNAACATGGCACCNAGCCAAACTCTA :  66
TrF3Ha22 : ACCNNAAACNCCA-AAACGAGNCCGTTTCCT-CTC-AACATGGCACCAAGCCAAACTCTA :  62
TrF3Ha23 : AC--CNNACNCCA-AAACGAGCCCGTTTCCT-CTN-AACATGGCACCAAGCCAAACTCTA :  60
TrF3Ha24 : AC--CAAAC-CCA-AAACGAGCCCGTTTCCT-NTC-AACATGGCACCAAGCCAAACTCTA :  58
TrF3Ha25 : AC--CAAACACCA-AAACGAGNCCGTTTCCT-NTC-AACATGGCACCAAGCCAAACTCTA :  59
TrF3Ha26 : NCCACAAAAACCAAAA-CGAGCCCGTTTCC--TATCAACATGGCACCAAGCCAAACTCTA :  59
TrF3Ha27 : ACANCAAACNCCANAAACGAGCCCGTTTCNTNCTCNAACATGGCACCAAGCCAAACTCTA :  62
TrF3Ha28 : ACANCAAACACCANAAACGAGNCCGTTTCCTNNTCNAACATGGCACCAAGCCAAACTCTA :  62
TrF3Ha29 : ACCNNAAACNC-AGNNCCGTTTCN-TNNTN---A--A-CATGGC-CC-AGCCAAACTCTA :  51
TrF3Ha30 : A-CCCCACC-T-NAAACCGAGACCGTTNCCT-NT-NAACATGGCACCAAGCCAAACTCTA :  55
TrF3Ha31 : -GCNNAAACACCANAAACGAGCCCGTTTCCTNNTCGAACATGGCACCAAGCCAAACTCTA :  59
TrF3Ha32 : -CAACACCCCCCA-AAACGAGCCCGTTTCCT-NTC-AACATGGCACCAAGCCAAACTCTA :  56
TrF3Ha33 : ----CAAAC-C-AAAACNGAGNCCGTTTCCTA-TN-AACATGGCACCAAGCCAAACTCTA :  52
TrF3Ha34 : -----NAAC-C-AAAACG-AGNCCGTTTCNTNCTC-AACATGGCTCCTAGCCAAACTCTA :  51
TrF3Ha35 : ------CAAACCAAAACNGAGCCCGTNTTCNNTNTNAACATGGCNACCAGCCAAACCCTA :  54
TrF3Ha36 : -------AACACCNACACGAGNCCGTTTCNTNNTNNAACATGGCNCCNAGCCAAACTCTA :  53
TrF3Ha37 : --------AACCAAANCCGAGNCCGTTTCCNNNTNTNAACATGGCNCCAAGCCAAACCCTA :  52
TrF3Ha38 : --------AACCAAAANCGAGNCCGTNTTCNNNATNAACATGGCNCCNAGCCAAACCCTA :  52
TrF3Ha39 : -----------------------------------------------------------T :   1
TrF3Ha40 : ------------------------------------------------------------ :   -
TrF3Ha41 : ------------------------------------------------------------ :   -
```

FIGURE 75 (cont)

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```
                    *       140         *        160         *        180
TrF3Ha1  : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :173
TrF3Ha2  : AGTTATCTCTCACAACAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :166
TrF3Ha3  : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :179
TrF3Ha4  : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :178
TrF3Ha5  : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :138
TrF3Ha6  : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :131
TrF3Ha7  : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :133
TrF3Ha8  : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :132
TrF3Ha9  : AGTTATCTNGGACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGACCGT :130
TrF3Ha10 : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :133
TrF3Ha11 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :126
TrF3Ha12 : AGTTATCTCTC-CAACAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :116
TrF3Ha13 : AGTTATCTCTCACCACAAAACACTCTTGAGTNAAGTTTCGTTAGGGAAGAAGATGAGCGT :124
TrF3Ha14 : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :129
TrF3Ha15 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :131
TrF3Ha16 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :127
TrF3Ha17 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :129
TrF3Ha18 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :128
TrF3Ha19 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :120
TrF3Ha20 : AGTTATCTCTCACAACAAAAAACCGTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :126
TrF3Ha21 : AGTTATCTCTNNCAACAAAACACTCTTGAGTCNAGTTTCGTTAGGGAAGAAGATGAGCGT :126
TrF3Ha22 : AGTTATCTCTCACAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :122
TrF3Ha23 : AGTTATCTCTC-CAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :119
TrF3Ha24 : AGTTATCTCTN-CAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :117
TrF3Ha25 : AGTTATCTCTC-CCACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :118
TrF3Ha26 : AGTTATCTCTCACAACAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :119
TrF3Ha27 : AGTTATCTCTCNCAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :122
TrF3Ha28 : AGTTATCTCTCNCAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :122
TrF3Ha29 : AGTTATCTCTC-CAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :110
TrF3Ha30 : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :115
TrF3Ha31 : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :119
TrF3Ha32 : AGTTATCTCTCACAACAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :116
TrF3Ha33 : AGTTATCTCTCACAACAAAAAACCGTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :112
TrF3Ha34 : AGTTATCTCTC-CCACAAAACACTCTTGAGTCA-GTTTCGTTAGGGAAGAAGATGAGCGT :109
TrF3Ha35 : AGTTATCTCTCACAACAAAAGACTCTTGAGTCNAGTTTCGTTAGGGAAGAAGATGAGCGT :114
TrF3Ha36 : AGTTATCTCTCNCAACAAAACACTCTCGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :113
TrF3Ha37 : AGTTATCTCTCACAACAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :112
TrF3Ha38 : AGTTATCTCTCACAACAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :112
TrF3Ha39 : NGATNTNTCTNNNNACNAAACNCTCNTCAGTNANGTTTCGTTCGGAANGAAGATGAGCGT :  61
TrF3Ha40 : ------------------------------------------------------------ :   -
TrF3Ha41 : ------------------------------------------------------------ :   -
```

FIGURE 75 (cont)

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```
                           *       200         *        220         *        240
TrF3Ha1  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 233
TrF3Ha2  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 226
TrF3Ha3  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 239
TrF3Ha4  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 238
TrF3Ha5  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 198
TrF3Ha6  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 191
TrF3Ha7  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 193
TrF3Ha8  : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 192
TrF3Ha9  : CCAAAAGTTGCCTACAATACCTTCAGCACCGAGATTCCAATCNTTTCTCTTGCTGGAATT : 190
TrF3Ha10 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 193
TrF3Ha11 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 186
TrF3Ha12 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 176
TrF3Ha13 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 184
TrF3Ha14 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 189
TrF3Ha15 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 191
TrF3Ha16 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 187
TrF3Ha17 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 189
TrF3Ha18 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 188
TrF3Ha19 : CCAAAAGTTGCCTACAATAACTTCAGCAACNAGATTCCAATCATTTCTCTTGCTGGAATT : 180
TrF3Ha20 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 186
TrF3Ha21 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 186
TrF3Ha22 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 182
TrF3Ha23 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 179
TrF3Ha24 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 177
TrF3Ha25 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 178
TrF3Ha26 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 179
TrF3Ha27 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 182
TrF3Ha28 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 182
TrF3Ha29 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 170
TrF3Ha30 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 175
TrF3Ha31 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 179
TrF3Ha32 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 176
TrF3Ha33 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 172
TrF3Ha34 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTNCTCTTGCTGGAATT : 169
TrF3Ha35 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 174
TrF3Ha36 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 173
TrF3Ha37 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 172
TrF3Ha38 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTTCTCTTGCTGGAATT : 172
TrF3Ha39 : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATNATTTCTCTTGCTGGAATT : 121
TrF3Ha40 : ------------------------------------------------------------ :   -
TrF3Ha41 : ------------------------------------------------------------ :   -
```

FIGURE 75 (cont)

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```
                          *        260         *        280         *        300
TrF3Ha1  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :293
TrF3Ha2  : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :286
TrF3Ha3  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :299
TrF3Ha4  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :298
TrF3Ha5  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :258
TrF3Ha6  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :251
TrF3Ha7  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :253
TrF3Ha8  : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :252
TrF3Ha9  : GATGAGGTTGATGGCCGAAAAACANAAATNTTTACCAAGATTGGNGGGGCTTGTNAAAAT :250
TrF3Ha10 : GATGAGGTTGATGGNCNCACANCACACATCTGNNCCANATTGCTCGAACCTNGCGANAGN :253
TrF3Ha11 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :246
TrF3Ha12 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :236
TrF3Ha13 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :244
TrF3Ha14 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :249
TrF3Ha15 : GATGAGGTTGATGGTCGAAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :251
TrF3Ha16 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :247
TrF3Ha17 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :249
TrF3Ha18 : GATGAGGTTGATGGNNNNCGNACNNCGNNATGTGGNNAGAGCAGCNNN------------ :236
TrF3Ha19 : GATGAGGTTGATGGTCGNAGAACANAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :240
TrF3Ha20 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :246
TrF3Ha21 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :246
TrF3Ha22 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :242
TrF3Ha23 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :239
TrF3Ha24 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :237
TrF3Ha25 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :238
TrF3Ha26 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :239
TrF3Ha27 : GATGAGGTTGATGGTCGAAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :242
TrF3Ha28 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :242
TrF3Ha29 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :230
TrF3Ha30 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :235
TrF3Ha31 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :239
TrF3Ha32 : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :236
TrF3Ha33 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :232
TrF3Ha34 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :229
TrF3Ha35 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :234
TrF3Ha36 : GATGAGGTTGATGGTCGAAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :233
TrF3Ha37 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :232
TrF3Ha38 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :232
TrF3Ha39 : GATGAGGTTGATGGTCGCAGAACAGAGATATGTAACAAGATTGTTGAAGCTTGTGAGAAT :181
TrF3Ha40 : -------------------------------GTNACCAGNNTGTTG-ANCTTGTGAGNAT : 28
TrF3Ha41 : ------------------------------------------------------------ :  -
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FIGURE 75 (cont)

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                      *       320         *       340         *       360
TrF3Ha1  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 353
TrF3Ha2  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 346
TrF3Ha3  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 359
TrF3Ha4  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 358
TrF3Ha5  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 318
TrF3Ha6  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 311
TrF3Ha7  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 313
TrF3Ha8  : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 312
TrF3Ha9  : TGGGGTNTTTTTCAGGTTGGTGATCATGGGGTNNA-ACAAAACTTGTTTCCCANAAANCC : 309
TrF3Ha10 : CGCCCGTNCCTCNCN--------------------------------------------- : 267
TrF3Ha11 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 306
TrF3Ha12 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 296
TrF3Ha13 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 304
TrF3Ha14 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 309
TrF3Ha15 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 311
TrF3Ha16 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 307
TrF3Ha17 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 309
TrF3Ha18 : ------------------------------------------------------------ :   -
TrF3Ha19 : TGGGGTATTTTTCANGTTGTTGATCATGGNGTN--------------------------- : 273
TrF3Ha20 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 306
TrF3Ha21 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 306
TrF3Ha22 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 302
TrF3Ha23 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 299
TrF3Ha24 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 297
TrF3Ha25 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 298
TrF3Ha26 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 299
TrF3Ha27 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 302
TrF3Ha28 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 302
TrF3Ha29 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 290
TrF3Ha30 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 295
TrF3Ha31 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 299
TrF3Ha32 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 296
TrF3Ha33 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 292
TrF3Ha34 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAANCTTGTTTCTGAGATGACC : 289
TrF3Ha35 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 294
TrF3Ha36 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAACTTGTTTCTGAGATGACC : 293
TrF3Ha37 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 292
TrF3Ha38 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 292
TrF3Ha39 : TGGGGTATTTTTCAGGTTGGTGATCATGGTGTTGATACAAAGCTTGTTTCTGAGATGACT : 241
TrF3Ha40 : TGGGGTATTTTTCAGGTTGTTGATCATGGTGTTGATACAAGACTTGTTTCTGAGATGACC :  88
TrF3Ha41 : ------------------------------------------------------------ :   -
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FIGURE 75 (cont)

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                   *       380         *       400         *       420
TrF3Ha1  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :413
TrF3Ha2  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :406
TrF3Ha3  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :419
TrF3Ha4  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :418
TrF3Ha5  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :378
TrF3Ha6  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :371
TrF3Ha7  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :373
TrF3Ha8  : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :372
TrF3Ha9  : CNTTTTGNTAAANAGTTTTTTGCTTTNCCCCCGGAANAAAACCTCCGGTTTNACTTNNCC :369
TrF3Ha10 : ------------------------------------------------------------ :  -
TrF3Ha11 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha12 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :356
TrF3Ha13 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTNC :364
TrF3Ha14 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :369
TrF3Ha15 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :371
TrF3Ha16 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :367
TrF3Ha17 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :369
TrF3Ha18 : ------------------------------------------------------------ :  -
TrF3Ha19 : ------------------------------------------------------------ :  -
TrF3Ha20 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha21 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha22 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :362
TrF3Ha23 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :359
TrF3Ha24 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :357
TrF3Ha25 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :358
TrF3Ha26 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :359
TrF3Ha27 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :362
TrF3Ha28 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :362
TrF3Ha29 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :350
TrF3Ha30 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTNC :355
TrF3Ha31 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :359
TrF3Ha32 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :356
TrF3Ha33 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :352
TrF3Ha34 : CGTTTTGCTAGAGAGTTTTTTGCTNTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :349
TrF3Ha35 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :354
TrF3Ha36 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :353
TrF3Ha37 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :352
TrF3Ha38 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :352
TrF3Ha39 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCGCCGGAAGAGAAGCTCCGGTTTGACATGTCC :301
TrF3Ha40 : CGTTTTGCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :148
TrF3Ha41 : ------------------------------------------------------------ :  -
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FIGURE 75 (cont)

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                      *       440         *       460         *       480
TrF3Ha1  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :473
TrF3Ha2  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :466
TrF3Ha3  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :479
TrF3Ha4  : GGTGGTAAAAAGGGTGGNTTNATTGTCTGTANTNGTNTCCNAGGACAACCNGNGNAGGAT :478
TrF3Ha5  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :438
TrF3Ha6  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :431
TrF3Ha7  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :433
TrF3Ha8  : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :432
TrF3Ha9  : GGGGGNAAAAAAGGGGGGCGTTTNATTNGNCNTTAAGNCCCNCCCCAA-GGGANAANCCC :428
TrF3Ha10 : ------------------------------------------------------------ :  -
TrF3Ha11 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :426
TrF3Ha12 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :416
TrF3Ha13 : GGTGGTAAAAAGGGTGGTTTCATTGNCTCTAGTCATCTNCAAGGANAAGCANNGAANGAT :424
TrF3Ha14 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :429
TrF3Ha15 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :431
TrF3Ha16 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :427
TrF3Ha17 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :429
TrF3Ha18 : ------------------------------------------------------------ :  -
TrF3Ha19 : ------------------------------------------------------------ :  -
TrF3Ha20 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :426
TrF3Ha21 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :426
TrF3Ha22 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :422
TrF3Ha23 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :419
TrF3Ha24 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :417
TrF3Ha25 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :418
TrF3Ha26 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :419
TrF3Ha27 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :422
TrF3Ha28 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :422
TrF3Ha29 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :410
TrF3Ha30 : GGTGGNAAAAAGGNTGGCTTCANTGCCTGTANCCATCTCCAAGGAGAAGCACCCNANGAN :415
TrF3Ha31 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :419
TrF3Ha32 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :416
TrF3Ha33 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCGTCTCCAAGGAGAAGCAGTGAAAGAT :412
TrF3Ha34 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTNCAAGGANAAGCANTGAAGGAT :409
TrF3Ha35 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :414
TrF3Ha36 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :413
TrF3Ha37 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :412
TrF3Ha38 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAAGAT :412
TrF3Ha39 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTNNTCATCTCCAAGGAGAAGCAGNGAAAGAT :361
TrF3Ha40 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT :208
TrF3Ha41 : ------------------------------------------------------------ :  -
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FIGURE 75 (cont)

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```
                    *       500         *       520         *       540
TrF3Ha1  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :533
TrF3Ha2  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :526
TrF3Ha3  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :539
TrF3Ha4  : TGCAGAGAGCTNNN---------------------------------------------- :492
TrF3Ha5  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :498
TrF3Ha6  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :491
TrF3Ha7  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :493
TrF3Ha8  : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :492
TrF3Ha9  : ANNNAAG-GNT-TTGGAANANNCNNNN--------------------------------- :453
TrF3Ha10 : ------------------------------------------------------------ :  -
TrF3Ha11 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :486
TrF3Ha12 : TGGAGCGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :476
TrF3Ha13 : TGGAGAGAGCTNGNGACATATTTTTN---------------------------------- :450
TrF3Ha14 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :489
TrF3Ha15 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :491
TrF3Ha16 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :487
TrF3Ha17 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :489
TrF3Ha18 : ------------------------------------------------------------ :  -
TrF3Ha19 : ------------------------------------------------------------ :  -
TrF3Ha20 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :486
TrF3Ha21 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :486
TrF3Ha22 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :482
TrF3Ha23 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :479
TrF3Ha24 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :477
TrF3Ha25 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :478
TrF3Ha26 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :479
TrF3Ha27 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :482
TrF3Ha28 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :482
TrF3Ha29 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :470
TrF3Ha30 : TGN--------------------------------------------------------- :418
TrF3Ha31 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :479
TrF3Ha32 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAATAAAGAGATTATTCAAGGTGG :476
TrF3Ha33 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :472
TrF3Ha34 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :469
TrF3Ha35 : TGGAGCGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :474
TrF3Ha36 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :473
TrF3Ha37 : TGGAGCGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :472
TrF3Ha38 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :472
TrF3Ha39 : TGGAGANAGCTAGTGACATATTTNTCATACCCAATTAAACAAAGAGATTATNCAAGGTGG :421
TrF3Ha40 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :268
TrF3Ha41 : ------------------------------------------------------------ :  -
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FIGURE 75 (cont)

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```
                     *       560         *       580         *       600
TrF3Ha1  : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCT------- :586
TrF3Ha2  : CCAGACAAGCCAGAAGAATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :586
TrF3Ha3  : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :599
TrF3Ha4  : ------------------------------------------------------------ :  -
TrF3Ha5  : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :558
TrF3Ha6  : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :551
TrF3Ha7  : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :553
TrF3Ha8  : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :552
TrF3Ha9  : ------------------------------------------------------------ :  -
TrF3Ha10 : ------------------------------------------------------------ :  -
TrF3Ha11 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :546
TrF3Ha12 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :536
TrF3Ha13 : ------------------------------------------------------------ :  -
TrF3Ha14 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :549
TrF3Ha15 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :551
TrF3Ha16 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :547
TrF3Ha17 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :549
TrF3Ha18 : ------------------------------------------------------------ :  -
TrF3Ha19 : ------------------------------------------------------------ :  -
TrF3Ha20 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :546
TrF3Ha21 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :546
TrF3Ha22 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :542
TrF3Ha23 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :539
TrF3Ha24 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGC-- :535
TrF3Ha25 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :538
TrF3Ha26 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :539
TrF3Ha27 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :542
TrF3Ha28 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :542
TrF3Ha29 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :530
TrF3Ha30 : ------------------------------------------------------------ :  -
TrF3Ha31 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :539
TrF3Ha32 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :536
TrF3Ha33 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACANAAAAATACAGTGAAAACCTAATGAAT :532
TrF3Ha34 : CCAGACAAGCCAGAAGGATGGAAAGAGGTNACAGAAAAATACAGCGAAAACCTAATGAAT :529
TrF3Ha35 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :534
TrF3Ha36 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :533
TrF3Ha37 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :532
TrF3Ha38 : CCAGACAAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :532
TrF3Ha39 : TCANACNAGCCAGAAGGATGGAAAGAAGTAACAGAAAAATACAGTGAAAACCTAATGAAT :481
TrF3Ha40 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTAATGAAT :328
TrF3Ha41 : ------------------------------------------------------------ :  -
```

FIGURE 75 (cont)

```
                          *        620         *         640         *         660
TrF3Ha1   : ------------------------------------------------------------ :   -
TrF3Ha2   : TTAGCTTGCAG------------------------------------------------- : 597
TrF3Ha3   : TTAGCT------------------------------------------------------ : 605
TrF3Ha4   : ------------------------------------------------------------ :   -
TrF3Ha5   : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 618
TrF3Ha6   : TTAGCTTGCAAGCTATTGGAAG-------------------------------------- : 573
TrF3Ha7   : TTAGCTTGCAAACTATTGGAAGNTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 613
TrF3Ha8   : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 612
TrF3Ha9   : ------------------------------------------------------------ :   -
TrF3Ha10  : ------------------------------------------------------------ :   -
TrF3Ha11  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAG-------------------------- : 580
TrF3Ha12  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGGATTAGAAAN---------- : 586
TrF3Ha13  : ------------------------------------------------------------ :   -
TrF3Ha14  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 609
TrF3Ha15  : TTAGCTTGCAAACTATTGGAAGTTTTATCAG----------------------------- : 582
TrF3Ha16  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 607
TrF3Ha17  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGGTTN---------------- : 593
TrF3Ha18  : ------------------------------------------------------------ :   -
TrF3Ha19  : ------------------------------------------------------------ :   -
TrF3Ha20  : TTAGCTTGCAAGCTATTGGAAGTTTT---------------------------------- : 572
TrF3Ha21  : TTAGCTTGCAAACTATTGGAAGTTTTATC------------------------------- : 575
TrF3Ha22  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAG------ : 596
TrF3Ha23  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 599
TrF3Ha24  : ------------------------------------------------------------ :   -
TrF3Ha25  : TTAGCTTGCAAACTATTGGAN--------------------------------------- : 559
TrF3Ha26  : TTAGCTTGCAAGCTATTGGAAGTTTT---------------------------------- : 565
TrF3Ha27  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAN----------- : 591
TrF3Ha28  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 602
TrF3Ha29  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 590
TrF3Ha30  : ------------------------------------------------------------ :   -
TrF3Ha31  : TTAGCTTGCAAACTATTGGAAGTTTTATCAG----------------------------- : 570
TrF3Ha32  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 596
TrF3Ha33  : TTANCTTGCAAGCTATTGGAAGTTTTATCACAAGCANTGGGATTACAAAAAGAAGCTGTT : 592
TrF3Ha34  : TTANCTN----------------------------------------------------- : 536
TrF3Ha35  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAAT---------------------- : 572
TrF3Ha36  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGG-------------------- : 573
TrF3Ha37  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGG------------------- : 573
TrF3Ha38  : TTAGCTTGCAAGCTATTGGAAGTTTTATCAGAAGCAATGGGATTAGAAAAAG-------- : 584
TrF3Ha39  : TTACCTNGCAAGCTATTGGAAGTTTTATAATAANCNATGGNATTAAGA------------ : 529
TrF3Ha40  : TTAGCTTGCAAACTATTGGAAGTTTTATCAGAAGCAATGGGTTTAGAAAAAGAAGCTCTA : 388
TrF3Ha41  : ------------------------------------------------------------ :   -
```

FIGURE 75 (cont)

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```
                             *         680         *         700         *         720
TrF3Ha1  : ------------------------------------------------------------ :   -
TrF3Ha2  : ------------------------------------------------------------ :   -
TrF3Ha3  : ------------------------------------------------------------ :   -
TrF3Ha4  : ------------------------------------------------------------ :   -
TrF3Ha5  : ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT : 678
TrF3Ha6  : ------------------------------------------------------------ :   -
TrF3Ha7  : ACAAANGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT : 673
TrF3Ha8  : ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT : 672
TrF3Ha9  : ------------------------------------------------------------ :   -
TrF3Ha10 : ------------------------------------------------------------ :   -
TrF3Ha11 : ------------------------------------------------------------ :   -
TrF3Ha12 : ------------------------------------------------------------ :   -
TrF3Ha13 : ------------------------------------------------------------ :   -
TrF3Ha14 : ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGNTATAAATTATTACCCAAAATGCCCT : 669
TrF3Ha15 : ------------------------------------------------------------ :   -
TrF3Ha16 : ACA--------------------------------------------------------- : 610
TrF3Ha17 : ------------------------------------------------------------ :   -
TrF3Ha18 : ------------------------------------------------------------ :   -
TrF3Ha19 : ------------------------------------------------------------ :   -
TrF3Ha20 : ------------------------------------------------------------ :   -
TrF3Ha21 : ------------------------------------------------------------ :   -
TrF3Ha22 : ------------------------------------------------------------ :   -
TrF3Ha23 : ACAAAAGCATGTG----------------------------------------------- : 612
TrF3Ha24 : ------------------------------------------------------------ :   -
TrF3Ha25 : ------------------------------------------------------------ :   -
TrF3Ha26 : ------------------------------------------------------------ :   -
TrF3Ha27 : ------------------------------------------------------------ :   -
TrF3Ha28 : ACAAAAG----------------------------------------------------- : 609
TrF3Ha29 : ACAAAAG----------------------------------------------------- : 597
TrF3Ha30 : ------------------------------------------------------------ :   -
TrF3Ha31 : ------------------------------------------------------------ :   -
TrF3Ha32 : ACAAAAGCATGT------------------------------------------------ : 608
TrF3Ha33 : ACAANANCNT-------------------------------------------------- : 602
TrF3Ha34 : ------------------------------------------------------------ :   -
TrF3Ha35 : ------------------------------------------------------------ :   -
TrF3Ha36 : ------------------------------------------------------------ :   -
TrF3Ha37 : ------------------------------------------------------------ :   -
TrF3Ha38 : ------------------------------------------------------------ :   -
TrF3Ha39 : ------------------------------------------------------------ :   -
TrF3Ha40 : ACAAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAATTATTACCCAAAATGCCCT : 448
TrF3Ha41 : ----------------------ATCNAAAAGTTGTGATAAANTATTACCCNAAATGCCCT :  38
```

FIGURE 75 (cont)

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```
                      *       740         *       760         *       780
TrF3Ha1   : ------------------------------------------------------------ :   -
TrF3Ha2   : ------------------------------------------------------------ :   -
TrF3Ha3   : ------------------------------------------------------------ :   -
TrF3Ha4   : ------------------------------------------------------------ :   -
TrF3Ha5   : GAACCTGACCTT------------------------------------------------ :690
TrF3Ha6   : ------------------------------------------------------------ :   -
TrF3Ha7   : GAACCTGACCTCCCACTT-GCCGTAAACGNCACACTGACCCNGA---------------- :716
TrF3Ha8   : GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAN----------- :721
TrF3Ha9   : ------------------------------------------------------------ :   -
TrF3Ha10  : ------------------------------------------------------------ :   -
TrF3Ha11  : ------------------------------------------------------------ :   -
TrF3Ha12  : ------------------------------------------------------------ :   -
TrF3Ha13  : ------------------------------------------------------------ :   -
TrF3Ha14  : GAACCTGACCTC------------------------------------------------ :681
TrF3Ha15  : ------------------------------------------------------------ :   -
TrF3Ha16  : ------------------------------------------------------------ :   -
TrF3Ha17  : ------------------------------------------------------------ :   -
TrF3Ha18  : ------------------------------------------------------------ :   -
TrF3Ha19  : ------------------------------------------------------------ :   -
TrF3Ha20  : ------------------------------------------------------------ :   -
TrF3Ha21  : ------------------------------------------------------------ :   -
TrF3Ha22  : ------------------------------------------------------------ :   -
TrF3Ha23  : ------------------------------------------------------------ :   -
TrF3Ha24  : ------------------------------------------------------------ :   -
TrF3Ha25  : ------------------------------------------------------------ :   -
TrF3Ha26  : ------------------------------------------------------------ :   -
TrF3Ha27  : ------------------------------------------------------------ :   -
TrF3Ha28  : ------------------------------------------------------------ :   -
TrF3Ha29  : ------------------------------------------------------------ :   -
TrF3Ha30  : ------------------------------------------------------------ :   -
TrF3Ha31  : ------------------------------------------------------------ :   -
TrF3Ha32  : ------------------------------------------------------------ :   -
TrF3Ha33  : ------------------------------------------------------------ :   -
TrF3Ha34  : ------------------------------------------------------------ :   -
TrF3Ha35  : ------------------------------------------------------------ :   -
TrF3Ha36  : ------------------------------------------------------------ :   -
TrF3Ha37  : ------------------------------------------------------------ :   -
TrF3Ha38  : ------------------------------------------------------------ :   -
TrF3Ha39  : ------------------------------------------------------------ :   -
TrF3Ha40  : GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCCTGGCACAATTACTCTTTTG :508
TrF3Ha41  : GAACCTGACCTCACACTTGGCCTTAAACGCCACACTGACCCTGGNACAATTACTCTTTTG : 98
```

FIGURE 75 (cont)

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```
                        *       800         *       820         *       840
TrF3Ha1    : ------------------------------------------------------------ :   -
TrF3Ha2    : ------------------------------------------------------------ :   -
TrF3Ha3    : ------------------------------------------------------------ :   -
TrF3Ha4    : ------------------------------------------------------------ :   -
TrF3Ha5    : ------------------------------------------------------------ :   -
TrF3Ha6    : ------------------------------------------------------------ :   -
TrF3Ha7    : ------------------------------------------------------------ :   -
TrF3Ha8    : ------------------------------------------------------------ :   -
TrF3Ha9    : ------------------------------------------------------------ :   -
TrF3Ha10   : ------------------------------------------------------------ :   -
TrF3Ha11   : ------------------------------------------------------------ :   -
TrF3Ha12   : ------------------------------------------------------------ :   -
TrF3Ha13   : ------------------------------------------------------------ :   -
TrF3Ha14   : ------------------------------------------------------------ :   -
TrF3Ha15   : ------------------------------------------------------------ :   -
TrF3Ha16   : ------------------------------------------------------------ :   -
TrF3Ha17   : ------------------------------------------------------------ :   -
TrF3Ha18   : ------------------------------------------------------------ :   -
TrF3Ha19   : ------------------------------------------------------------ :   -
TrF3Ha20   : ------------------------------------------------------------ :   -
TrF3Ha21   : ------------------------------------------------------------ :   -
TrF3Ha22   : ------------------------------------------------------------ :   -
TrF3Ha23   : ------------------------------------------------------------ :   -
TrF3Ha24   : ------------------------------------------------------------ :   -
TrF3Ha25   : ------------------------------------------------------------ :   -
TrF3Ha26   : ------------------------------------------------------------ :   -
TrF3Ha27   : ------------------------------------------------------------ :   -
TrF3Ha28   : ------------------------------------------------------------ :   -
TrF3Ha29   : ------------------------------------------------------------ :   -
TrF3Ha30   : ------------------------------------------------------------ :   -
TrF3Ha31   : ------------------------------------------------------------ :   -
TrF3Ha32   : ------------------------------------------------------------ :   -
TrF3Ha33   : ------------------------------------------------------------ :   -
TrF3Ha34   : ------------------------------------------------------------ :   -
TrF3Ha35   : ------------------------------------------------------------ :   -
TrF3Ha36   : ------------------------------------------------------------ :   -
TrF3Ha37   : ------------------------------------------------------------ :   -
TrF3Ha38   : ------------------------------------------------------------ :   -
TrF3Ha39   : ------------------------------------------------------------ :   -
TrF3Ha40   : CTTCAAGATCAAGTTGGTGGTCTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA : 568
TrF3Ha41   : CTTCAAGATCAAGTTGGTGGCCTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA : 158
```

FIGURE 75 (cont)

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```
                      *       860         *       880         *       900
TrF3Ha1   : ------------------------------------------------------------ :   -
TrF3Ha2   : ------------------------------------------------------------ :   -
TrF3Ha3   : ------------------------------------------------------------ :   -
TrF3Ha4   : ------------------------------------------------------------ :   -
TrF3Ha5   : ------------------------------------------------------------ :   -
TrF3Ha6   : ------------------------------------------------------------ :   -
TrF3Ha7   : ------------------------------------------------------------ :   -
TrF3Ha8   : ------------------------------------------------------------ :   -
TrF3Ha9   : ------------------------------------------------------------ :   -
TrF3Ha10  : ------------------------------------------------------------ :   -
TrF3Ha11  : ------------------------------------------------------------ :   -
TrF3Ha12  : ------------------------------------------------------------ :   -
TrF3Ha13  : ------------------------------------------------------------ :   -
TrF3Ha14  : ------------------------------------------------------------ :   -
TrF3Ha15  : ------------------------------------------------------------ :   -
TrF3Ha16  : ------------------------------------------------------------ :   -
TrF3Ha17  : ------------------------------------------------------------ :   -
TrF3Ha18  : ------------------------------------------------------------ :   -
TrF3Ha19  : ------------------------------------------------------------ :   -
TrF3Ha20  : ------------------------------------------------------------ :   -
TrF3Ha21  : ------------------------------------------------------------ :   -
TrF3Ha22  : ------------------------------------------------------------ :   -
TrF3Ha23  : ------------------------------------------------------------ :   -
TrF3Ha24  : ------------------------------------------------------------ :   -
TrF3Ha25  : ------------------------------------------------------------ :   -
TrF3Ha26  : ------------------------------------------------------------ :   -
TrF3Ha27  : ------------------------------------------------------------ :   -
TrF3Ha28  : ------------------------------------------------------------ :   -
TrF3Ha29  : ------------------------------------------------------------ :   -
TrF3Ha30  : ------------------------------------------------------------ :   -
TrF3Ha31  : ------------------------------------------------------------ :   -
TrF3Ha32  : ------------------------------------------------------------ :   -
TrF3Ha33  : ------------------------------------------------------------ :   -
TrF3Ha34  : ------------------------------------------------------------ :   -
TrF3Ha35  : ------------------------------------------------------------ :   -
TrF3Ha36  : ------------------------------------------------------------ :   -
TrF3Ha37  : ------------------------------------------------------------ :   -
TrF3Ha38  : ------------------------------------------------------------ :   -
TrF3Ha39  : ------------------------------------------------------------ :   -
TrF3Ha40  : GTTCAACCAGTTGAAGGTGCTTTTGTTGTTAATCTTGGAGACCATGGTCACTATCTAAGT : 628
TrF3Ha41  : GTTCAACCAGTTGAAGGTGCTTTTGTTGTTAATCTTGGAGACCATGGTCATTATCTAAGT : 218
```

FIGURE 75 (cont)

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```
                         *       920         *       940         *       960
TrF3Ha1   : ------------------------------------------------------------ :   -
TrF3Ha2   : ------------------------------------------------------------ :   -
TrF3Ha3   : ------------------------------------------------------------ :   -
TrF3Ha4   : ------------------------------------------------------------ :   -
TrF3Ha5   : ------------------------------------------------------------ :   -
TrF3Ha6   : ------------------------------------------------------------ :   -
TrF3Ha7   : ------------------------------------------------------------ :   -
TrF3Ha8   : ------------------------------------------------------------ :   -
TrF3Ha9   : ------------------------------------------------------------ :   -
TrF3Ha10  : ------------------------------------------------------------ :   -
TrF3Ha11  : ------------------------------------------------------------ :   -
TrF3Ha12  : ------------------------------------------------------------ :   -
TrF3Ha13  : ------------------------------------------------------------ :   -
TrF3Ha14  : ------------------------------------------------------------ :   -
TrF3Ha15  : ------------------------------------------------------------ :   -
TrF3Ha16  : ------------------------------------------------------------ :   -
TrF3Ha17  : ------------------------------------------------------------ :   -
TrF3Ha18  : ------------------------------------------------------------ :   -
TrF3Ha19  : ------------------------------------------------------------ :   -
TrF3Ha20  : ------------------------------------------------------------ :   -
TrF3Ha21  : ------------------------------------------------------------ :   -
TrF3Ha22  : ------------------------------------------------------------ :   -
TrF3Ha23  : ------------------------------------------------------------ :   -
TrF3Ha24  : ------------------------------------------------------------ :   -
TrF3Ha25  : ------------------------------------------------------------ :   -
TrF3Ha26  : ------------------------------------------------------------ :   -
TrF3Ha27  : ------------------------------------------------------------ :   -
TrF3Ha28  : ------------------------------------------------------------ :   -
TrF3Ha29  : ------------------------------------------------------------ :   -
TrF3Ha30  : ------------------------------------------------------------ :   -
TrF3Ha31  : ------------------------------------------------------------ :   -
TrF3Ha32  : ------------------------------------------------------------ :   -
TrF3Ha33  : ------------------------------------------------------------ :   -
TrF3Ha34  : ------------------------------------------------------------ :   -
TrF3Ha35  : ------------------------------------------------------------ :   -
TrF3Ha36  : ------------------------------------------------------------ :   -
TrF3Ha37  : ------------------------------------------------------------ :   -
TrF3Ha38  : ------------------------------------------------------------ :   -
TrF3Ha39  : ------------------------------------------------------------ :   -
TrF3Ha40  : AATGGACGGTTCAAAAATGCTGACCATCAAGCAGTGGTGAATTCGAACTACAGCCGNTTA : 688
TrF3Ha41  : AATGGACGGTTCAAAAATGCTGACCACCAAGCAGTGGTGAATTCGAACTACAGCCGTTTA : 278
```

FIGURE 75 (cont)

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```
                      *       980         *        1000         *        1020
TrF3Ha1    : ------------------------------------------------------------ :  -
TrF3Ha2    : ------------------------------------------------------------ :  -
TrF3Ha3    : ------------------------------------------------------------ :  -
TrF3Ha4    : ------------------------------------------------------------ :  -
TrF3Ha5    : ------------------------------------------------------------ :  -
TrF3Ha6    : ------------------------------------------------------------ :  -
TrF3Ha7    : ------------------------------------------------------------ :  -
TrF3Ha8    : ------------------------------------------------------------ :  -
TrF3Ha9    : ------------------------------------------------------------ :  -
TrF3Ha10   : ------------------------------------------------------------ :  -
TrF3Ha11   : ------------------------------------------------------------ :  -
TrF3Ha12   : ------------------------------------------------------------ :  -
TrF3Ha13   : ------------------------------------------------------------ :  -
TrF3Ha14   : ------------------------------------------------------------ :  -
TrF3Ha15   : ------------------------------------------------------------ :  -
TrF3Ha16   : ------------------------------------------------------------ :  -
TrF3Ha17   : ------------------------------------------------------------ :  -
TrF3Ha18   : ------------------------------------------------------------ :  -
TrF3Ha19   : ------------------------------------------------------------ :  -
TrF3Ha20   : ------------------------------------------------------------ :  -
TrF3Ha21   : ------------------------------------------------------------ :  -
TrF3Ha22   : ------------------------------------------------------------ :  -
TrF3Ha23   : ------------------------------------------------------------ :  -
TrF3Ha24   : ------------------------------------------------------------ :  -
TrF3Ha25   : ------------------------------------------------------------ :  -
TrF3Ha26   : ------------------------------------------------------------ :  -
TrF3Ha27   : ------------------------------------------------------------ :  -
TrF3Ha28   : ------------------------------------------------------------ :  -
TrF3Ha29   : ------------------------------------------------------------ :  -
TrF3Ha30   : ------------------------------------------------------------ :  -
TrF3Ha31   : ------------------------------------------------------------ :  -
TrF3Ha32   : ------------------------------------------------------------ :  -
TrF3Ha33   : ------------------------------------------------------------ :  -
TrF3Ha34   : ------------------------------------------------------------ :  -
TrF3Ha35   : ------------------------------------------------------------ :  -
TrF3Ha36   : ------------------------------------------------------------ :  -
TrF3Ha37   : ------------------------------------------------------------ :  -
TrF3Ha38   : ------------------------------------------------------------ :  -
TrF3Ha39   : ------------------------------------------------------------ :  -
TrF3Ha40   : TCAATAGCAA-------------------------------------------------- :698
TrF3Ha41   : TCAATAGCAACATTTCAAAATCCAGCTCCCGATGCAACTGTATACCCTTTGAAGATTAGA :338
```

FIGURE 75 (cont)

```
                          *        1040         *        1060         *        1080
TrF3Ha1  : ------------------------------------------------------------ :   -
TrF3Ha2  : ------------------------------------------------------------ :   -
TrF3Ha3  : ------------------------------------------------------------ :   -
TrF3Ha4  : ------------------------------------------------------------ :   -
TrF3Ha5  : ------------------------------------------------------------ :   -
TrF3Ha6  : ------------------------------------------------------------ :   -
TrF3Ha7  : ------------------------------------------------------------ :   -
TrF3Ha8  : ------------------------------------------------------------ :   -
TrF3Ha9  : ------------------------------------------------------------ :   -
TrF3Ha10 : ------------------------------------------------------------ :   -
TrF3Ha11 : ------------------------------------------------------------ :   -
TrF3Ha12 : ------------------------------------------------------------ :   -
TrF3Ha13 : ------------------------------------------------------------ :   -
TrF3Ha14 : ------------------------------------------------------------ :   -
TrF3Ha15 : ------------------------------------------------------------ :   -
TrF3Ha16 : ------------------------------------------------------------ :   -
TrF3Ha17 : ------------------------------------------------------------ :   -
TrF3Ha18 : ------------------------------------------------------------ :   -
TrF3Ha19 : ------------------------------------------------------------ :   -
TrF3Ha20 : ------------------------------------------------------------ :   -
TrF3Ha21 : ------------------------------------------------------------ :   -
TrF3Ha22 : ------------------------------------------------------------ :   -
TrF3Ha23 : ------------------------------------------------------------ :   -
TrF3Ha24 : ------------------------------------------------------------ :   -
TrF3Ha25 : ------------------------------------------------------------ :   -
TrF3Ha26 : ------------------------------------------------------------ :   -
TrF3Ha27 : ------------------------------------------------------------ :   -
TrF3Ha28 : ------------------------------------------------------------ :   -
TrF3Ha29 : ------------------------------------------------------------ :   -
TrF3Ha30 : ------------------------------------------------------------ :   -
TrF3Ha31 : ------------------------------------------------------------ :   -
TrF3Ha32 : ------------------------------------------------------------ :   -
TrF3Ha33 : ------------------------------------------------------------ :   -
TrF3Ha34 : ------------------------------------------------------------ :   -
TrF3Ha35 : ------------------------------------------------------------ :   -
TrF3Ha36 : ------------------------------------------------------------ :   -
TrF3Ha37 : ------------------------------------------------------------ :   -
TrF3Ha38 : ------------------------------------------------------------ :   -
TrF3Ha39 : ------------------------------------------------------------ :   -
TrF3Ha40 : ------------------------------------------------------------ :   -
TrF3Ha41 : GAGGGTGAAAAATCTGTGTTGGAAGAACCAATCACTTTTGCTGAAATGTATAGAAGGAAG :398
```

FIGURE 75 (cont)

```
                     *       1100         *       1120         *       1140
TrF3Ha1   : ------------------------------------------------------------ :   -
TrF3Ha2   : ------------------------------------------------------------ :   -
TrF3Ha3   : ------------------------------------------------------------ :   -
TrF3Ha4   : ------------------------------------------------------------ :   -
TrF3Ha5   : ------------------------------------------------------------ :   -
TrF3Ha6   : ------------------------------------------------------------ :   -
TrF3Ha7   : ------------------------------------------------------------ :   -
TrF3Ha8   : ------------------------------------------------------------ :   -
TrF3Ha9   : ------------------------------------------------------------ :   -
TrF3Ha10  : ------------------------------------------------------------ :   -
TrF3Ha11  : ------------------------------------------------------------ :   -
TrF3Ha12  : ------------------------------------------------------------ :   -
TrF3Ha13  : ------------------------------------------------------------ :   -
TrF3Ha14  : ------------------------------------------------------------ :   -
TrF3Ha15  : ------------------------------------------------------------ :   -
TrF3Ha16  : ------------------------------------------------------------ :   -
TrF3Ha17  : ------------------------------------------------------------ :   -
TrF3Ha18  : ------------------------------------------------------------ :   -
TrF3Ha19  : ------------------------------------------------------------ :   -
TrF3Ha20  : ------------------------------------------------------------ :   -
TrF3Ha21  : ------------------------------------------------------------ :   -
TrF3Ha22  : ------------------------------------------------------------ :   -
TrF3Ha23  : ------------------------------------------------------------ :   -
TrF3Ha24  : ------------------------------------------------------------ :   -
TrF3Ha25  : ------------------------------------------------------------ :   -
TrF3Ha26  : ------------------------------------------------------------ :   -
TrF3Ha27  : ------------------------------------------------------------ :   -
TrF3Ha28  : ------------------------------------------------------------ :   -
TrF3Ha29  : ------------------------------------------------------------ :   -
TrF3Ha30  : ------------------------------------------------------------ :   -
TrF3Ha31  : ------------------------------------------------------------ :   -
TrF3Ha32  : ------------------------------------------------------------ :   -
TrF3Ha33  : ------------------------------------------------------------ :   -
TrF3Ha34  : ------------------------------------------------------------ :   -
TrF3Ha35  : ------------------------------------------------------------ :   -
TrF3Ha36  : ------------------------------------------------------------ :   -
TrF3Ha37  : ------------------------------------------------------------ :   -
TrF3Ha38  : ------------------------------------------------------------ :   -
TrF3Ha39  : ------------------------------------------------------------ :   -
TrF3Ha40  : ------------------------------------------------------------ :   -
TrF3Ha41  : ATGACCAAAGACCTTGAAATTGCTAGGATGAAGAAGTTGGCTAAGGAACAACAACTTAGG :458
```

FIGURE 75 (cont)

```
                     *      1160         *      1180         *      1200
TrF3Ha1   : ------------------------------------------------------------ :    -
TrF3Ha2   : ------------------------------------------------------------ :    -
TrF3Ha3   : ------------------------------------------------------------ :    -
TrF3Ha4   : ------------------------------------------------------------ :    -
TrF3Ha5   : ------------------------------------------------------------ :    -
TrF3Ha6   : ------------------------------------------------------------ :    -
TrF3Ha7   : ------------------------------------------------------------ :    -
TrF3Ha8   : ------------------------------------------------------------ :    -
TrF3Ha9   : ------------------------------------------------------------ :    -
TrF3Ha10  : ------------------------------------------------------------ :    -
TrF3Ha11  : ------------------------------------------------------------ :    -
TrF3Ha12  : ------------------------------------------------------------ :    -
TrF3Ha13  : ------------------------------------------------------------ :    -
TrF3Ha14  : ------------------------------------------------------------ :    -
TrF3Ha15  : ------------------------------------------------------------ :    -
TrF3Ha16  : ------------------------------------------------------------ :    -
TrF3Ha17  : ------------------------------------------------------------ :    -
TrF3Ha18  : ------------------------------------------------------------ :    -
TrF3Ha19  : ------------------------------------------------------------ :    -
TrF3Ha20  : ------------------------------------------------------------ :    -
TrF3Ha21  : ------------------------------------------------------------ :    -
TrF3Ha22  : ------------------------------------------------------------ :    -
TrF3Ha23  : ------------------------------------------------------------ :    -
TrF3Ha24  : ------------------------------------------------------------ :    -
TrF3Ha25  : ------------------------------------------------------------ :    -
TrF3Ha26  : ------------------------------------------------------------ :    -
TrF3Ha27  : ------------------------------------------------------------ :    -
TrF3Ha28  : ------------------------------------------------------------ :    -
TrF3Ha29  : ------------------------------------------------------------ :    -
TrF3Ha30  : ------------------------------------------------------------ :    -
TrF3Ha31  : ------------------------------------------------------------ :    -
TrF3Ha32  : ------------------------------------------------------------ :    -
TrF3Ha33  : ------------------------------------------------------------ :    -
TrF3Ha34  : ------------------------------------------------------------ :    -
TrF3Ha35  : ------------------------------------------------------------ :    -
TrF3Ha36  : ------------------------------------------------------------ :    -
TrF3Ha37  : ------------------------------------------------------------ :    -
TrF3Ha38  : ------------------------------------------------------------ :    -
TrF3Ha39  : ------------------------------------------------------------ :    -
TrF3Ha40  : ------------------------------------------------------------ :    -
TrF3Ha41  : GACTTGGAGGAGAACAAGACTAAATATGAGGCCAAACCTTTGAATGAGATCTTTGCTTAA : 518
```

FIGURE 75 (cont)

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```
                      *       1220         *       1240         *       1260
TrF3Ha1  : ------------------------------------------------------------ :   -
TrF3Ha2  : ------------------------------------------------------------ :   -
TrF3Ha3  : ------------------------------------------------------------ :   -
TrF3Ha4  : ------------------------------------------------------------ :   -
TrF3Ha5  : ------------------------------------------------------------ :   -
TrF3Ha6  : ------------------------------------------------------------ :   -
TrF3Ha7  : ------------------------------------------------------------ :   -
TrF3Ha8  : ------------------------------------------------------------ :   -
TrF3Ha9  : ------------------------------------------------------------ :   -
TrF3Ha10 : ------------------------------------------------------------ :   -
TrF3Ha11 : ------------------------------------------------------------ :   -
TrF3Ha12 : ------------------------------------------------------------ :   -
TrF3Ha13 : ------------------------------------------------------------ :   -
TrF3Ha14 : ------------------------------------------------------------ :   -
TrF3Ha15 : ------------------------------------------------------------ :   -
TrF3Ha16 : ------------------------------------------------------------ :   -
TrF3Ha17 : ------------------------------------------------------------ :   -
TrF3Ha18 : ------------------------------------------------------------ :   -
TrF3Ha19 : ------------------------------------------------------------ :   -
TrF3Ha20 : ------------------------------------------------------------ :   -
TrF3Ha21 : ------------------------------------------------------------ :   -
TrF3Ha22 : ------------------------------------------------------------ :   -
TrF3Ha23 : ------------------------------------------------------------ :   -
TrF3Ha24 : ------------------------------------------------------------ :   -
TrF3Ha25 : ------------------------------------------------------------ :   -
TrF3Ha26 : ------------------------------------------------------------ :   -
TrF3Ha27 : ------------------------------------------------------------ :   -
TrF3Ha28 : ------------------------------------------------------------ :   -
TrF3Ha29 : ------------------------------------------------------------ :   -
TrF3Ha30 : ------------------------------------------------------------ :   -
TrF3Ha31 : ------------------------------------------------------------ :   -
TrF3Ha32 : ------------------------------------------------------------ :   -
TrF3Ha33 : ------------------------------------------------------------ :   -
TrF3Ha34 : ------------------------------------------------------------ :   -
TrF3Ha35 : ------------------------------------------------------------ :   -
TrF3Ha36 : ------------------------------------------------------------ :   -
TrF3Ha37 : ------------------------------------------------------------ :   -
TrF3Ha38 : ------------------------------------------------------------ :   -
TrF3Ha39 : ------------------------------------------------------------ :   -
TrF3Ha40 : ------------------------------------------------------------ :   -
TrF3Ha41 : TTAATTAGTCTTAATTTAAATAATTAATAAATTTTAGACTTAATTTACATATAATAATTT : 578
```

FIGURE 75 (cont)

```
TrF3Ha1  : - :   -
TrF3Ha2  : - :   -
TrF3Ha3  : - :   -
TrF3Ha4  : - :   -
TrF3Ha5  : - :   -
TrF3Ha6  : - :   -
TrF3Ha7  : - :   -
TrF3Ha8  : - :   -
TrF3Ha9  : - :   -
TrF3Ha10 : - :   -
TrF3Ha11 : - :   -
TrF3Ha12 : - :   -
TrF3Ha13 : - :   -
TrF3Ha14 : - :   -
TrF3Ha15 : - :   -
TrF3Ha16 : - :   -
TrF3Ha17 : - :   -
TrF3Ha18 : - :   -
TrF3Ha19 : - :   -
TrF3Ha20 : - :   -
TrF3Ha21 : - :   -
TrF3Ha22 : - :   -
TrF3Ha23 : - :   -
TrF3Ha24 : - :   -
TrF3Ha25 : - :   -
TrF3Ha26 : - :   -
TrF3Ha27 : - :   -
TrF3Ha28 : - :   -
TrF3Ha29 : - :   -
TrF3Ha30 : - :   -
TrF3Ha31 : - :   -
TrF3Ha32 : - :   -
TrF3Ha33 : - :   -
TrF3Ha34 : - :   -
TrF3Ha35 : - :   -
TrF3Ha36 : - :   -
TrF3Ha37 : - :   -
TrF3Ha38 : - :   -
TrF3Ha39 : - :   -
TrF3Ha40 : - :   -
TrF3Ha41 : T : 579
```

FIGURE 75 (cont)

```
                      *        20         *        40         *        60
TrF3Hb : GNAGCATAACATAAACCCTGTNCCCGATTNATGTAACACAATCTCCCCTTTTCTTATTAC :  60

                      *        80         *       100         *       120
TrF3Hb : AAGTAAAATACCATAACACAATAATATGAATACCATAATCTTGAATCATACAAACAACCT : 120

                      *       140         *       160         *       180
TrF3Hb : TGGATCAAACAAAACAACAACCATGGTTGATCTAGAAACAGAACCAAGTTCACCATTTAT : 180

                      *       200         *       220         *       240
TrF3Hb : TCAATCCCCAGAACACAGACCAAAATCCTCAATAATCATTGCTGAAGGTATCCCTCTAAT : 240

                      *       260         *       280         *       300
TrF3Hb : TGATCTCACTCCTATAAACTACAAAGATGAAATCATCACCAACCCACTTTCCATTGAAGA : 300

                      *       320         *       340         *       360
TrF3Hb : CTTAGTCAAAGAAATAGGCAAAGCATGTAAAGAATGGGGTTTCTTTCAAGTGATTAATCA : 360

                      *       380         *       400         *       420
TrF3Hb : CAAAGTTCCTTTGGATAAACGTGAAAGGATTGAAGAATCTTCAAAGAAGTTTTTTGAACT : 420

                      *       440         *       460         *       480
TrF3Hb : TAGTTTGGAGGAAAAACTTAAGGTGAGAAGAGATGAAGTTAATTTGCTTGGTTATTTTGA : 480

                      *       500         *       520         *       540
TrF3Hb : AGCTGAGCATACAAAAAATGTTAGGGACTGGAAGGAAATTTATGATTTTAATGTGCAACA : 540

                      *       560         *       580         *       600
TrF3Hb : ACCAACTTTTATACCACCTTCGGATGACCAAAGTTTTCAGTTTCAATGGGAAAATCGATG : 600

TrF3Hb : G : 601
```

FIGURE 76

```
                         *        20          *        40          *        60
TrF3Hb : MNTIILNHTNNLGSNKTTTMVDLETEPSSPFIQSPEHRPKSSIIIAEGIPLIDLTPINYK :  60

                         *        80          *       100          *       120
TrF3Hb : DEIITNPLSIEDLVKEIGKACKEWGFFQVINHKVPLDKRERIEESSKKFFELSLEEKLKV : 120

                         *       140          *       160          *
TrF3Hb : RRDEVNLLGYFEAEHTKNVRDWKEIYDFNVQQPTFIPPSDDQSFQFQWENRW : 172
```

FIGURE 77

```
                    *        20         *        40         *        60
TrF3Hc : TTACCCAACAATNATGTGTGACTGATGTTAGTGTACCAGGAAAGATGGGAGAGGTGGATC :  60

                    *        80         *       100         *       120
TrF3Hc : CAGCTTTCTTCAAATCCAGAAAATAGGCCAAAACTTTCCATAATCCAAGCTGAAGGAATT : 120

                    *       140         *       160         *       180
TrF3Hc : CCTGTAATCAATCTCTCCCCATTAATTCACCACACAGTTCAAGACTCCTCTGCCATTGAA : 180

                    *       200         *       220         *       240
TrF3Hc : AGCTTAGTCAAAGAAATAGGAAATGCTTGCAAGGAATGGGGTTTCTTCCAAGTAACAAAC : 240

                    *       260         *       280         *       300
TrF3Hc : CATGGTGTCCCTCTAAATCTAAGGCTCAGACTCGAGGAAGCTACCAAAGTTTTCTTTGCA : 300

                    *       320         *       340         *       360
TrF3Hc : CAGAGTTTGGAGGAGAAGAGGAAGCTTACCGTAGATGATAACAGTTTGCCTGGTTATCAT : 360

                    *       380         *       400         *       420
TrF3Hc : GATACAGAGCACACCAAGAATGTCAGAGACTGGAAAGAAGTGTTTGATTTTTATCCAAA : 420

                    *       440         *       460         *       480
TrF3Hc : GACCCCACTTTGATTCCTCTGAATTCTGATGAACATGATGATCGAGTCACTCAATGGACT : 480

                    *       500         *       520         *       540
TrF3Hc : AATCCATCCCCTCAATATCCTCCAAACTTCAAAGTTATTTGGAAGAGTATATTAAAGAG : 540

                    *       560         *       580
TrF3Hc : ATGGAAAAGCTAGGCTTTAAGTTGCTAGAGCTTATAGCTTTGAGC : 585
```

FIGURE 78

```
                       *        20         *        40         *        60
TrF3Hc : MLVYQERWERWIQLSSNPENRPKLSIIQAEGIPVINLSPLIHHTVQDSSAIESLVKEIGN :  60

                       *        80         *       100         *       120
TrF3Hc : ACKEWGFFQVTNHGVPLNLRLRLEEATKVFFAQSLEEKRKLTVDDNSLPGYHDTEHTKNV : 120

                       *       140         *       160         *       180
TrF3Hc : RDWKEVFDFLSKDPTLIPLNSDEHDDRVTQWTNPSPQYPPNFKVILEEYIKEMEKLGFKL : 180

TrF3Hc : LELIALS : 187
```

FIGURE 79

```
                   *        20         *        40         *        60
TrF3'Ha : GGGAATGGTGGAGGCGAATGTGACCCTAGGGCTGATGAATTAGTAATGGTAGTTGAGCTT :  60

                   *        80         *       100         *       120
TrF3'Ha : ATGGCGTTAGCTGGAGTTTTCAATATTGGTGATTTTGTTCCTGCTTTGGAATGGTTAGAT : 120

                   *       140         *       160         *       180
TrF3'Ha : ATTCAAGGTGTACAAGGAAAAATGAAGAAATTACATAAAAGATTTGATGCATTTTTAACT : 180

                   *       200         *       220         *       240
TrF3'Ha : AGCATTATTGAAGATCACATGATTTCCAAGAGTGAGAAGCATAATGACTTATTGAGTACG : 240

                   *       260         *       280         *       300
TrF3'Ha : TTGTTATCACTAAAAGAAAAAGTTGATGAGGATGGTGACAAACTTAATGATACTGAGATC : 300

                   *       320         *       340         *       360
TrF3'Ha : AAAGCATTACTCTTGAACATGTTCACAGCTGGAACAGACACATCATCAAGCACAACAGAG : 360

                   *       380         *       400         *       420
TrF3'Ha : TGGGCTATTGCTGAACTAATAAAAAATCCAAAACTAATGATTCGTGTTCAAAATGAGTTG : 420

                   *       440         *       460         *       480
TrF3'Ha : GACACTGTTGTGGGCCGAGACAAGCTTGTAACTGAACAAGACTTGGCCCATCTTCCTTAC : 480

                   *       500         *       520         *       540
TrF3'Ha : TTAGAGGCTGTAATAAAGGAGACATTTCGTCTCCATCCATCAACCCCTCTTTCTCTCCCA : 540

                   *       560         *       580         *       600
TrF3'Ha : CGTGTTGCAACAAATAGTTGTGAAATCCTCGACTATCACATTCCCAAAGGTGCAACTCTC : 600

TrF3'Ha : TTGG : 604
```

FIGURE 80

```
                      *        20         *        40         *        60
TrF3'Ha  : GNGGGECDPRADELVMVVELMALAGVFNIGDFVPALEWLDIQGVQGKMKKLHKRFDAFLT  : 60

                      *        80         *       100         *       120
TrF3'Ha  : SIIEDHMISKSEKHNDLLSTLLSLKEKVDEDGDKLNDTEIKALLLNMFTAGTDTSSSTTE  :120

                      *       140         *       160         *       180
TrF3'Ha  : WAIAELIKNPKLMIRVQNELDTVVGRDKLVTEQDLAHLPYLEAVIKETFRLHPSTPLSLP  :180

                      *       200
TrF3'Ha  : RVATNSCEILDYHIPKGATLL :201
```

FIGURE 81

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```
                    *        20         *        40         *        60
TrF3'Ha1 : GGGAATGGTGGAGGCGAATGTGACCCTAGGGCTGATGAATTTAAGTAATGGTAGTTGAGC : 60
TrF3'Ha2 : ---AATGGTGGAGGTGAATGTGACCCTAGGGCTGATGAATTTAAGTNATGGTAGTTGAGC : 57

                    *        80         *       100         *       120
TrF3'Ha1 : TTATGGCGTTAGCTGGAGTTTTCAATATTGGTGATTTTGTTCCTGCTTTGGAATGGTTAG :120
TrF3'Ha2 : TTATGGCGTTAGCTGGAGTTTTCAATATTGGTGATTTTGTTCCTGCTTTGGAATGGTTAG :117

                    *       140         *       160         *       180
TrF3'Ha1 : ATATTCAAGGTGTACAAGGAAAAATGAAGAAATTACATAAAAGATTTGATGCATTTTTAA :180
TrF3'Ha2 : ATATTCAAGGTGTACAAGGAAAAATGAAGAAATTACATAAAAGATTTGATGCATTTTTAA :177

                    *       200         *       220         *       240
TrF3'Ha1 : CTAGCATTATTGAAGATCACATGATTTCCAAGAGTGAGAAGCATAATGACTTATTGAGTA :240
TrF3'Ha2 : CTAGCATTATTGAAGATCACATGATTTCCAAGAGTGAGAAGCATAATGACTTATTGAGTA :237

                    *       260         *       280         *       300
TrF3'Ha1 : CGTTGTTATCACTAAAAGAAAAAGTTGATGAGGATGGTGACAAACTTAATGATACTGAGA :300
TrF3'Ha2 : CGTTGTTATCACTAAAAGAAAAAGTTGATGAGGATGGTGACAAACTTAATGATACTGAGA :297

                    *       320         *       340         *       360
TrF3'Ha1 : TCAAAGCATTACTCTTGAACATGTTCACAGCTGGAACAGACACATCATCAAGCACAACAG :360
TrF3'Ha2 : TCAAAGCATTACTCTTGAACATGTTCACAGCTGGAACAGACACATCATCAAGCACAACAG :357

                    *       380         *       400         *       420
TrF3'Ha1 : AGTGGGCTATTGCTGAACTAATAAAAAATCCAAAACTAATGATTCGTGTTCAAAATGAGT :420
TrF3'Ha2 : AGTGGGCTATTGCTGAACTAATAAAAAATCCAAAACTAATGATTCGTGTTCAAAATGAGT :417

                    *       440         *       460         *       480
TrF3'Ha1 : TGGACACTGTTGTGGGCCGAGACAAGCTTGTAACTGAACAAGACTTGGCCCATCTTCCTT :480
TrF3'Ha2 : TGGACACTGTTGTGGGCCGAGACAAGCTTGTAACTGAACAAGACTTGGCCCATCTTCCTT :477

                    *       500         *       520         *       540
TrF3'Ha1 : ACTTAGAGGCTGTAATAAAGGAGACATTTCGTCTCCATCCATCAACCCCTCTTTCTCTCC :540
TrF3'Ha2 : ACTTAGAGGCTGTAATAAAGGAGACATTTCGTCTCCATCCATCAACCCCTCTTTCTCTCC :537

                    *       560         *       580         *       600
TrF3'Ha1 : CACGTGTTGCAACAAATAGTTGTGAAATCCTCGACTATCAC------------------- :581
TrF3'Ha2 : CACGTGTTGCAACAAATAGTTGTGAAATCCTCGACTATCACATTCCCAAAGGTGCAACTC :597

TrF3'Ha1 : ------ :   -
TrF3'Ha2 : TCTTGG :603
```

FIGURE 82

```
                        *        20          *        40          *        60
TrPALa : GNAGGAAATTTCAACTAAATATTGCCTTTAATTCTTTNTNATANATNTTTGAATTTCNTT :  60

                        *        80          *       100          *       120
TrPALa : CTCCCTAAAAATTCTATAGCTACCACATCANCACAACATAACANNAATTAAGAAATATTN : 120

                        *       140          *       160          *       180
TrPALa : TATNTACTATTTTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAAACAATGGCAAG : 180

                        *       200          *       220          *       240
TrPALa : ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT : 240

                        *       260          *       280          *       300
TrPALa : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG : 300

                        *       320          *       340          *       360
TrPALa : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGTCTTGGTGGCGAGACACTGACGATT : 360

                        *       380          *       400          *       420
TrPALa : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT : 420

                        *       440          *       460          *       480
TrPALa : AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGAGTATGAACAAAGGTACAGAC : 480

                        *       500          *       520          *       540
TrPALa : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCGCACCGCCGAACCAAACAAGGTGGT : 540

                        *       560          *       580          *       600
TrPALa : GCTTTGCAGAAAGAGCTCATAAGGTNTTTTGAATGCAGGAATATTTGGAAATGGAACNTG : 600

                        *       620
TrPALa : AGACAAAGCCACACACTACCC : 621
```

FIGURE 83

```
                    *        20         *        40         *        60
TrPALa : MEVVAAAITKNNGKIDSFCLNHANANNMKVNGADPLNWGVAAEAMKGSHLDEVKRMVEEY :  60

                    *        80         *       100         *       120
TrPALa : RKPVVRLGGETLTISQVAAIAAHDGATVELSESARAGVKASSDWVMESMNKGTDSYGVTT : 120

                    *       140         *
TrPALa : GFGATSHRRTKQGGALQKELIRFECRNIWKWNRQSHTLP : 159
```

FIGURE 84

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```
                    *        20         *        40         *        60
TrPALa1  : GNNGGAAATTNCAACTAAATATTGCCTTTAATTCTTTNTNATANATNTTTGAATTTCCTT  : 60
TrPALa2  : GNAGGAAATTACAACTAAATATTNCCTTTAATTCTTTATNATANATNTTTGAATTTCNTT  : 60
TrPALa3  : ----------TCAAGAAATTACACTCTTTNNTTCTTTNTAATNTTTGTTTTNATTTCNTT  : 50

                    *        80         *       100         *       120
TrPALa1  : CTCCCTAAAAATTCTATAGCTACCACATCANCACAACATAACANNAATTAAGAAATATTN  :120
TrPALa2  : CTCCCTAAAAATTCTATAGCTACCACATCANCACAACATAACANNAATTAAGAAATATTN  :120
TrPALa3  : CTCTCTNGAAATACTATAGTTACCAAAACATAACAAAGTAACACTTATTACTAGCTATTA  :110

                    *       140         *       160         *       180
TrPALa1  : TATNTACTATTTTAAGATATGGAAGTAGTAGCANCAGCAATCACAAAAAACAATGGCAAG  :180
TrPALa2  : TATNTACTATNTTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAAACAATGGCAAG  :180
TrPALa3  : TTTCTATCAATTTAAGNNATGGAAGTAGTAGCAGCAGCAATCACAAAAAACAACGGAAAG  :170

                    *       200         *       220         *       240
TrPALa1  : ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT  :240
TrPALa2  : ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT  :240
TrPALa3  : ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGCTGAT  :230

                    *       260         *       280         *       300
TrPALa1  : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG  :300
TrPALa2  : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG  :300
TrPALa3  : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAAGGAAGTCACTTGGATGAGGTGAAG  :290

                    *       320         *       340         *       360
TrPALa1  : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGTCTTGGTGGCGAGACGCTGACGATT  :360
TrPALa2  : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGTCTTGGTGGCGAGACACTAACGATT  :360
TrPALa3  : TGTATGGTGGAGGAGTATCGAAAACCGGTTGTCCGTCTTGGTGGCGAGACACTGACGATT  :350

                    *       380         *       400         *       420
TrPALa1  : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGANCTATCGGAATCTGCT  :420
TrPALa2  : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT  :420
TrPALa3  : TCTCAAGTGGCTGCCATTGCTGCACACGATGGTGCCACGGTGGAGCTATCGGAATCTGCT  :410

                    *       440         *       460         *       480
TrPALa1  : AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGAGCATGAACAAAGGTACAGAC  :480
TrPALa2  : AGAGCCGGCGTTAAGGCAAGCAGTGACTGGGTTATGGAGAGTATGAACAAAGGTACCGAC  :480
TrPALa3  : AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAAAGTATGAACAAAGGTACTGAC  :470

                    *       500         *       520         *       540
TrPALa1  : AGTTATGGTGTCACTACCGGGTTCGGCGCTACCTCNCACCGCCGAACCAAACAAGGTGGT  :540
TrPALa2  : AGCTACGGTGTCCCAACAGGGTTCGGCGCTACCTCGCACCGCCGAACCAAACAAGGTGGT  :540
TrPALa3  : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCGCACCGCCGAACCAAACAAGGTGGT  :530

                    *       560         *       580         *       600
TrPALa1  : GCTTTGCANAAAGAGCTCATAAGCTAATTTGCTTGTGTCAAT------------------  :582
TrPALa2  : GCTTTGCAGAAAGAGCTCATAAGGTNTTTTGAATGCTGGAATATTTGGAAATGGAACNTG  :600
TrPALa3  : GCTTTGCAGAAAGAGCTCATAAGGTNTTTTGAATGCAGGAATATTTGGAAATGGAACTTG  :590

                    *       620
TrPALa1  : ---------------------  :  -
TrPALa2  : AGTCNAAGCCACACACTACCC  :621
TrPALa3  : ANACAAATCC-----------  :600
```

FIGURE 85

```
                             *        20          *        40          *        60
TrPALb : GNAGGAAANAATTNTATTGTTATTATTTCCCCCCACACAACGGAAANAATTNTATTGTTN :  60

                             *        80          *       100          *       120
TrPALb : CTTATTTCCCCCCACACAACATAACNAATACATTNTCCTCTCCTCTCATCACAATTATTA : 120

                             *       140          *       160          *       180
TrPALb : CTTTCTACACACCCCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG : 180

                             *       200          *       220          *       240
TrPALb : GCCATGCTGAAGCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG : 240

                             *       260          *       280          *       300
TrPALb : CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT : 300

                             *       320          *       340          *       360
TrPALb : ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA : 360

                             *       380          *       400          *       420
TrPALb : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCCAGGGCCGGCGTTA : 420

                             *       440          *       460          *       480
TrPALb : AGGCGAGTAGTGATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 480

                             *       500          *       520          *       540
TrPALb : CCACCGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG : 540

                             *       560          *       580          *       600
TrPALb : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC : 600

                             *       620          *       640          *       660
TrPALb : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAGAGG : 660

                             *       680          *
TrPALb : AATATTTCTTGAATGGCCTTTGTAAATTTTTGG : 693
```

FIGURE 86

```
                          *        20         *        40         *        60
TrPALb : MEGITNGHAEATFCVTKSVGDPLNWGAAAESLMGSHLDEVKRMVEEYRNPLVKIGGETLT :  60

                          *        80         *       100         *       120
TrPALb : IAQVAGIASHDSGVRVELSESARAGVKASSDWVMDSMNNGTDSYGVTTGFGATSHRRTKQ : 120

                          *       140         *       160         *
TrPALb : GGALQKELIRFLNAGIFGNGTESNCTLPHTATRAAMLVRINTLLQEEYFLNGLCKFL : 177
```

FIGURE 87

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```
                    *        20         *        40         *        60
TrPALb1 : GNAGGAAANAATTNTATTGTTATTATTTCCCCCCACACAACAAAACAAATACNATTATTN : 60
TrPALb2 : ---------------------------------------GAGGAAANAATTNTATTGTTN : 21
TrPALb3 : ---------------------------------------CCTTGAATNATTGNTTTGNCN : 21
TrPALb4 : -----------------------------------------GGAAANAATTATNTTGTTN : 19
TrPALb5 : -----------------------------------------GGAAANAATTATATTGTTC : 19
TrPALb6 : ------------------------------------------GAAANAATTNTNTTGTTN : 18
TrPALb7 : ------------------------------------------GAAANAATTNTNTTGTTC : 18
TrPALb8 : ------------------------------------------------------------ :  -

                    *        80         *       100         *       120
TrPALb1 : CTNNCCTCNCATCACANATTATTACNNTTNCNTACNACNCNNCTNNCCTCTCAACTATTA :120
TrPALb2 : NTTATTCCTACCCACACAACATAACAAATACATTNTCCTCTCCTCTCATCACAATTATTA : 81
TrPALb3 : CACCCAACACAACANCATANACAAAATACNATTTCNTGCTNCNCTACTNGCATCACAATTATTA : 81
TrPALb4 : NNTATTTCCCCCCACACNACATAACNAATACATTNTCTTCTCCTCTNATCACAATTATTA : 79
TrPALb5 : CTTATTTCCNCCCACACAACATAACAAATACATTNTCCTCTCCTCTCATCACAATTATTA : 79
TrPALb6 : ATTATTTCCNCCCACACAACATAACNAATACATTATTCTCTCCTCTCATCACAATTATTA : 78
TrPALb7 : CTTATTTCCCCCCACACAACATAACAAATACATTNTCCTCTCCTCTCATCACAATTATTA : 78
TrPALb8 : ------------------ANATANANAATCNNNATNTNCTCTCCTCTANTAACNATNNTNN : 42

                    *       140         *       160         *       180
TrPALb1 : NTANCTANGCANAAANGCACCCAANTACNANTGGCTAGCNGCNTTNCANAANAAANACCAATG :180
TrPALb2 : CTTTCTACANNCCCCCCTCTCAAGTATTATTAACTAACATAATGGAGGGAATTACCAATG :141
TrPALb3 : CTTTCTANNCACCCCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACTAATG :141
TrPALb4 : CTTTCTACANNCCCCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACTAATG :139
TrPALb5 : CTTTCTACACCCCCCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG :139
TrPALb6 : CTTTCTANNCACCCNCCTCTCAACTATTATTAACTANCATAATGGAGGGAATTACCAATG :138
TrPALb7 : CTTTCTACACCCCCCCCTCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG :138
TrPALb8 : CTTTCNNNNCNCCCNCCTCTNAACTATTANTAACTNNCATAATGGAGGGAANTACCAATG :102

                    *       200         *       220         *       240
TrPALb1 : GCCATGCTGAANCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :240
TrPALb2 : GCCATGCTGAAGCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :201
TrPALb3 : GCCATGCTGAAGCAACTTTTTGCGTNACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :201
TrPALb4 : GCCATGCTGAAGCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :199
TrPALb5 : GCCATGCTGAAGCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :199
TrPALb6 : GCCATGCTGAAACAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :198
TrPALb7 : GCCATGCTGAAGCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :198
TrPALb8 : GCCATGCTGAANCAACTTTTTGCGTGACCAAAAGTGTTGGTGATCCACTCAACTGGGGTG :162

                    *       260         *       280         *       300
TrPALb1 : CAGCCGCGGAGTCGTTGANGGGGNAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAGT :300
TrPALb2 : CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT :261
TrPALb3 : CAGCCGCGGAGTCGNTGATGGGGAGTNATTTGGATGAGGTGAANCGTATGGTGGAGGAAT :261
TrPALb4 : CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT :259
TrPALb5 : CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT :259
TrPALb6 : CAGCCGCGGAGTCGTTGACGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAGT :258
TrPALb7 : CAGCCGCGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAAT :258
TrPALb8 : CAGCCGCGGAGTCGTCGACGGGGAGTCATTTGGATGAGGTGAAGCGTATGGTGGAGGAGT :222

                    *       320         *       340         *       360
TrPALb1 : ACCGTAATCCNTTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :360
TrPALb2 : ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :321
TrPALb3 : ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :321
TrPALb4 : ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :319
TrPALb5 : ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :319
TrPALb6 : ACCGTAATCCNTTGGNTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :318
TrPALb7 : ACCGTAATCCATTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :318
TrPALb8 : ACCGTAATCCNTTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA :282
```

FIGURE 88

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```
                  *      380        *      400        *       420
TrPALb1 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCCGAGTCCGCAAGGGCCGGCGTTA :420
TrPALb2 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCGAGGGCCGGCGTTA :381
TrPALb3 : TTGCTTCTCATGATAGNGNTGTGAGGGTGGAGCTGTCTGAGTNCGCCAGGGCCGGCGTTA :381
TrPALb4 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCCAGGGCCGGCGTTA :379
TrPALb5 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCCAGGGCCGGCGTTA :379
TrPALb6 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGNNCGAGTCCGCAAGGGCCGGCGTTA :378
TrPALb7 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGAGTCCGCCAGGGCCGGCGTTA :378
TrPALb8 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCCGAGTCCGCAAGGGCCGGCGTTA :342

                  *      440        *      460        *       480
TrPALb1 : AGGCGAGTAGTGATTGGGTGATGGATAGCATGAACAATGGGACTGATAGTTACGGTGTTA :480
TrPALb2 : AGGCGAGTAGTGATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTACGGTGTTA :441
TrPALb3 : ANGCGAGTAGTGATTGNGTGATGGACAGNATGAACAATGGGACTGATAGTTATGGTGTTA :441
TrPALb4 : AGGCGAGTAGTGATTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGNGTNA :439
TrPALb5 : AGGCGAGTAGTGGTTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA :439
TrPALb6 : AGGCGAGTACTGATTGGGTGATGNATAACATGAACAATGGGACTGATNGGTNCGGNGCNA :438
TrPALb7 : AGGCGAGTAGTGGTTGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA :438
TrPALb8 : AGGCGAGTAGTGATTGGGTGATGGATAGCATGAACAATGGGACTGATAGTTACGGTGTTA :402

                  *      500        *      520        *       540
TrPALb1 : CCACCGGTTTTGGTGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG :540
TrPALb2 : CCACCGGTTTCGGTGCCACCTCTCACCGGAGAACCAAGCAAGGTGGTGCCTTGCAGAAGG :501
TrPALb3 : CCACCGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAAAAGG :501
TrPALb4 : CCACCGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG :499
TrPALb5 : CCACTGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG :499
TrPALb6 : CNN--------------------------------------------------------- :441
TrPALb7 : CCACTGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG :498
TrPALb8 : CCACCGGTTTTGGTGCCACCTCTCACCGGAGAACCAAGCAGGGTGGTGCCTTGCAGAAGG :462

                  *      560        *      580        *       600
TrPALb1 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAN-------- :592
TrPALb2 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC :561
TrPALb3 : AGCTAATTATGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC :561
TrPALb4 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC :559
TrPALb5 : AGCTAATTAGGTTTTTGAATGCCGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC :559
TrPALb6 : ------------------------------------------------------------ :   -
TrPALb7 : AGCTAATTAGGTTTTTGAATGCCGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC :558
TrPALb8 : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTTTACAC :522

                  *      620        *      640        *       660
TrPALb1 : ------------------------------------------------------------ :   -
TrPALb2 : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAG--- :618
TrPALb3 : TGCNACACACAGCAACCANAGNTGCATTGCTTTGGTGCANNATCACNCTTCTTCTNNAGG :621
TrPALb4 : TACCACACACGGCAACCAGAGCTGCAATGCT----------------------------- :590
TrPALb5 : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTTCAAG--- :616
TrPALb6 : ------------------------------------------------------------ :   -
TrPALb7 : TACCACACC--------------------------------------------------- :567
TrPALb8 : TACCACACAC-------------------------------------------------- :532

                  *      680        *
TrPALb1 : ---------------------------------- :   -
TrPALb2 : ---------------------------------- :   -
TrPALb3 : AATATTTCTTGAATGGCCTTTGTAAATTTTTGG :654
TrPALb4 : ---------------------------------- :   -
TrPALb5 : ---------------------------------- :   -
TrPALb6 : ---------------------------------- :   -
TrPALb7 : ---------------------------------- :   -
TrPALb8 : ---------------------------------- :   -
```

FIGURE 88 (cont)

```
                    *        20         *        40         *        60
TrPALc : AACAAGATCGTTATGCCTTAGAACTTCACCTCAATGGCTTGGTCCTTTGATTGAAGTGAT :  60

                    *        80         *       100         *       120
TrPALc : AAGATTTTCAACCAAATCAATTGAAAGAGAAATTAACTCGGTCAACGACAACCCTTTGAT : 120

                    *       140         *       160         *       180
TrPALc : CGATGTTTCAAGGAACAAGGCCATTCATGGTGGTAACTTTCAAGGAACACCTATTGGAGT : 180

                    *       200         *       220         *       240
TrPALc : TTCAATGGATAACACACGTTTAGCTCTTGCTTCAATTGGTAAACTCATGTTTGCTCAATT : 240

                    *       260         *       280         *       300
TrPALc : CTCTGAACTTGTTAATGATTTTTACAACAACGGGTTGCCTTCGAATCTTACTGCTAGTAG : 300

                    *       320         *       340         *       360
TrPALc : GAACCCGAGCTTGGACTATGGTTTCAAGGGATCGGAAATTGCCATGGCTTCGTATTGTTC : 360

                    *       380         *       400         *       420
TrPALc : CGAGTTACAATATCTTGCTAATCCTGTCACCACCCATGTCCAAAGTGCCGAGCAACACAA : 420

                    *       440         *       460         *       480
TrPALc : CCAAGATGTTAACTCTTTGGGTTTGATTTCATCTAGAAAAACAAATGAAGCTATTGAGAT : 480

                    *       500         *       520         *       540
TrPALc : TCTCAAGCTCATGTCTTCCACTTTCTTGATTGCATTATGTCAAGCAATCGACTTAAGGCA : 540

                    *       560         *
TrPALc : CTTGGAGGAAAATCTCAGGAACACCGTCAAGAACACGGT : 579
```

FIGURE 89

```
                      *        20         *        40         *        60
TrPALc : TRSLCLRTSPQWLGPLIEVIRFSTKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGV :  60

                      *        80         *       100         *       120
TrPALc : SMDNTRLALASIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGSEIAMASYCS : 120

                      *       140         *       160         *       180
TrPALc : ELQYLANPVTTHVQSAEQHNQDVNSLGLISSRKTNEAIEILKLMSSTFLIALCQAIDLRH : 180

                      *
TrPALc : LEENLRNTVKNT : 192
```

FIGURE 90

```
                         *        20         *        40         *        60
TrPALd : GGTCAATNCAGCTTNGGAGATCTAGTCCCCCTTTCTTACTNTGCTGGTTTACTAACTGGA :  60

                         *        80         *       100         *       120
TrPALd : AGACCNAATTCTAAAGCTCATGGGCCTACAGGAGAAGTACTTAATGCAAAAGAAGCTTTT : 120

                         *       140         *       160         *       180
TrPALd : CAATTGGCTGGAATCAATACCGAGTTCTTTGAATTACAACCAAAAGAAGGTCTTGCACTT : 180

                         *       200         *       220         *       240
TrPALd : GTTAATGGAACTGCTGTTGGTTCTGGTTTAGCTTCTATTGTTCTTTTTGAGGCTAACATA : 240

                         *       260         *       280         *       300
TrPALd : TTGGCGGTGTTGTCTGAAGTTCTATCGGCAATTTTCGCTGAAGTTATGCAAGGGAAGCCC : 300

                         *       320         *       340         *       360
TrPALd : GAATTTACTGATCATTTGACACATAAGTTGAAGCACCACCCTGGTCAAATTGAGGCTGCT : 360

                         *       380         *       400         *       420
TrPALd : GCTATTATGGAACACATTTTGGATGGGAGTGCTTATGTTAAAGACGCGAAGAAGTTGCAT : 420

                         *       440         *       460         *       480
TrPALd : GAGATGGACCCTTTACAGAAGCCAAAGCAAGATAGATATGCACTTAGAACTTCACCACAA : 480

                         *       500         *       520         *       540
TrPALd : TGGCTTGGTCCTTTGATTGAAGTGATTAGATTTTCAACCAAGTCAATTGAGAGAGAGATC : 540

                         *       560         *       580         *
TrPALd : AACTCTGTCAATGACAACCCTTTGATTGATGTTTCGAGAAACAAGGCTTTG : 591
```

FIGURE 91

```
                       *        20         *        40         *        60
TrPALd : GQXSXGDLVPLSYXAGLLTGRXNSKAHGPTGEVLNAKEAFQLAGINTEFFELQPKEGLAL :  60

                       *        80         *       100         *       120
TrPALd : VNGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIEAA : 120

                       *       140         *       160         *       180
TrPALd : AIMEHILDGSAYVKDAKKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREI : 180

                       *
TrPALd : NSVNDNPLIDVSRNKAL : 197
```

FIGURE 92

```
                     *        20         *        40         *        60
TrPALe : GNNGGAAATTNCAACTCNATTNTTTCTTTNTATAATNTTTGAATTTCCTTCTCTCTCAAA :  60

                     *        80         *       100         *       120
TrPALe : TTCTATAGCTACTCTACCACATCACACAACATAACAAATTAAGAAATATTCATTACTATA : 120

                     *       140         *       160         *       180
TrPALe : CTATTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAAACAACGGCAAGATTGATTC : 180

                     *       200         *       220         *       240
TrPALe : ATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGATGCTGATCCTTTGAA : 240

                     *       260         *       280         *       300
TrPALe : TTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAACGTATGGT : 300

                     *       320         *       340         *       360
TrPALe : GGAGGAGTACCGGAAGCCGATTGTCCGTCTTGGTGGCGAGACGCTGACGATTTCTCAGGT : 360

                     *       380         *       400         *       420
TrPALe : GGCTGCCATTGCTGCACACGATGGTGCGATGGTTGAGCTGTCGGAATCTGCTAGAGCCGG : 420

                     *       440         *       460         *       480
TrPALe : CGTTAAGGCAAGCAGTGATTGGGTTATGGAGAGTATGAACAAAGGTACTGACAGTTATGG : 480

                     *       500         *       520         *       540
TrPALe : TGTCACCACAGGGTTCGGCGCTACCTCNCACCGCCGAACCAAACAAGGTGGTGCTTTACA : 540

                     *       560         *       580         *
TrPALe : GAAAGGGCTCATAAGGTTTTTGAATGCTGGAATATTTGNAAATGNAACTGAN : 592
```

FIGURE 93

```
                     *        20         *        40         *        60
TrPALe : MEVVAAAITKNNGKIDSFCLNHANANNMKVNDADPLNWGVAAEAMKGSHLDEVKRMVEEY :  60

                     *        80         *       100         *       120
TrPALe : RKPIVRLGGETLTISQVAAIAAHDGAMVELSESARAGVKASSDWVMESMNKGTDSYGVTT : 120

                     *       140         *
TrPALe : GFGATXHRRTKQGGALQKGLIRFLNAGIFXNXTX : 154
```

FIGURE 94

```
                      *        20         *        40         *        60
TrPALf : CNATTGTTAGTNGTTTCCNCCCACCCACATAACAAATACATAATTCTCTCCTCTGATCAC :  60

                      *        80         *       100         *       120
TrPALf : AATTATTACTTTACTACACCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT : 120

                      *       140         *       160         *       180
TrPALf : ACCAATGGCCATGCTGAAACAACTTTTAGCGTGACCAAAAGTGNNGGNGATCCACTCAAC : 180

                      *       200         *       220         *       240
TrPALf : TGGCGNGCAGCCGCGGAGTCGTCGACGGGGAGTCATTTGGATGAGGTGAAGCGTATGGNG : 240

                      *       260         *       280         *       300
TrPALf : GAGGAGTACCGTAATCCGNTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTNNGGTA : 300

                      *       320         *       340         *       360
TrPALf : NCTGGAATTGCTTCTCATGATAGTGGAGTGAGGGTGGAGCTGTCCGAGTTCGCAAGGGCC : 360

                      *       380         *       400         *       420
TrPALf : GGCGTTAAGGCGAGTAGTGATTGNGTGATGGATAGCATGAACAATGGGACTGATAGTTAC : 420

                      *       440         *       460         *       480
TrPALf : GGTGTTACCACCGCNTTTGGTGCCACCTGTCACCGGAGAACCAAGCCANGGTGGTGCCTT : 480

                      *       500         *       520         *       540
TrPALf : GCAGAAGGAGCTAAATTNNGGTGTTTTGAANGCTGGNAATANTTTGGCNNTGGTTCAGAA : 540

                      *       560
TrPALf : ATCTNAACTTGTNCACTTACCACACC : 566
```

FIGURE 95

```
                        *        20         *        40         *        60
TrPALf : MEGITNGHAETTFSVTKSXXDPLNWXAAAESSTGSHLDEVKRMXEEYRNPXVKIGGETLT :  60

                        *        80         *       100         *       120
TrPALf : IAXVXGIASHDSGVRVELSEFARAGVKASSDXVMDSMNNGTDSYGVTTXFGATCHRRTKP : 120

                        *       140         *
TrPALf : XWCLAEGAKXXCFEXWXXFGXGSEIXTCXLTT : 152
```

FIGURE 96

```
                     *        20         *        40         *        60
TrPALf1 : CNATTGTTAGTNGTTTCCNCCCACCNACATAACNAATACNTANTTCTCTCCTCTGATCAC : 60
TrPALf2 : -------------------------CCCATAACAAATACATTATTCTCTCCTCTGATCAC : 35

                     *        80         *       100         *       120
TrPALf1 : AATTATTACTTTNCTACACCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT :120
TrPALf2 : AATTATTACTTTACTACACCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT : 95

                     *       140         *       160         *       180
TrPALf1 : ACCAATGGCCATGCTGAAACAACTTTTTGCGTGACCAAAAGTGTNGGNGATNNANTGNNC :180
TrPALf2 : ACCAATGGCCATGCTGAAACAACTTTTATCGTGACCAAAAGTGNTGGTGATCCACTCAAC :155

                     *       200         *       220         *       240
TrPALf1 : TGTCGNGN---------------------------------------------------- :188
TrPALf2 : TGGGGTGCAGCCGCGGAGTCGTCGACGGGGAGTCATTTGGATGAGGTGAAGCGTATGGNG :215

                     *       260         *       280         *       300
TrPALf1 : ------------------------------------------------------------ :  -
TrPALf2 : GAGGAGTACCGTAATCCGNTGGTTAAAATTGGCGGCGAGACGCTTACCATTGCTNNGGTA :275

                     *       320         *       340         *       360
TrPALf1 : ------------------------------------------------------------ :  -
TrPALf2 : NCTGGAATTGCTTCTCATGATAGTGGAGTGAGGGTGGAGCTGTCCGAGTTCGCAAGGGCC :335

                     *       380         *       400         *       420
TrPALf1 : ------------------------------------------------------------ :  -
TrPALf2 : GGCGTTAAGGCGAGTAGTGATTGNGTGATGGATAGCATGAACAATGGGACTGATAGTTAC :395

                     *       440         *       460         *       480
TrPALf1 : ------------------------------------------------------------ :  -
TrPALf2 : GGTGTTACCACCGCNTTTGGTGCCACCTGTCACCGGAGAACCAAGCCANGGTGGTGCCTT :455

                     *       500         *       520         *       540
TrPALf1 : ------------------------------------------------------------ :  -
TrPALf2 : GCAGAAGGAGCTAAATTNNGGTGTTTTGAANGCTGGNAATANTTTGGCNNTGGTTCAGAA :515

                     *       560
TrPALf1 : -------------------------- :  -
TrPALf2 : ATCTNAACTTGTNCACTTACCACACC :541
```

FIGURE 97

```
                    *        20         *        40         *        60
TrVRa : GTAAGAGTTGAGAAAAAANACCAATAAAGTAAACNCTATNTAGAAAGAGAGTCAAAAATG :    60

                    *        80         *       100         *       120
TrVRa : GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGGTTCATGGATC :   120

                    *       140         *       160         *       180
TrVRa : ATCAAGAGTCTTCTTGAAAATGGATACTCTGTTAATACCACTATTAGAGCTGATCCAGAA :   180

                    *       200         *       220         *       240
TrVRa : CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTC :   240

                    *       260         *       280         *       300
TrVRa : TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCGGG :   300

                    *       320         *       340         *       360
TrVRa : ATATTCCACACCGCTTCACCAATCGATTTCGCCGTGAGTGAGCCAGAAGAAATAGTGACA :   360

                    *       380         *       400         *       420
TrVRa : AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAAGCATGTGTGAATTCAAAGACAGTG :   420

                    *       440         *       460         *       480
TrVRa : AAGAGATTTATTTACACTTCAAGNGGTTCTGCTGTTTCATTCAATGGAAAAAACAAAGAT :   480

                    *       500         *       520         *       540
TrVRa : GNNTNGGATGAGAGTGATTGGAGTGATGTTGATTTGCTTAGAAGTGTTAAACCATTTGGT :   540

                    *       560         *       580         *       600
TrVRa : TGGAGTTATGGNGTGTTCAAGACTTTGGCTGAGAAAGCAGTGCTTGAATTTGGTCNACAA :   600

                    *       620         *       640         *       660
TrVRa : AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTATTGTTGGAGGTTTTGTTTGTCCC :   660

                    *       680         *       700         *       720
TrVRa : AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT :   720

                    *       740         *       760         *       780
TrVRa : GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA :   780

                    *       800         *       820         *       840
TrVRa : CTTGAGAATCCTGTTCCAGGAGGTAGATATAATTGTTCACCATTCTTTGTATCTATTGAA :   840

                    *       860         *       880         *       900
TrVRa : GAAATGTCACAGCTTCTCTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG :   900

                    *       920         *       940         *       960
TrVRa : TTGAAGGAAATTAAAGGGGCAAGATTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT :   960

                    *       980         *      1000         *      1020
TrVRa : GGTTTTGAGTTTAAGTATAGTGTCGATGATATGTTCGATGATGCGATTCAATGCTGCAAG :  1020

                    *      1040         *      1060         *      1080
TrVRa : GAAAAAGGCTATCTCTAAGCATGTATTTGAAAATTCCATGAAGTTGAGAAAACAATAATG :  1080

                    *      1100         *      1120         *      1140
TrVRa : TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT :  1140

                    *      1160         *      1180
TrVRa : CAATCAAATAATGAAATAATCTGTTCATTTTTCCGAAAAAAAAAA : 1185
```

FIGURE 98

```
                    *        20          *        40          *        60
TrVRa : MAEGKGRVCVTGGTGFLGSWIIKSLLENGYSVNTTIRADPERKRDVSFLTNLPGASERLH :  60

                    *        80          *       100          *       120
TrVRa : FFNADLDDPESFNEAIEGCVGIFHTASPIDFAVSEPEEIVTKRTVDGALGILKACVNSKT : 120

                    *       140          *       160          *       180
TrVRa : VKRFIYTSXGSAVSFNGKNKDXXDESDWSDVDLLRSVKPFGWSYXVFKTLAEKAVLEFGX : 180

                    *       200          *       220          *       240
TrVRa : QNGIDVVTLILPFIVGGFVCPKLPDSVEKALVLVLGKKEQIGIISFHMVHVDDVARAHIY : 240

                    *       260          *       280          *       300
TrVRa : LLENPVPGGRYNCSPFFVSIEEMSQLLSAKYPEYQILSVDELKEIKGARLPDLNSKKLVD : 300

                    *       320
TrVRa : AGFEFKYSVDDMFDDAIQCCKEKGYL : 326
```

FIGURE 99

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```
                *        20         *        40         *        60
TrVRa1 : GTAGTAGTTGAGAAAAAATACNAATAAAGTAAACNCTATNTAGAAAGAGAGTCAAAAATG :  60
TrVRa2 : ---AGAGTTGAGAAAAAANNCCAATAAAGTAAACNCTATNTAGAAAGAGAGTNNAAAATG :  57
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                *        80         *       100         *       120
TrVRa1 : GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGGTTCATGGATC : 120
TrVRa2 : GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGGTTCATGGATC : 117
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                *       140         *       160         *       180
TrVRa1 : ATCAAGAGTCTTCTTGAAAATGGATACTCTGTTAATACCACTATTAGAGCTGATCCAGAA : 180
TrVRa2 : ATCAAGAGTCTTCTTGAAAATGGATACTCTGTTAATACCACTATTAGAGCTGATCCAGAA : 177
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                *       200         *       220         *       240
TrVRa1 : CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTC : 240
TrVRa2 : CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTC : 237
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                *       260         *       280         *       300
TrVRa1 : TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCGGG : 300
TrVRa2 : TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCGGG : 297
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                *       320         *       340         *       360
TrVRa1 : ATATTCCACACCGCTTCACCAATCGATTTCGCCGTGAGTGAGCCAGAAGAAATAGTGACA : 360
TrVRa2 : ATATTCCACACCGCTTCACCAATCGATTTCGCCGTGAGTGAGCCAGAAGAAATAGTGACA : 357
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                *       380         *       400         *       420
TrVRa1 : AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAAGCATGTGTGAATTCAAAGACAGTG : 420
TrVRa2 : AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAAGCATGTGTGAATTCAAAGACAGTG : 417
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -
```

FIGURE 100

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```
                     *       440         *       460         *       480
TrVRa1 : AAGAGATTTATTTACACTTCAAGNGGTTCTGCTGTTTCATTCAATGNAAAAANCAAAGAT : 480
TrVRa2 : AAGAGATTTATTTACACTTCAAGTGGTTCTGCTGTTTCATTCAATGGAAAAAACAAAGAT : 477
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                     *       500         *       520         *       540
TrVRa1 : GNNTNNNATGANA----------------------------------------------- : 493
TrVRa2 : GTTTTGGATGAGAGTGATTGGAGTGATGTTGATTTGCTTAGAAGTGTTAAACCATTTGGT : 537
TrVRa3 : ------------------------------------------------------------ :   -
TrVRa4 : ------------------------------------------------------------ :   -
TrVRa5 : ------------------------------------------------------------ :   -
TrVRa6 : ------------------------------------------------------------ :   -

                     *       560         *       580         *       600
TrVRa1 : ------------------------------------------------------------ :   -
TrVRa2 : TGGAGTTATGGTGTNTTCAAGACTTTGGCTGAGAAAGCAGTGCTTGAATTTGGTCAACAA : 597
TrVRa3 : -----------GNGTGTTTAAGACTTTAGCTGAGAAAGCAGTGCTTGAATTTGGTNNACAA :  50
TrVRa4 : -------------------AGACGTTNGCTGAGAAAGCNGTGCTTGAATTTGGTCNACAA :  41
TrVRa5 : -----------------------------------------NNTTGAATTTGGNCNACAA :  19
TrVRa6 : -----------------------------------------NNTTGAATTTGGTNNACAA :  19

                     *       620         *       640         *       660
TrVRa1 : ------------------------------------------------------------ :   -
TrVRa2 : AATG-------------------------------------------------------- : 601
TrVRa3 : AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTATTGTTGGAGGTTTTGTTTGTCCT : 110
TrVRa4 : AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTATTGTTGGAGGTTTTGTTTGTCCT : 101
TrVRa5 : AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTNTTGTTGGAGGTTTTGTTTGTCCC :  79
TrVRa6 : AATGGGATTGATGTTGTTACTTTGATTCTTCCTTTTNTTGTTGGAGGTTTTGTTTGTCCC :  79

                     *       680         *       700         *       720
TrVRa1 : ------------------------------------------------------------ :   -
TrVRa2 : ------------------------------------------------------------ :   -
TrVRa3 : AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT : 170
TrVRa4 : AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT : 161
TrVRa5 : AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT : 139
TrVRa6 : AAGCTTCCTGATTCTGTTGAGAAAGCTCTTGTTTTGGTACTAGGCAAAAAGGAACAAATT : 139

                     *       740         *       760         *       780
TrVRa1 : ------------------------------------------------------------ :   -
TrVRa2 : ------------------------------------------------------------ :   -
TrVRa3 : GGTATTATAAGTTTCCACATGGTACATGTGGATGATGTGGCTAGAGCACATATCTATCTA : 230
TrVRa4 : GGTATTATAAGTTTCCACATGGTACATGTGGATGATGTGGCTAGAGCACATATCTATCTA : 221
TrVRa5 : GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA : 199
TrVRa6 : GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA : 199

                     *       800         *       820         *       840
TrVRa1 : ------------------------------------------------------------ :   -
TrVRa2 : ------------------------------------------------------------ :   -
TrVRa3 : CTTGAGAATCCTGTTCCAGGAGGTAGATATAATTGTTCACCATTCTTTGTATCTATTGAA : 290
TrVRa4 : CTTGAGAATCCTGTTCCAGGAGGTAGATATAATTGTTCACCATTCTTTGTATCTATTGAA : 281
TrVRa5 : CTTGAGAATCCTGTTCCAGGAGGTAGATATAATTGTTCACCATTCTTTGTATCTATTGAA : 259
TrVRa6 : CTTGAGAATCCTGTTCCAGGAGGTAGATATAATTGTTCACCATTCTTTGTATCTATTGAA : 259
```

FIGURE 100 (cont)

```
                        *       860         *       880         *        900
TrVRa1 : ------------------------------------------------------------ :    -
TrVRa2 : ------------------------------------------------------------ :    -
TrVRa3 : GAAATGTCACAGCTTCTTTCAGCCAAATATCCAGAATATCAAATACTATCTGTAGATGAG : 350
TrVRa4 : GAAATGTCACAGCTTCTTTCAGCCAAATATCCAGAATATCAAATACTATCTGTAGATGAG : 341
TrVRa5 : GAAATGTCACAGCTTCTCTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG : 319
TrVRa6 : GAAATGTCACAGCTTCTCTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG : 319

                        *       920         *       940         *        960
TrVRa1 : ------------------------------------------------------------ :    -
TrVRa2 : ------------------------------------------------------------ :    -
TrVRa3 : TTGAAGGAAATTAAAGGGGCAAGGTTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT : 410
TrVRa4 : TTGAAGGAAATTAAAGGGGCAAGGTTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT : 401
TrVRa5 : TTGAAGGAAATTAAAGGTGCAAGATTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT : 379
TrVRa6 : TTGAAGGAAATTAAAGGTGCAAGATTGCCAGATTTGAACTCGAAGAAGCTCGTGGACGCT : 379

                        *       980         *      1000         *       1020
TrVRa1 : ------------------------------------------------------------ :    -
TrVRa2 : ------------------------------------------------------------ :    -
TrVRa3 : GGTTTTGAGTTTAAGTATAGTGTCGATGATATGTTCGATGATGCGATTCAATGCTGCAAG : 470
TrVRa4 : GGTTTTGAGTTTAAGTATAGTGTCGATGATATGTTCGATGATGCGATTCAATGCTGCAAG : 461
TrVRa5 : GGTTTTGAGTTTAAGTATAGTGTCGATGATATGTTTGATGATGCGATTCAATGCTGCAAG : 439
TrVRa6 : GGTTTTGAGTTTAAGTATAGTGTCGATGATATGTTTGATGATGCGATTCAATGCTGCAAG : 439

                        *      1040         *      1060         *       1080
TrVRa1 : ------------------------------------------------------------ :    -
TrVRa2 : ------------------------------------------------------------ :    -
TrVRa3 : GAAAAAGGCTATCTCTAAGCATGTGTTTGAAAATTCCATGAAGTTGAGAAAACAATAGTG : 530
TrVRa4 : GAAAAAGGCTATCTCTAAGCATGTGTTTGAAAATTCCATGAAGTTGAGAAAACAATAGTG : 521
TrVRa5 : GAAAAAGGCTATCTCTAAGCATGTATTTGAAAATTCCATGAAGTTGAGAAAACAATAATG : 499
TrVRa6 : GAAAAAGGCTATCTCTAAGCATGTATTTGAAAATTCCATGAAGTTGAGAAAACAATAATG : 499

                        *      1100         *      1120         *       1140
TrVRa1 : ------------------------------------------------------------ :    -
TrVRa2 : ------------------------------------------------------------ :    -
TrVRa3 : TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT : 590
TrVRa4 : TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT : 581
TrVRa5 : TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT : 559
TrVRa6 : TGCCTAAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCATTAAGTTATTTGTGAT : 559

                        *      1160         *      1180
TrVRa1 : --------------------------------------------- :    -
TrVRa2 : --------------------------------------------- :    -
TrVRa3 : CAATCAAATAATGAAATAATCTG---------------------- :  613
TrVRa4 : CAATCAAATAATGAAATAATC------------------------ :  602
TrVRa5 : CAATCAAATAATGAAN----------------------------- :  575
TrVRa6 : CAATCAAATAATGAAATAATCTGTTCATTTTTCCGAAAAAAAAAA :  604
```

FIGURE 100 (cont)

```
                    *        20         *        40         *        60
LpDFRa : GTSYWTTCGAGTTTGAGAGAATGGCTTCCAGGGCAAGGTGTGTGTTACTGGGGCCTCTGG :  60

                    *        80         *       100         *       120
LpDFRa : CTTTGTTGCTTCTTGGCTTGTCAAAAGACTACTCGAGTCCGGTTATAATGTTCTAGGGAC : 120

                    *       140         *       160         *       180
LpDFRa : AGTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACTTAGCAGGGGCCAA : 180

                    *       200         *       220         *       240
LpDFRa : GGAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAGAAGGGAGCTTCGATGATGCTGT : 240

                    *       260         *       280         *       300
LpDFRa : GATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAA : 300

                    *       320         *       340         *       360
LpDFRa : GGAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAA : 360

                    *       380         *       400         *       420
LpDFRa : GAATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGA : 420

                    *       440         *       460         *       480
LpDFRa : TGAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTT : 480

                    *       500         *       520         *       540
LpDFRa : CTGTGAAAGTATCCAGGTATGGTATGGTGTCGCGAAGATCCTTGCTGAGAAATCAGCTTG : 540

                    *       560         *       580         *       600
LpDFRa : GGAGTTCGCCAAGGAGAACAACATCGACCTAGTGGCTGTTCTTCCAACGTTCGTGATTGG : 600

                    *       620         *       640         *       660
LpDFRa : ACCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAAAGG : 660

                    *       680         *
LpDFRa : AGAGACAGAGAAGTTCACCATGTTTKGGAAGGATG : 695
```

FIGURE 101

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```
                     *        20         *        40         *        60
LpDFRa  : VFSSLREWLPGQVCVTGASGFVASWLVKRLLESGYNVLGTVRDPGNQKKVAHLWNLAGAK :  60

                     *        80         *       100         *       120
LpDFRa  : ERLELVKADLLEEGSFDDAVMACEGVFHTASPIITKSDTKEEMLDSAINGTLNVLRSCKK : 120

                     *       140         *       160         *       180
LpDFRa  : NPFLKRVVLTSSSSTVRLRDEAEFPPNVLLDETSWSSVEFCESIQVWYGVAKILAEKSAW : 180

                     *       200         *       220         *
LpDFRa  : EFAKENNIDLVAVLPTFVIGPNLSSELGPTVLDVLGLFKGETEKFTMFGKD : 231
```

FIGURE 102

```
                   *        20         *        40         *        60
LpDFRa1 : ----------GTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 50
LpDFRa2 : ------TCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 54
LpDFRa3 : -------------------GTNGGCTTCCAGGGCCGGTGTGTGTTACTGGGGCCTCTGGC : 41
LpDFRa4 : --GCATTCGAGTTTGAGAGAATGGCTTCCAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 58
LpDFRa5 : GTCTTTCCAGTTTGAGCAGAATGGCTTCNAGGGCAGGTGTGTGTTACTGGGGCCTCTGGC : 60

                   *        80         *       100         *       120
LpDFRa1 : TTTGTTGCTTCTTGGCTTGTCAAAAGACTACTCGAGTCCGGTTATAATGTTCTAGGGACA :110
LpDFRa2 : TTTGTTGCTTCTTGGCTTGTCAAAAGACTACTCGAGTCCGGTTATAATGTTCTAGGGACA :114
LpDFRa3 : TTTGTTGCTTCTTGGCTTGTNAAA-GACTACTCGAGTCCGGTTATAATGTTCTAGGGACA :100
LpDFRa4 : TTTGTTGCTTCCTGGCTTGTCAAAAGACTTCTCGAGTCCGGTTATAATGTTCTAGGGACA :118
LpDFRa5 : TTTGTTGCTTCCTGGCTTGTCAAAAGACTTCTCGAGTCCGGTTATAATGTTCTAGGGACA :120

                   *       140         *       160         *       180
LpDFRa1 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACTTAGCAGGGGCCAAG :170
LpDFRa2 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACTTAGCAGGGGCCAAG :174
LpDFRa3 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACTTAGCAGGGGCCAAG :160
LpDFRa4 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAGCTTAGCAGGGGCCAAG :178
LpDFRa5 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAGCTTAGCAGGGGCCAAG :180

                   *       200         *       220         *       240
LpDFRa1 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAGAAGGGAGCTTCGATGATGCTGTG :230
LpDFRa2 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAGAAGGGAGCTTCGATGATGCTGTG :234
LpDFRa3 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAGAAGGGAGCTTCGATGATGCTGTG :220
LpDFRa4 : GAAAGGCTGGAGCTTGTCAGAGCTGACCTCTTGGAAGAAGGGAGCTTCGATGATGCCGTG :238
LpDFRa5 : GAAAGGCTGGAGCTTGTCAGAGCTGACCTCTTGGAAGAAGGGAGCTTCGATGATGCCGTG :240

                   *       260         *       280         *       300
LpDFRa1 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :290
LpDFRa2 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :294
LpDFRa3 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :280
LpDFRa4 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :298
LpDFRa5 : ATGGCCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG :300

                   *       320         *       340         *       360
LpDFRa1 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAAG :350
LpDFRa2 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAAG :354
LpDFRa3 : GAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGNGCTGAGATCGNGCAAGAAG :340
LpDFRa4 : GAAGAAATGCTTGATTCTGCAATAAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAAG :358
LpDFRa5 : GAAGAAATGCTTGATTCTGCAATAAACGGCNCTCTAAACGTGCTGNNATCCCGGTNAAAA :360

                   *       380         *       400         *       420
LpDFRa1 : AATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGAT :410
LpDFRa2 : AATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGAT :414
LpDFRa3 : AATNCTTTTCTNAAAAGGGNTGNTCTCACGTCATCATCGCCACCCGNGANGCTGANGGAT :400
LpDFRa4 : AATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGAT :418
LpDFRa5 : AAAAN------------------------------------------------------- :365

                   *       440         *       460         *       480
LpDFRa1 : GAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTTC :470
LpDFRa2 : GAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTTC :474
LpDFRa3 : GAANCTGANTTCCCACCCAACGNGN----------------------------------- :425
LpDFRa4 : GAAGCTGAATTCCCACCCAACGTGTTGCTGGATGAAACATCATGGAGCTCCGTGGAGTTC :478
LpDFRa5 : ------------------------------------------------------------ :  -
```

FIGURE 103

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```
                          *       500         *       520         *       540
LpDFRa1 : TGTGAAAGTATCCAGGTATGGTATGGTGTCGCGAAGATCCTTGCTGAGAAATCAGCTTGG :530
LpDFRa2 : TGTGAAAGTATCCAGGTATGGTATGGTGTCGCGAAGATCCTTGCTGAGAAATCAGCTTGG :534
LpDFRa3 : ------------------------------------------------------------ :   -
LpDFRa4 : TGTGAAAGTATCCAGGTATGGTACGGTGTCGCAAAGATCCTTGCCGAGAAATCAGCCTGG :538
LpDFRa5 : ------------------------------------------------------------ :   -

                          *       560         *       580         *       600
LpDFRa1 : GAGTTCGCCAAGGAGAACAACATCGACCTAGTGGCTGTTCTTCCAACGTTCGTGATTGGA :590
LpDFRa2 : GAGTTCGCCAAGGAGAACAACATCGACCTAGTGGCTGTTCTTCCAACGTTCGTGATTGGA :594
LpDFRa3 : ------------------------------------------------------------ :   -
LpDFRa4 : GAGTTTGCCAAGGAGAACAACATCGACCTAGTGGCTGTTCTTCCAACATTCGTGATTGGA :598
LpDFRa5 : ------------------------------------------------------------ :   -

                          *       620         *       640         *       660
LpDFRa1 : CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAAAGGA :650
LpDFRa2 : CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAANGGA :654
LpDFRa3 : ------------------------------------------------------------ :   -
LpDFRa4 : CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTTAGATGTCCTTGGCTTATTTAAAGGA :658
LpDFRa5 : ------------------------------------------------------------ :   -

                          *       680         *
LpDFRa1 : GAGACAGAGAAGTTCAC----------------- : 667
LpDFRa2 : GAGACAGAGAAGTTCACCATGTTTTGGAAGGATG : 688
LpDFRa3 : ---------------------------------- :   -
LpDFRa4 : GAGACAGAGAAGTTCACCATGTTTGGGAAGGAN- : 691
LpDFRa5 : ---------------------------------- :   -
```

FIGURE 103 (cont)

```
                     *        20          *        40          *        60
LpDFRb : GTCCTCGCCTACGAGCGCCCCGACGCCCGCGGCCGCTACCTCTGCATCGGGGCCGTGCTG :  60

                     *        80          *       100          *       120
LpDFRb : CACCGCGCGCACTTCCTAAAGCTTCTCAAGGACCTCTTCCCGCAGTACTCCTTCACCGCC : 120

                     *       140          *       160          *       180
LpDFRb : AAGTGCGAAGACGACGGCAAGCCCATGGCGAAGCCGTACAAGTTCTCCNACCAGAGGCTC : 180

                     *       200          *       220          *       240
LpDFRb : AGGGACCTGGGATTAAAATTCACTCCGCTGGCGGAAAGTTTGTACGAGACCGTGACGTGC : 240

                     *       260          *       280          *       300
LpDFRb : CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCATGGCGCCAAAGCGTGCATACCTA : 300

                     *       320          *       340          *       360
LpDFRb : TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT : 360

                     *       380          *       400          *       420
LpDFRb : TCACCATGGAATTGTGTATTTCACAAAGTTTGAATTCTTATTTTTTTATTATGAAGAAA : 420

                     *       440          *       460          *       480
LpDFRb : TACGGAAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT : 480

                     *       500          *       520
LpDFRb : CTTGTTCAAGAATGAATGATAAAGTATTTTTTGCAAAAAAAAAA : 524
```

FIGURE 104

```
                      *        20          *        40          *        60
LpDFRb : VLAYERPDARGRYLCIGAVLHRAHFLKLLKDLFPQYSFTAKCEDDGKPMAKPYKFSXQRL :  60

                      *        80          *       100
LpDFRb : RDLGLKFTPLAESLYETVTCLQKNGHLPLPAPMAPKRAYL : 100
```

FIGURE 105

```
                         *        20         *        40         *        60
LpDFRb1 : GTCCTCGCCTACGAGCGCCCCGACGCCCGCGGCCGCTACCTCTGCATCGGGGCCGTGCTG : 60
LpDFRb2 : ------------------------------------------------------------ :  -
LpDFRb3 : ------------------------------------------------------------ :  -

                         *        80         *       100         *       120
LpDFRb1 : CACCGCGCGCACTTCCTAAAGCTTCTCAAGGACCTCTTCCCGCAGTACTCCTTCACCGCC :120
LpDFRb2 : ------------------------------------------------------------ :  -
LpDFRb3 : ------------------------------------------------------------ :  -

                         *       140         *       160         *       180
LpDFRb1 : AAGTGCGAAGACGACGGCAAGCCCATGGCGAAGCCGTACAAGTTCTCCAACCAGAGGCTC :180
LpDFRb2 : ------------------------------AAGCCGTACAAGTTCTCCNACCAGNNGCTC : 30
LpDFRb3 : -----------------------------------------GTTCTCNNACCAGAGGCTC : 19

                         *       200         *       220         *       240
LpDFRb1 : AGGGACCTGGGATTAAAATTCACTCCGCTGGCGGAAAGTTTGTACGAGACCGTGACGTGC :240
LpDFRb2 : AGGGACCTGGGATTAAAATTCACTCCGCTGGCGGAAAGTTTGTACGAGACCGTGACGTGC : 90
LpDFRb3 : AGGGACCTGGGATTAAAATTCACTCCGCTGGCGGAAAGTTTGTACGAGACCGTGACGTGC : 79

                         *       260         *       280         *       300
LpDFRb1 : CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCGTGGCGCCAAAGCGTGCATACCTA :300
LpDFRb2 : CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCATGGCGCCAAAGCGTGCATACCTA :150
LpDFRb3 : CTGCAAAAAAATGGCCACCTGCCTCTGCCCGCTCCCATGGCGCCAAAGCGTGCATACCTA :139

                         *       320         *       340         *       360
LpDFRb1 : TAATANTACGAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT :360
LpDFRb2 : TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT :210
LpDFRb3 : TAATACTACAAAGACACGGCCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCCGAGGT :199

                         *       380         *       400         *       420
LpDFRb1 : TCACCATGGAATTGTGTATTTCAGAAAGTTTGAATTCTTATTTTTTTTATTATGAAGGAA :420
LpDFRb2 : TCACCATGGAATTGTGTATTTCACAAAGTTTGAATTCTTATTTTTTTTATTATGAAGAAA :270
LpDFRb3 : TCACCATGGAATTGTGTATTTCACAAAGTTTGAATTCTTATTTTTTTTATTATGAAGAAA :259

                         *       440         *       460         *       480
LpDFRb1 : TACGGATAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT :480
LpDFRb2 : TACGGAAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT :330
LpDFRb3 : TACGGAAAACCAATACTGTATACCAGAGGCAAGTGTAACAATGTAAATAGTCGTGTAAAT :319

                         *       500         *       520
LpDFRb1 : CNTGTTCAAGATTGAATGATAAAGTATTTTTTGCAAAANAAAAA :524
LpDFRb2 : CTTGTTCAAGAATGAATGATAAAGTATTTTTTGCAAAAAAAAAA :374
LpDFRb3 : CTTGTTCAAGAATGAATGATAAAGTATTTTTTGCAAAAAAAAAN :363
```

FIGURE 106

```
                 *        20         *        40         *        60
LpF3Ha : TCTCNAGACACACTGTGTAACCACGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA :   60
                 *        80         *       100         *       120
LpF3Ha : TCAGCTAACCATTCCTCAACTAGAATAAGCATGGCTCCGGCGATGTCCAACCCTCTCCTC :  120
                 *       140         *       160         *       180
LpF3Ha : AGTGATCGGGTGGCACGCTCCAAGAAAGTCCCATCTAGCCACGTTAGAGCGGTGGGAGAC :  180
                 *       200         *       220         *       240
LpF3Ha : CGCCCAGACCTCGCCAATGTCGACCACGAGTCCGGCGCGGGCATTCCGCTCATCGACCTG :  240
                 *       260         *       280         *       300
LpF3Ha : AAGCAGCTCGAAGGTCCAGGGCGCCGCAGGGTCGTCGAGGCCATCGGCTCCGCGTGCGAG :  300
                 *       320         *       340         *       360
LpF3Ha : AACGATGGGTTTTTCATGGTGACGAATCATGGCATCCCAGAGGCGGTCGTGGAGGGGATG :  360
                 *       380         *       400         *       420
LpF3Ha : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGGAGTCGGAGCGGCTCAAGTGCTACTCC :  420
                 *       440         *       460         *       480
LpF3Ha : GACGACCCCAAGAAGGCGGTCCGGCTGTCGACGAGCTTCAACGTGCGCACGGAGAAGGTG :  480
                 *       500         *       520         *       540
LpF3Ha : AGCAACTGGCGCGACTTCCTCCGGCTGCATTGCTACCCTCTTGAGAGCTTCGTCGACCAG :  540
                 *       560         *       580         *       600
LpF3Ha : TGGCCGTCGAACCCGCCCGCCTTCAGGCAAGTCGTCGGCACCTACTCGACGGAAGCGAGA :  600
                 *       620         *       640         *       660
LpF3Ha : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC :  660
                 *       680         *       700         *       720
LpF3Ha : ATGGTGAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAACTACTACCCGCCGTGC :  720
                 *       740         *       760         *       780
LpF3Ha : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCACACGGACCCCAACGCCCTCACCATC :  780
                 *       800         *       820         *       840
LpF3Ha : CTCCTCATGGATCCCCACGTCTCCGGCCTCCAGGTCCTCAGGGACGGCGCCAAGTGGATC :  840
                 *       860         *       880         *       900
LpF3Ha : GCCGTCCACCCACGCCCCAACGCCCTGGTCATCAACCTAGGCGACCAGCTACAGGCGCTG :  900
                 *       920         *       940         *       960
LpF3Ha : AGCAACGGCGCGTACAAGAGCGTGTGGCACCGGGCAGTGGTGAACGCGGAGCAGGAGCGT :  960
                 *       980         *      1000         *      1020
LpF3Ha : CTGTCGGTGGCATCTTTCCTGTGCCCGTGCAACAGCGCGGTTATCTGCCCCGCGCCGAGG : 1020
                 *      1040         *      1060         *      1080
LpF3Ha : CTCGTCGGCGACGGGGAGGACCCCGTCTACCGGAGCTACACCTACGACGAGTACTACAAG : 1080
                 *      1100         *      1120         *      1140
LpF3Ha : AGGTTTTGGAGCAGGAACCTGGATCAGGAGCACTGCCTCGAGCTCTTCAGGAGTCAGCAC : 1140
```

FIGURE 107

```
                    *        1160          *        1180          *        1200
LpF3Ha : TGATGCTTGAACCTTGAGTTACTAGCTAGCTCTCCTTAACAGTGCAAATCCATGGCCCAA :1200

                    *        1220          *        1240          *        1260
LpF3Ha : GAGGGCCCCGATTGCATGGTTACTTATGTTGTTTGAACTGGTATTGCTTAAGTGCCTAAT :1260

                    *        1280          *        1300          *        1320
LpF3Ha : AACATTGCTACATTCTACTNCTATCTTGTCCGTTTAAAATTATAAGATGGCCTAACCTTT :1320

                    *        1340          *        1360          *        1380
LpF3Ha : TTCTTAATTGTATGCATNCTGAACATATTTAAGTGTGTGTGTTCAGACAGTTTAGTCTGC :1380

LpF3Ha : A :1381
```

FIGURE 107 (cont)

```
                    *        20         *        40         *        60
LpF3Ha : MSNPLLSDRVARSKKVPSSHVRAVGDRPDLANVDHESGAGIPLIDLKQLEGPGRRRVVEA :  60

                    *        80         *       100         *       120
LpF3Ha : IGSACENDGFFMVTNHGIPEAVVEGMLSVAREFFHLPESERLKCYSDDPKKAVRLSTSFN : 120

                    *       140         *       160         *       180
LpF3Ha : VRTEKVSNWRDFLRLHCYPLESFVDQWPSNPPAFRQVVGTYSTEARALALRLLEAISESL : 180

                    *       200         *       220         *       240
LpF3Ha : GLERGHMVKAMGRHAQHMAVNYYPPCPQPELTYGLPGHTDPNALTILLMDPHVSGLQVLR : 240

                    *       260         *       280         *       300
LpF3Ha : DGAKWIAVHPRPNALVINLGDQLQALSNGAYKSVWHRAVVNAEQERLSVASFLCPCNSAV : 300

                    *       320         *       340
LpF3Ha : ICPAPRLVGDGEDPVYRSYTYDEYYKRFWSRNLDQEHCLELFRSQH : 346
```

FIGURE 108

```
                   *        20         *        40         *        60
LpF3Ha1 : TCTCNAGACACACTGTGTAACCACGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA :  60
LpF3Ha2 : --TCTAGACACACTGTGTAACCNCGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA :  58
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
LpF3Ha1 : TCAGCTAACCATTCCTCAACTAGAATAAGCATGGCTCCGGCGATGTCCAACCCTCTCCTC : 120
LpF3Ha2 : TCAGCTAACCATTCCTCAACTAGAATAAGCATGGCTCCGGCGATGTCCAACCCTCTCCTC : 118
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
LpF3Ha1 : AGTGATCGGGTGGCACGCTCCAAGAAAGTCCCATCTAGCCACGTTAGAGCGGTGGGAGAC : 180
LpF3Ha2 : AGTGATCGGGTGGCACGCTCCAAGAAAGTCCCATCTAGCCACGTTAGAGCGGTGGGAGAC : 178
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
LpF3Ha1 : CGCCCAGACCTCGCCAATGTCGACCACGAGTCCGGCGCGGGCATTCCGCTCATCGACCTG : 240
LpF3Ha2 : CGCCCAGACCTCGCCAATGTCGACCACGAGTCCGGCGCGGGCATTCCGCTCATCGACCTG : 238
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
LpF3Ha1 : AAGCAGCTCGAAGGTCCAGGGCGCCGCAGGGTCGTCGAGGCCATCGGCTCCGCGTGCGAG : 300
LpF3Ha2 : AAGCAGCTCGAAGGTCCAGGGCGCCGCAGGGTCGTCGAGGCCATCGGCTCCGCGTGCGAG : 298
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       320         *       340         *       360
LpF3Ha1 : AACGATGGGTTTTTCATGGTGACGAATCATGGCATCCCAGAGGCGGTCGTGGAGGGGATG : 360
LpF3Ha2 : AACGATGGGTTTTTCATGGTGACGAATCATGGCATCCCAGAGGCGGTCGTGGAGGGGATG : 358
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       380         *       400         *       420
LpF3Ha1 : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGGAGTCGGAGCGGCTCAAGTGCTACTCC : 420
LpF3Ha2 : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGGAGTCGGAGCGGCTCAAGTGCTACTCC : 418
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       440         *       460         *       480
LpF3Ha1 : GACGACCCCAAGAAGGCGGTCCGGCTGTCGACGAGCTTCAACGTGCGCACGGAGAAGGTG : 480
LpF3Ha2 : GACGACCCCAAGAAGGCGGTCCGGCTGTCGACGAGCTTCAACGTGCGCACGGAGAAGGTG : 478
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       500         *       520         *       540
LpF3Ha1 : AGCAACTGGCGCGACTTCCTCCGGCTGCATTGCTACCCTCTTGAGAGCTTCGTCGACCAG : 540
LpF3Ha2 : AGCAACTGGCGCGACTTCCTCCGGCTGCATTGCTACCCTCTTGAGAGCTTCGTCGACCAG : 538
LpF3Ha3 : ------------------------------------------------------------ :   -

                   *       560         *       580         *       600
LpF3Ha1 : TGGCCGTCGAACCCGCCCGCCTTCAGGCAAGTCGTCGGCACCTACTCGACGGAAGCGAGA : 600
LpF3Ha2 : TGGCCGTCGAACCCGCCCGCCTTCAGGCAAGTCGTCGGCACCTACTCGACGGAAGCGAGA : 598
LpF3Ha3 : ------------------------------------------------GCGGAAGTCCGC :  12

                   *       620         *       640         *       660
LpF3Ha1 : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC : 660
LpF3Ha2 : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC : 658
LpF3Ha3 : CTGCTGGCGCTTCGGCTTCTGGCCGCGATCTCGCTGGGGCTGGGGCTGGAGNGAGGGTAT :  72

                   *       680         *       700         *       720
LpF3Ha1 : ATGGTGAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAACTACTACCCGCCGTGC : 720
LpF3Ha2 : ATGGTGAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAACTACTACCCGCCGTGC : 718
LpF3Ha3 : CTGGAGAAGGTGCTGGGCCAGCACGAGCAGCACATGGCCGTGAACTACTACCCGCGGTGC : 132
```

FIGURE 109

```
                  *       740         *       760         *       780
LpF3Ha1 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCA------------------------- :755
LpF3Ha2 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCACACGGACCCCAATGCCCTCACCATN :778
LpF3Ha3 : CCCGAGCCGGACCTCACCTACGGCCTGCCCAAGCACACGGACCCCAACGCCCTCACCATC :192

                  *       800         *       820         *       840
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : CT---------------------------------------------------------- :780
LpF3Ha3 : CTCCTCATGGATCCCCACGTCTCCGGCCTCCAGGTCCTCAGGGACGGCGCCAAGTGGATC :252

                  *       860         *       880         *       900
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : GCCGTCCACCCACGCCCCAACGCCCTGGTCATCAACCTAGGCGACCAGCTACAGGCGCTG :312

                  *       920         *       940         *       960
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : AGCAACGGCGCGTACAAGAGCGTGTGGCACCGGGCAGTGGTGAACGCGGAGCAGGAGCGT :372

                  *       980         *      1000         *      1020
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : CTGTCGGTGGCATCTTTCCTGTGCCCGTGCAACAGCGCGGTTATCTGCCCCGCGCCGAGG :432

                  *      1040         *      1060         *      1080
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : CTCGTCGGCGACGGGGAGGACCCCGTCTACCGGAGCTACACCTACGACGAGTACTACAAG :492

                  *      1100         *      1120         *      1140
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : AGGTTTTGGAGCAGGAACCTGGATCAGGAGCACTGCCTCGAGCTCTTCAGGAGTCAGCAC :552

                  *      1160         *      1180         *      1200
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : TGATGCTTGAACCTTGAGTTACTAGCTAGCTCTCCTTAACAGTGCAAATCCATGGCCCAA :612

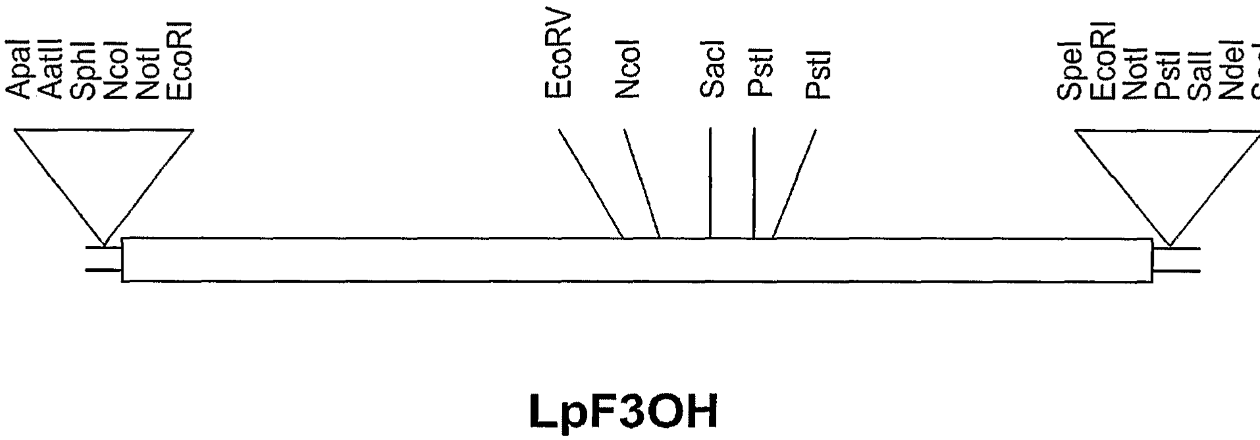
                  *      1220         *      1240         *      1260
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : GAGGGCCCCGATTGCATGGTTACTTATGTTGTTTGAACTGGTATTGCTTAAGTGCCTAAT :672

                  *      1280         *      1300         *      1320
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : AACATTGCTACATTCTACTNCTATCTTGTCCGTTTAAAATTATAAGATGGCCTAACCTTT :732

                  *      1340         *      1360         *      1380
LpF3Ha1 : ------------------------------------------------------------ :   -
LpF3Ha2 : ------------------------------------------------------------ :   -
LpF3Ha3 : TTCTTAATTGTATGCATNCTGAACATATTTAAGTGTGTGTGTTCAGACAGTTTAGTCTGC :792

LpF3Ha1 : - :   -
LpF3Ha2 : - :   -
LpF3Ha3 : A : 793
```

FIGURE 109 (cont)



ApaI
AatII
SphI
NcoI
NotI
EcoRI
EcoRV
NcoI
SacI
PstI
PstI
SpeI
EcoRI
NotI
PstI
SalI
NdeI
SacI
LpF3OH

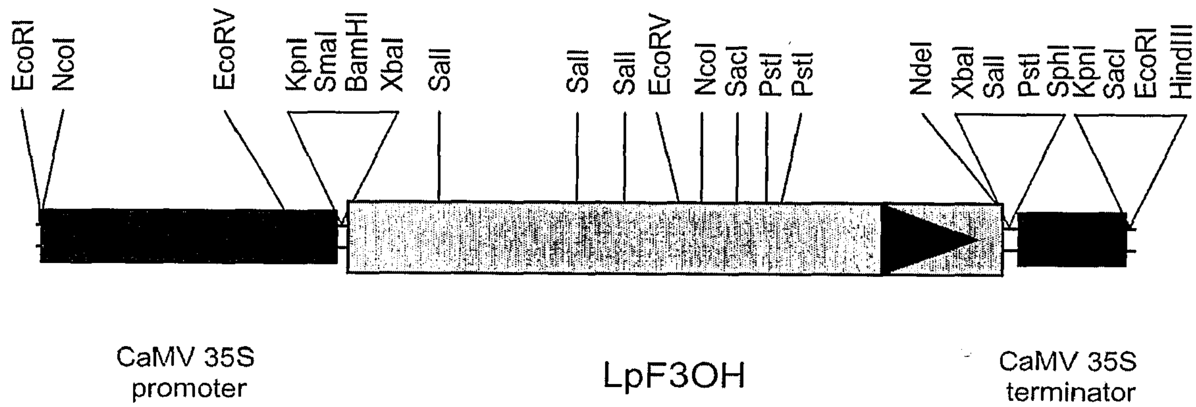
FIGURE 110

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GACTCTCAGA
  51 ACACACTGTG TAACCACGGT AGCGAGTGGC AAGACTAGCA GAAAGTACGG
 101 ACATCAGCTA ACCATTCCTC AACTAGAATA AGCATGGCTC CGGCGATGTC
 151 CAACCCTCTC CTCAGTGATC GGGTGGCACG CTCCAAGAAA GTCCCATCTA
 201 GCCACGTTAG AGCGGTGGGA GACCGCCCAG ACCTCGCCAA TGTCGACCAC
 251 GAGTCCGGCG CGGGCATTCC GCTCATCGAC CTGAAGCAGC TCGAAGGTCC
 301 AGGGCGCCGC AGGGTCGTCG AGGCCATCGG CTCCGCGTGC GAGAACGATG
 351 GGTTTTTCAT GGTGACGAAT CATGGCATCC CAGAGGCGGT CGTGGAGGGG
 401 ATGCTGAGCG TGGCGAGGGA GTTCTTCCAC CTGCCGGAGT CGGAGCGGCT
 451 CAAGTGCTAC TCCGACGACC CCAAGAAGGC GGTCCGGCTG TCGACGAGCT
 501 TCAACGTGCG CACGGAGAAG GTGAGCAACT GGCGCGACTT CCTCCGGCTG
 551 CATTGCTACC CTCTTGAGAG CTTCGTCGAC CAGTGGCCGT CGAACCCGCC
 601 CGCCTTCAGG CAAGTCGTCG GCACCTACTC GACGGAAGCG AGAGCGCTGG
 651 CGCTGAGGCT CCTGGAGGCG ATATCGGAGA GCCTAGGGCT GGAGAGAGGC
 701 CACATGGTGA AGGCCATGGG GCGGCACGCG CAGCACATGG CGGTGAACTA
 751 CTACCCGCCG TGCCCGCAGC CGGAGCTCAC CTACGGTCTG CCAGGGCACA
 801 AGGACCCCAA TGCCATCACG CTCCTCCTGC AGGACGGCGT CTCCGGCCTG
 851 CAGGTCCAGC GCGACGGCCG GTGGGTGGCC GTCAACCCGG TGCCCAACGC
 901 CCTCGTCATC AACATCGGCG ATCAGTTACA GGCGCTGAGC AACGACCGAT
 951 ACAAGAGCGT GAACCACAGA GTGATCGTCA ACAGCGCGAG CGAGAGGATT
1001 TCGGTGCCGA CGTTCTACTG CCCGTCGCCG GACACGGTGG TCGCGCCGGC
1051 CGACGCGCTG GTGGACGACG CCCACCCTCG GGCCTACCAG CCCTTCACGT
1101 ACCAGGAGTA CTACGAGGAG TTCTGGAAGA TGGGCCTTCA GTCAGCAAGT
1151 TGCCTCGACA GGTTCCGACG GATCGAGTGA TGGACAAGAC GTGGGCCGTT
1201 GTTATCTCCT GGGCCATGAG CGTTGCCGCA GCCGATGTGT CGCCATATGG
1251 TGGAGACGTT TCCTCCCTCC GGAAAAGAAA AATAAAACAG AGTGGAGACC
1301 ACTAGAACCG TCAGATAGCA TCCCAAAAAA AAAAAAAAAA AAAAAAAAAA
1351 AAAAGTACTC TGCGTTGTTA CCACTGCTTA ATCACTAGTG AATTC
```

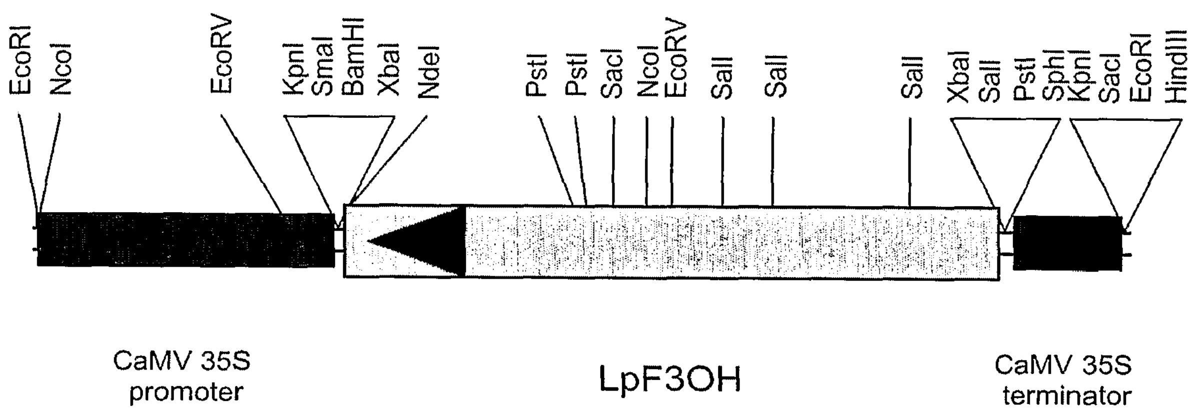
FIGURE 111

```
  1 MAPAMSNPLL SDRVARSKKV PSSHVRAVGD RPDLANVDHE SGAGIPLIDL
 51 KQLEGPGRRR VVEAIGSACE NDGFFMVTNH GIPEAVVEGM LSVAREFFHL
101 PESERLKCYS DDPKKAVRLS TSFNVRTEKV SNWRDFLRLH CYPLESFVDQ
151 WPSNPPAFRQ VVGTYSTEAR ALALRLLEAI SESLGLERGH MVKAMGRHAQ
201 HMAVNYYPPC PQPELTYGLP GHKDPNAITL LLQDGVSGLQ VQRDGRWVAV
251 NPVPNALVIN IGDQLQALSN DRYKSVNHRV IVNSASERIS VPTFYCPSPD
301 TVVAPADALV DDAHPRAYQP FTYQEYYEEF WKMGLQSASC LDRFRRIE
```

FIGURE 112

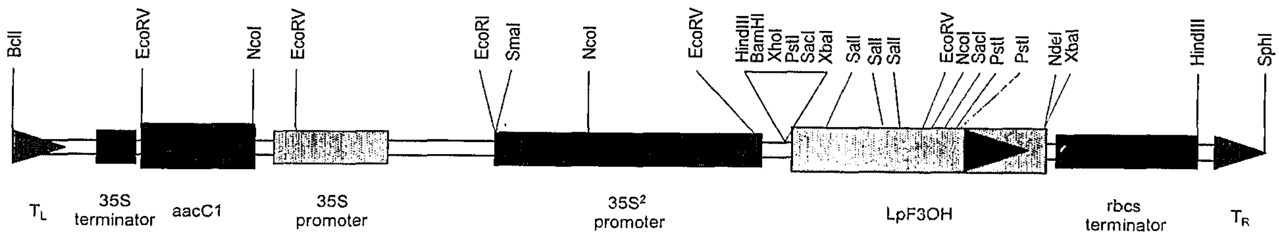


pDH51LpF3OH sense

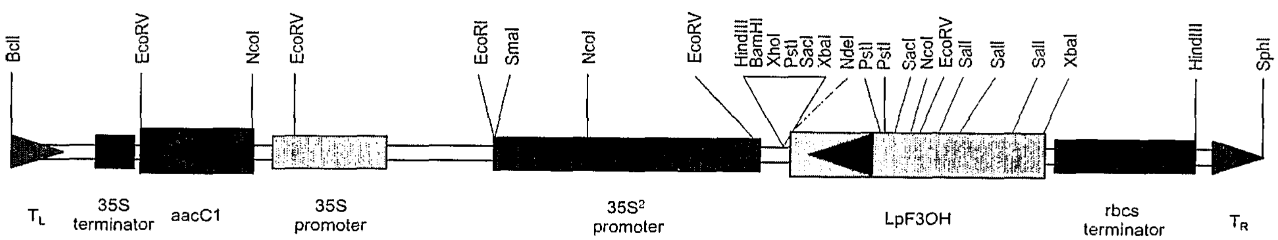


pDH51LpF3OH anti

FIGURE 113



pPZP221:35S²LpF3OH sense



pPZP221:35S²LpF3OH anti

FIGURE 114

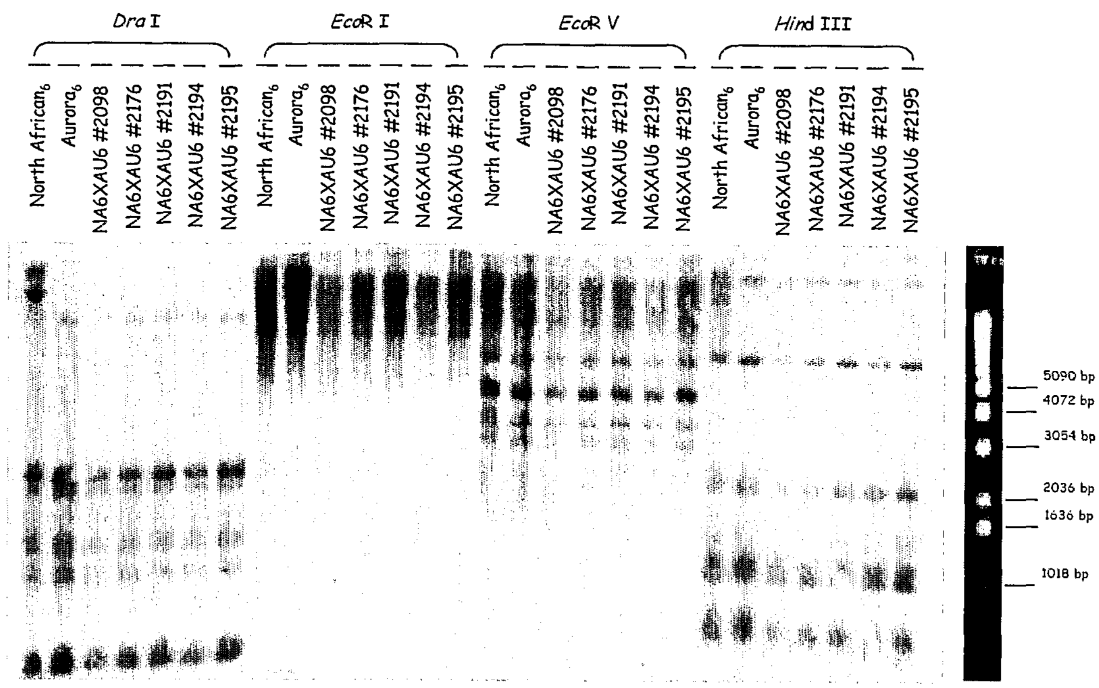
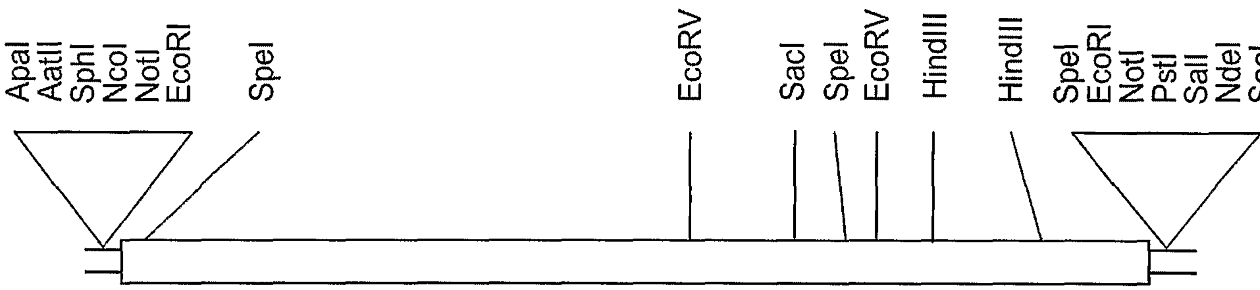

Dra I
EcoR I
EcoR V
Hind III
North African6
Aurora6
NA6XAU6 #2098
NA6XAU6 #2176
NA6XAU6 #2191
NA6XAU6 #2194
NA6XAU6 #2195
5090 bp
4072 bp
3054 bp
2036 bp
1636 bp
1018 bp

FIGURE 115



TrBANa

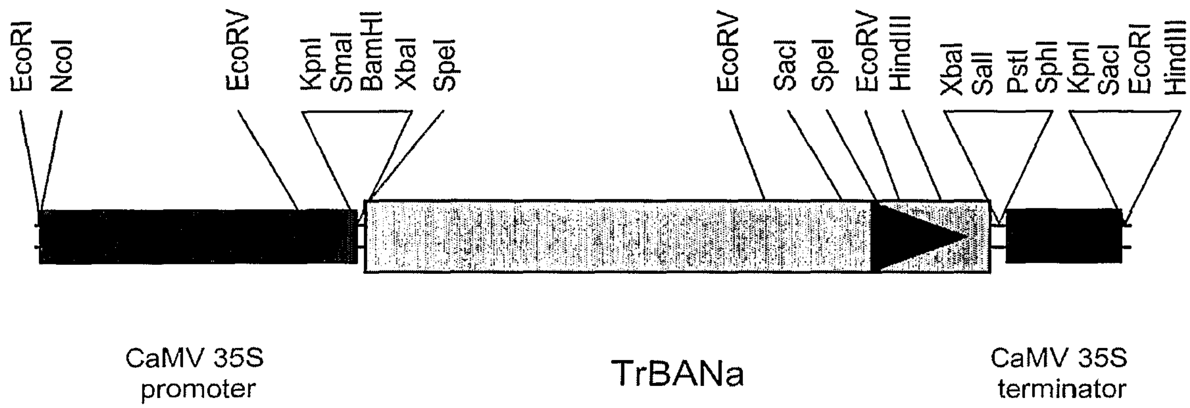
FIGURE 116

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG ATAAAAACTG
  51 CACTAGTGTG TATAAGTTTC TTGGTGAAAA AAGAGTTTGT AAATTAACAT
 101 CATGGCTAGT ATCAAACAAA TTGGAAACAA GAAAGCATGT GTGATTGGTG
 151 GCACTGGTTT TGTTGCATCT ATGTTGATCA AGCAGTTACT TGAAAAGGGT
 201 TATGCTGTTA ATACTACCGT TAGAGACCCA GATAGCCCTA AGAAAATATC
 251 TCACCTAGTG GCACTGCAAA GTTTGGGGGA ACTGAATCTA TTTAGAGCAG
 301 ACTTAACAGT TGAAGAAGAT TTTGATGCTC CTATAGCAGG ATGTGAACTT
 351 GTTTTTCAAC TTGCTACACC TGTGAACTTT GCTTCTCAAG ATCCTGAGAA
 401 TGACATGATA AAGCCAGCAA TCAAAGGTGT GTTGAATGTG TTGAAAGCAA
 451 TTGCAAGAGC AAAAGAAGTT AAAAGAGTTA TCTTAACATC TTCGGCAGCC
 501 GCGGTGACTA TAAATGAACT CAAAGGGACA GGTCATGTTA TGGATGAAAC
 551 CAACTGGTCT GATGTTGAAT TTCTCAACAC TGCAAAACCA CCCACTTGGG
 601 GTTATCCTGC CTCAAAAATG CTAGCTGAAA AGGCTGCATG GAAATTTGCT
 651 GAAGAAAATG ACATTGATCT AATCACTGTG ATACCTAGTT TAACAACTGG
 701 TCCTTCTCTC ACACCAGATA TCCCATCTAG TGTTGGCTTG GCAATGTCTC
 751 TAATAACAGG CAATGATTTT CTCATAAATG CTTTGAAAGG AATGCAGTTT
 801 CTGTCGGGTT CGTTATCCAT CACTCATGTT GAGGATATTT GCCGAGCTCA
 851 TATATTTCTT GCAGAGAAAG AATCAGCTTC TGGTAGATAC ATTTGCTGTG
 901 CTCACAATAC TAGTGTTCCC GAGCTTGCAA AGTTTCTCAA CAAACGATAT
 951 CCTCAGTATA AAGTTCCAAC TGAATTTGAT GATTGCCCCA GCAAGGCAAA
1001 GTTGATAATC TCTTCTGAAA AGCTTATCAA AGAAGGGTTC AGTTTCAAGC
1051 ATGGTATTGC CGAAACTTTC GACCAGACTG TCGAGTATTT TAAGACTAAG
1101 GGGGCACTGA AGAATTAGAT TTTGATATTT CTAATTCAAT AGCAAACTCT
1151 AAGCTTGTTA TGTGTTTGTG AAGTTCAGAG TGAAATATCA AATGAATAAG
1201 TGGAGAGAGC ACAATAAGAG GAGAGCACAA TAATTTTGGA AAAAAAAAAA
1251 AAAAAAAAAA AAAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1301 AGTGAATTC
```

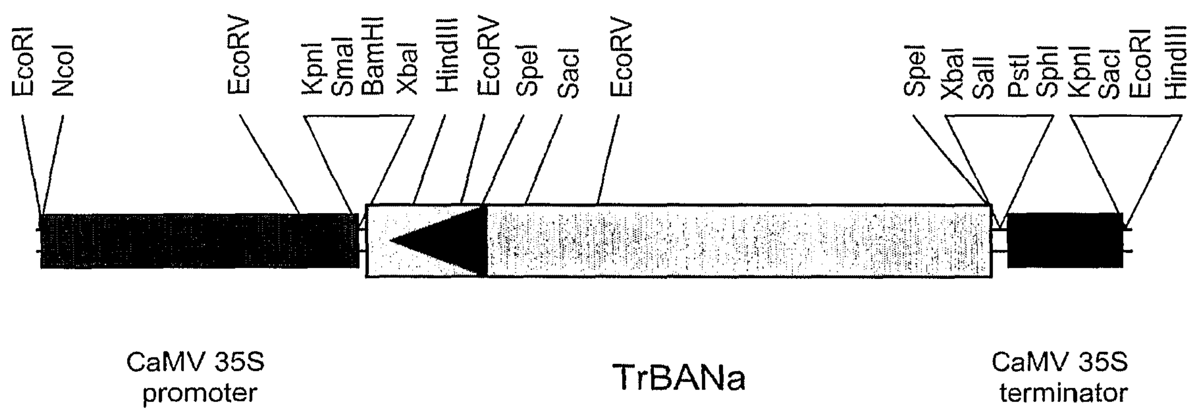
FIGURE 117

```
  1 MASIKQIGNK KACVIGGTGF VASMLIKQLL EKGYAVNTTV RDPDSPKKIS
 51 HLVALQSLGE LNLFRADLTV EEDFDAPIAG CELVFQLATP VNFASQDPEN
101 DMIKPAIKGV LNVLKAIARA KEVKRVILTS SAAAVTINEL KGTGHVMDET
151 NWSDVEFLNT AKPPTWGYPA SKMLAEKAAW KFAEENDIDL ITVIPSLTTG
201 PSLTPDIPSS VGLAMSLITG NDFLINALKG MQFLSGSLSI THVEDICRAH
251 IFLAEKESAS GRYICCAHNT SVPELAKFLN KRYPQYKVPT EFDDCPSKAK
301 LIISSEKLIK EGFSFKHGIA ETFDQTVEYF KTKGALKN
```

FIGURE 118

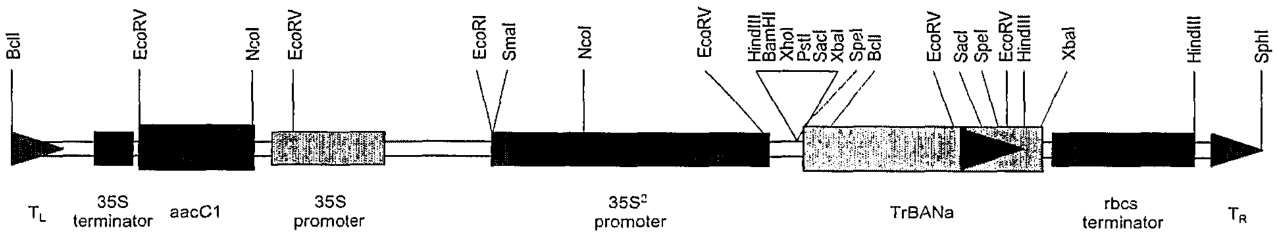


pDH51TrBANa sense

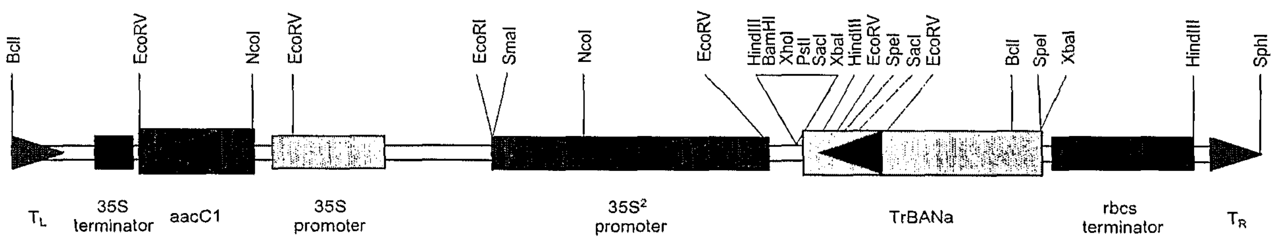


pDH51TrBANa anti

FIGURE 119

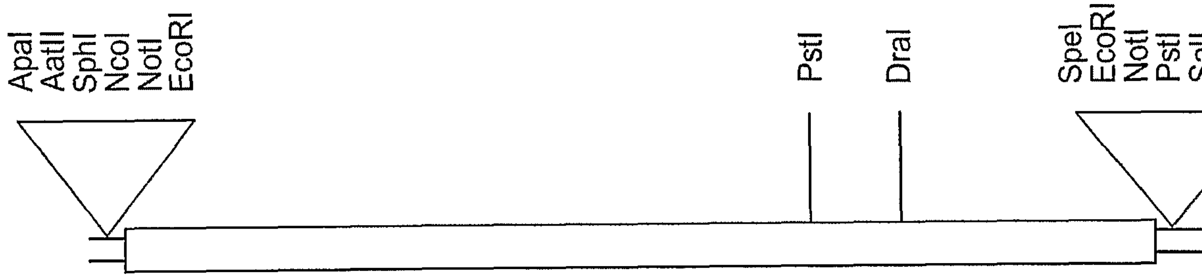


pPZP221:35S[2]TrBANa sense



pPZP221:35S[2]TrBANa anti

FIGURE 120



TrCHIa

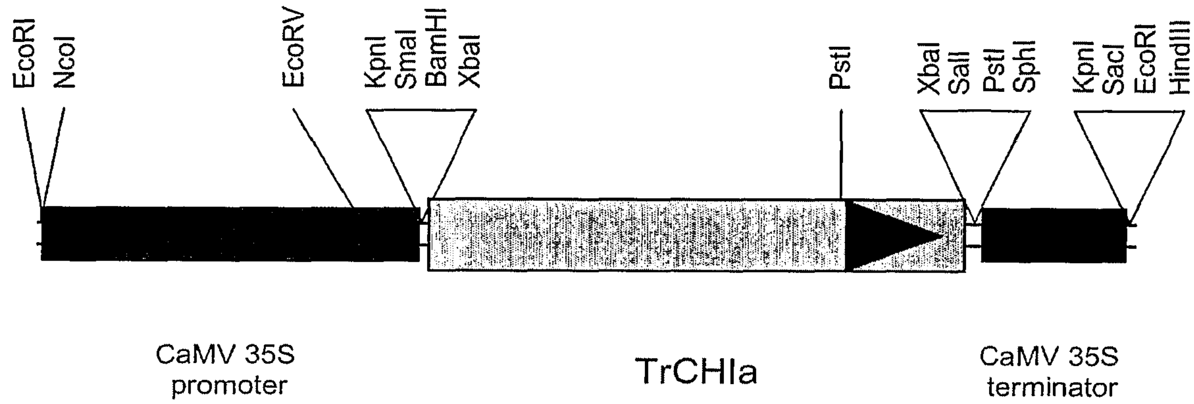
FIGURE 121

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GACTTAAACA
  51 TTGACACAAG TCCCAAATAA AAAAGATCTG AAACAACATA GTCACCCCAT
 101 TTTTTAACAT TAAACTAAAA ATATGTCGGC CATCACCGCA ATCCAAGTCG
 151 AGAACCTTGA ATTTCCGGCT GTGGTTACTT CTCCGGCCAC CGGTAAGTCA
 201 TATTTTCTTG GTGGTGCAGG GGAGAGAGGT TTGACTATTG AAGGAAACTT
 251 CATCAAGTTC ACTGCCATAG GAGTATATTT GGAAGATGTA GCAGTGGCTT
 301 CACTTGCCAC TAAATGGAAG GGTAAATCCT CTGAGGAGTT GCTTGAGACT
 351 CTTGACTTCT ATAGAGACAT CATTTCAGGA CCCTTTGAAA AGTTGATTCG
 401 AGGATCGAAG ATTAGGGAAT TGAGTGGTCC TGAGTACTCA AGGAAGGTTA
 451 ATGAAAACTG CGTGGCACAC TTAAAATCTG TTGGGACTTA TGGAGATGCT
 501 GAAGCTGAAG CTATGCAAAA ATTTGTTGAA GCCTTCAAGC CTATTAATTT
 551 TCCACCTGGT GCCTCTGTTT TTTACAGGCA ATCACCTGAT GGAATATTAG
 601 GGCTTAGTTT CTCTCAAGAT GCAAGTATAC CAGAAAAGGA GGCTGCAGTA
 651 ATAGAGAACA AGGCAGCTTC ATCGGCAGTG TTAGAAACTA TGATTGGTGA
 701 ACATGCTGTT TCTCCTGATT TAAAGCGTTG TTTGGCTGCA AGATTACCTG
 751 CCTTGTTGAA CGAGGGTACT TTCAAGATTG AATGAAAACT GATTATTATT
 801 ATCTCCAAAA GCATTGCAGC ACAAGATTGA GTCATTTATG AGCATGGACA
 851 TTTTTATGTC CACACATGTT TAACTTTTGT ATCTCTCTTT AGATTCTCAT
 901 CAATATCAAT AATACTAATA TGAAACGAAG TCAAAAAAAA AAAAAAAAAA
 951 AAAAAAAAAA AAAAGTACTC TGCGTTGTTA CCACTGCTTA ATCACTAGTG
1001 AATTC
```

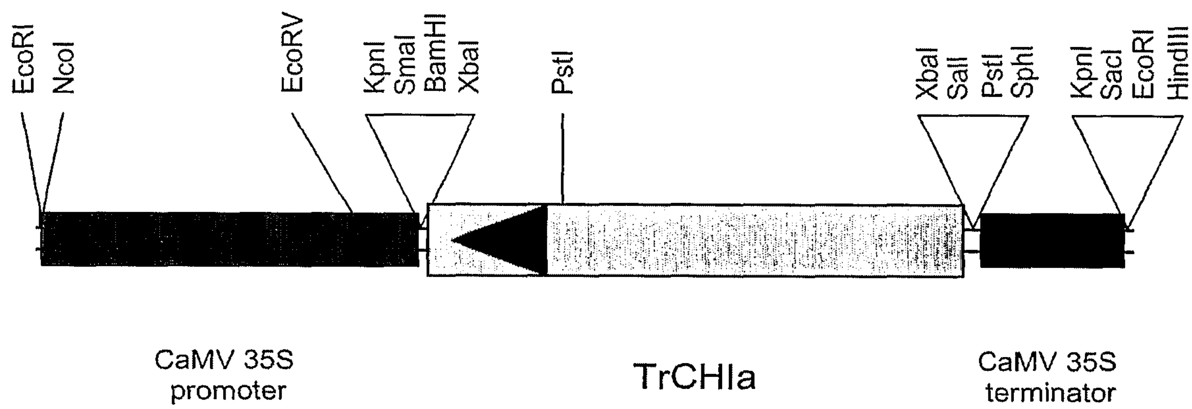
FIGURE 122

1	MSAITAIQVE	NLEFPAVVTS	PATGKSYFLG	GAGERGLTIE	GNFIKFTAIG
51	VYLEDVAVAS	LATKWKGKSS	EELLETLDFY	RDIISGPFEK	LIRGSKIREL
101	SGPEYSRKVN	ENCVAHLKSV	GTYGDAEAEA	MQKFVEAFKP	INFPPGASVF
151	YRQSPDGILG	LSFSQDASIP	EKEAAVIENK	AASSAVLETM	IGEHAVSPDL
201	KRCLAARLPA	LLNEGTFKIE			

FIGURE 123

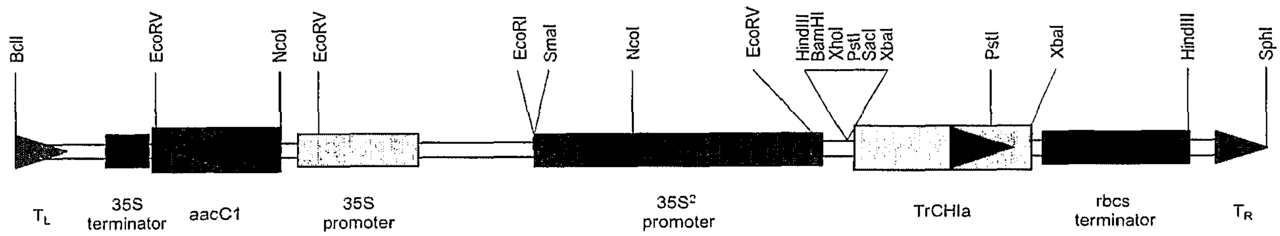


pDH51TrCHIa sense

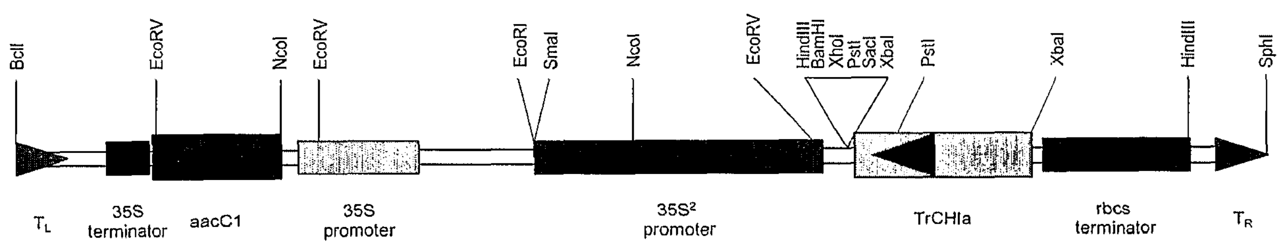


pDH51TrCHIa anti

FIGURE 124

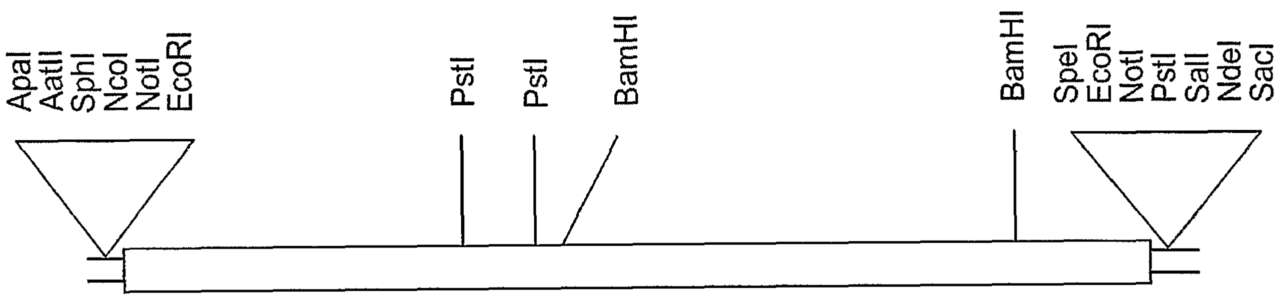


pPZP221:35S^{2}TrCHIa sense



pPZP221:35S^{2}TrCHIa anti

FIGURE 125



TrCHId

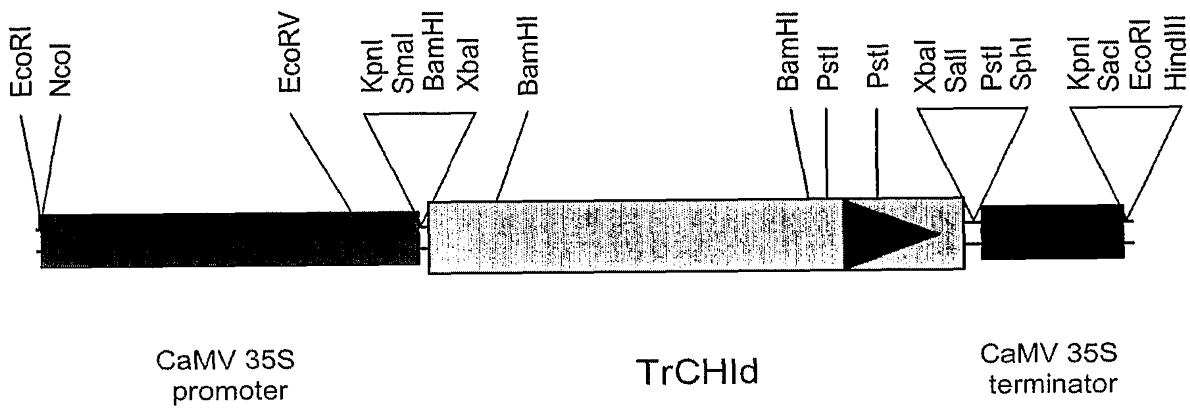
FIGURE 126

```
   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGACA
  51 TTACAACTCA CAACACCTTC TCCATTACCA TCTATCTTCT ACTAAGTTCA
 101 ACGAGATCAA TGGCACTTCC TTCTGTCACC GCTTTGAATA TCGAGAACAA
 151 TCTATTCCCT CCTACCGTCA CACCACCGGG ATCCACCAAC AATTTCTTCC
 201 TCGGCGGTGC AGGAGAGCGG GGTCTTCAAA TTCAAGACAA ATTTGTCAAA
 251 TTCACCGCTA TTGGTGTTTA TCTACAGGAC ATTGCTGTTC CTTACCTCGC
 301 CACTAAATGG AAGGGTAAGA CTGCTCAAGA GCTAACGGAA ACTGTTCCTT
 351 TCTTCAGGGA CATCGTTACA GGTCCATTTG AGAAATTTAT GCAGGTGACA
 401 ATGATCTTGC CATTGACTGG GCAACAATAC TCAGAGAAAG TGTCAGAAAA
 451 TTGTGTAGCT ATTTGGAAGT CTCTTGGGAT TTATACCGAC GAAGAAGCCA
 501 AAGCAATTGA GAAGTTTGTT TCTGTCTTCA AAGATGAAAC ATTCCCACCA
 551 GGCTCCTCTA TCCTTTTCAC AGTATTACCC AAAGGATTAG GATCACTAAC
 601 GATAAGTTTC TCTAAAGATG GATCCATTCC AGAGACCGAG TCTGCAGTTA
 651 TAGAGAATAA GCTACTCTCA CAAGCTGTGC TTGAGTCGAT GATAGGGGCG
 701 CACGGTGTCT CCCCTGCAGC AAAACAGAGT TTGGCCACCA GGTTATCCGA
 751 GTTATTCAAC GAGGTTGGTG ATGCTAGCAA CTGATTATAT CAACAAAACG
 801 AAAATGAAAG TCCTTTCTGC AATAAAGACC AAGCGGAAAT TTTATTTTAG
 851 GTGCACTTTG AAATGACCTC TTTGGCGACT TTTTCTTGTA CTAATAATAA
 901 AGAGTGTGTT TGTATCATGT TGTAATTTTA TTTTAGAAAA AGTGAGGTAA
 951 GAAAGGAGTC CTTATGTTTA TTTCAATTAT TGAAAAATTA TTTGCATGTA
1001 TAATTGATTT CAACTGATGT TATTTAATCA CGTTTTTTCT AAAAAAAAAA
1051 AAAAAAAAAA AAAAAAAAAA GTACTCTGCG TTGTTACCAC TGCTTAATCG
1101 AATTC
```

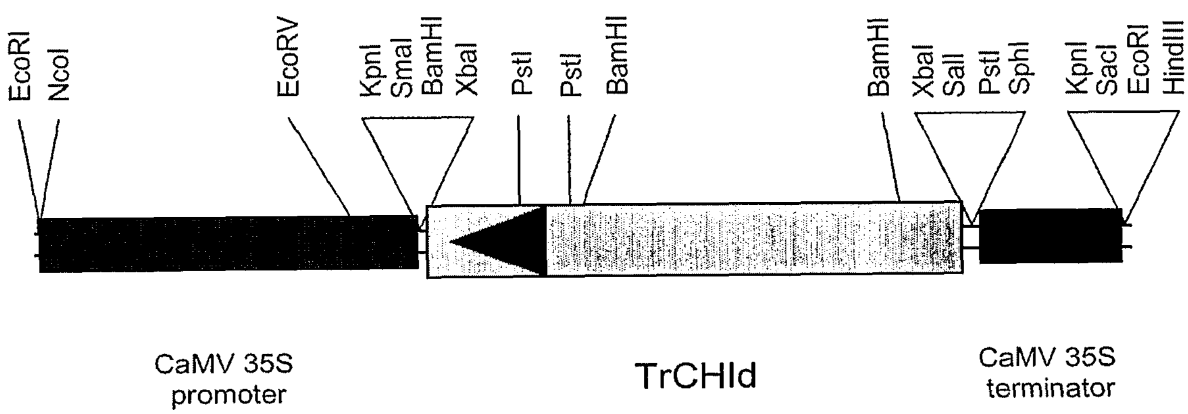
FIGURE 127

```
  1  MALPSVTALN IENNLFPPTV TPPGSTNNFF LGGAGERGLQ IQDKFVKFTA
 51  IGVYLQDIAV PYLATKWKGK TAQELTETVP FFRDIVTGPF EKFMQVTMIL
101  PLTGQQYSEK VSENCVAIWK SLGIYTDEEA KAIEKFVSVF KDETFPPGSS
151  ILFTVLPKGL GSLTISFSKD GSIPETESAV IENKLLSQAV LESMIGAHGV
201  SPAAKQSLAT RLSELFNEVG DASN
```

FIGURE 128



pDH51TrCHId sense



pDH51TrCHId anti

FIGURE 129

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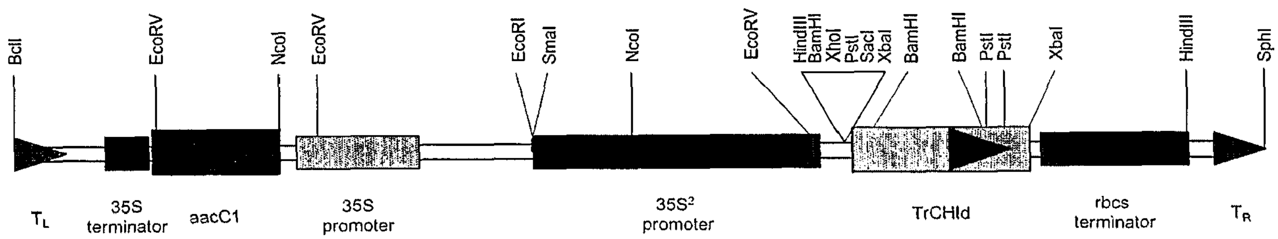
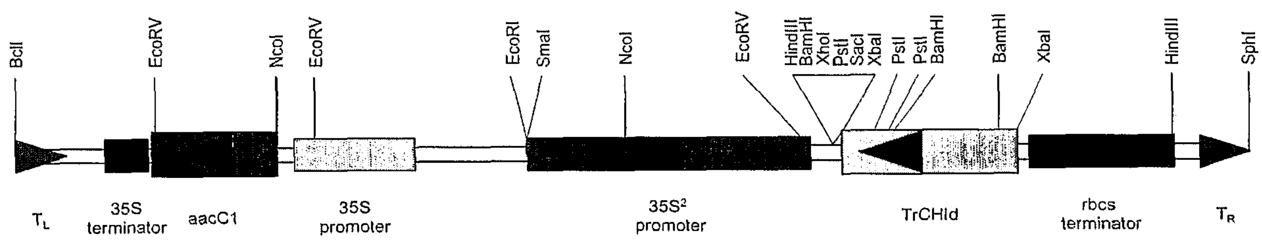


pPZP221:35S²TrCHId sense



pPZP221:35S²TrCHId anti

FIGURE 130

TrCHRc

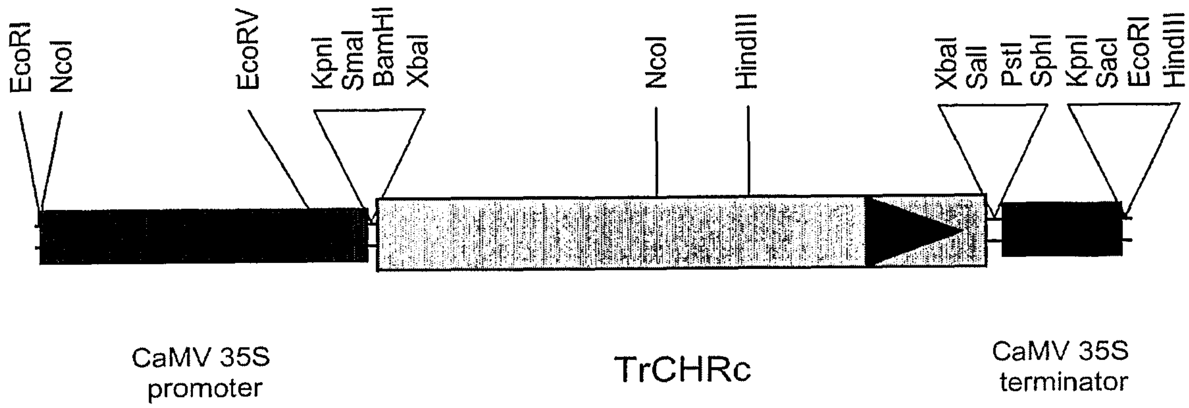
FIGURE 131

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATTCAAACA
  51 TAGCTCAAAG TGTGTAACAA ATTTCTTAAC TTAAAACATT TTCAACCCAA
 101 CAAAAAAAAA CAAAGACAAA AACATGGGTA GTGTTGAAAT TCCAACAAAG
 151 GTTCTTACTA ACAGTTCTAG TCAAGTGAAA ATGCCTGTGG TTGGAATGGG
 201 ATCAGCACCT GATTTCACAT GTAAGAAAGA CACAAAAGAT GCAATCATTG
 251 AAGCCATCAA ACAGGGTTAT AGACACTTTG ATACTGCTGC TGCTTATGGC
 301 TCAGAACAAG CTCTTGGTGA AGGTTTGAAA GAAGCAATTG AACTTGGTCT
 351 TGTCACTAGA GAAGACCTTT TTGTTACTTC TAAACTTTGG GTCACTGAAA
 401 ATCATCCTCA TCTTGTTGTT CCTGCTCTTC AAAAATCTCT CAAGACTCTT
 451 CAATTGGAGT ACTTGGACTT GTATTTGATC CATTGGCCAC TTAGTTCTCA
 501 GCCTGGAAAG TTTTCATTTC CAATTGATGT GGCAGATCTC TTGCCATTTG
 551 ATGTGAAGGG TGTTTGGGAA TCCATGGAAG AAGGCTTGAA ACTTGGACTC
 601 ACTAAAGCTA TTGGTGTTAG TAACTTCTCT GTCAAGAAAC TTCAAAATCT
 651 TGTCTCAGTT GCCACTGTTC TTCCTGCTGT CAATCAAGTG GAGATGAACC
 701 TTGCATGGCA ACAAAAGAAG CTTAGAGAAT TTTGCAATGC AAATGGAATA
 751 GTGTTAACTG CATTTTCACC ATTGAGAAAA GGTGCAAGCA GGGGACCAAA
 801 TGAAGTTATG GAAAATGATA TGCTTAAAGA GATTGCAGAT GCTCATGGAA
 851 AGTCTGTTGC ACAAATTTCA TTGAGATGGT TATATGAACA AGGAGTCACT
 901 TTTGTTCCCA AGAGCTATGA TAAGGAAAGA ATGGGTCAAA ATTTGGCTAT
 951 CTTTGATTGG ACATTGGCAA AAGAAGATCA TGAGAAAATT GATCAAATTA
1001 AGCAGAACCG TTTGATCCCT GGACCAACCA AGCCAGGACT CAGTGACCTA
1051 TGGGATGATG AAATATAAAG TGGAAGATGT TAAAAGTCCC TTAAGCTCAC
1101 TCAATATCTA TCTATTGTGT ACTTTTTGCA TTTGGGGTTT GAAATTGAGT
1151 CACCCTTGTT TCTGTATCGA TTTAAAATTT AAATAATCAA TTTTTCATTA
1201 CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AGTACTCTGC GTTGTTACCA
1251 CTGCTTAATC ACTAGTGAAT TC
```

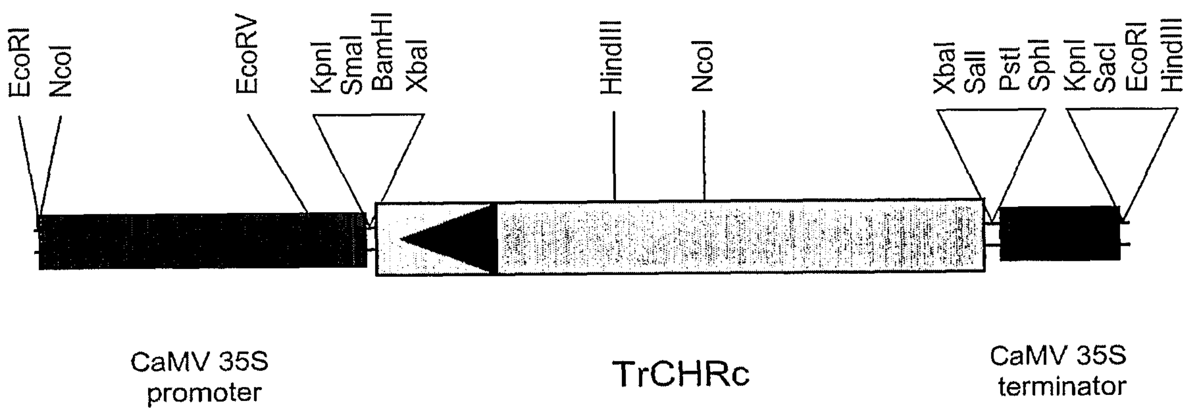
FIGURE 132

```
  1  MGSVEIPTKV LTNSSSQVKM PVVGMGSAPD FTCKKDTKDA IIEAIKQGYR
 51  HFDTAAAYGS EQALGEGLKE AIELGLVTRE DLFVTSKLWV TENHPHLVVP
101  ALQKSLKTLQ LEYLDLYLIH WPLSSQPGKF SFPIDVADLL PFDVKGVWES
151  MEEGLKLGLT KAIGVSNFSV KKLQNLVSVA TVLPAVNQVE MNLAWQQKKL
201  REFCNANGIV LTAFSPLRKG ASRGPNEVME NDMLKEIADA HGKSVAQISL
251  RWLYEQGVTF VPKSYDKERM GQNLAIFDWT LAKEDHEKID QIKQNRLIPG
301  PTKPGLSDLW DDEI
```

FIGURE 133

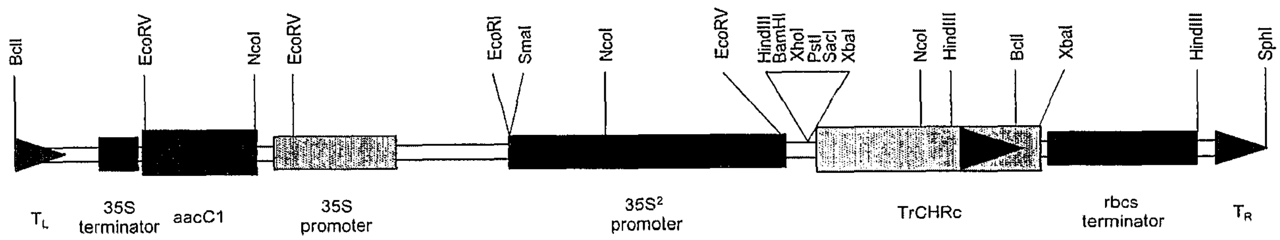


pDH51TrCHRc sense

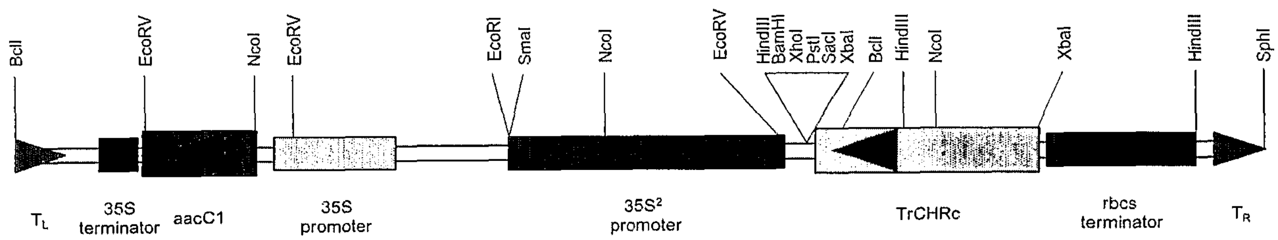


pDH51TrCHRc anti

FIGURE 134



pPZP221:35S²TrCHRc sense



pPZP221:35S²TrCHRc anti

FIGURE 135

TrCHSa1

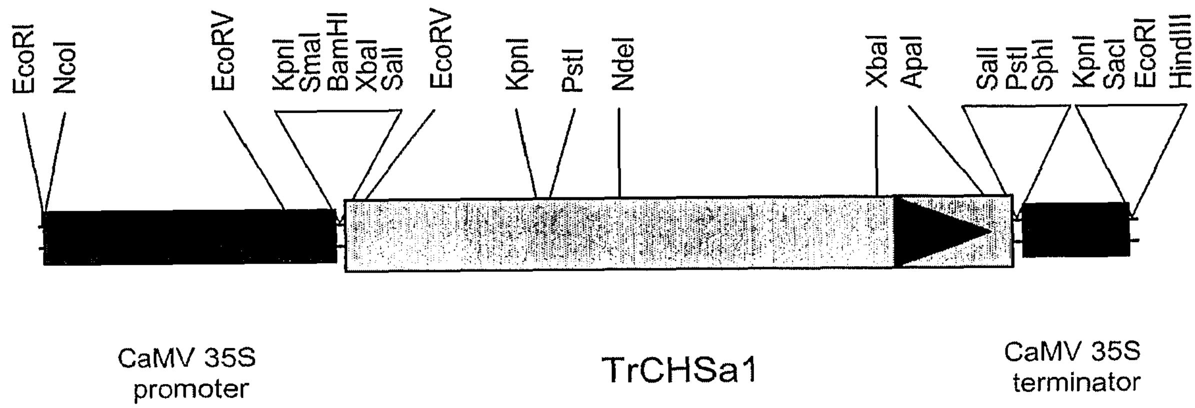
FIGURE 136

1 **GAATTC**GATT AAGCAGTGGT ATCAACGCAG AGTACGCGGG GACAACAACT
51 ATAACTTCCT GTTATTAACC AATTGAGTTC AAATTACATA CATAGCAGGA
101 ACTATACTAA AGATATCAAC ATGGTTAGTG TTTCTGAAAT TCGCAAGGCT
151 CAAAGGGCTG AAGGCCCTGC AACTATTTTG GCCATTGGTA CTGCAAATCC
201 AGCAAATCGT GTTGACCAGA GTACATATCC TGATTTCTAC TTCAAAATCA
251 CTAACAGTGA GCATAAGGTT GAGCTTAAAG AGAAATTTCA GCGCATGTGT
301 GATAAATCTA TGATCAAGAG CAGATACATG TATCTAACAG AAGAGATTTT
351 GAAAGAAAAT CCTAGTCTTT GTGAATACAT GGCACCTTCA TTGGATGCTA
401 GGCAAGACAT GGTGGTGGTT GAGGTACCTA GACTTGGGAA GGAGGCTGCA
451 GTGAAAGCTA TCAAAGAATG GGGTCAACCA AAGTCAAAGA TTACTCACTT
501 AATCTTTTGC ACCACAAGTG GTGTTGACAT GCCTGGTGCC GATTACCAAC
551 TCACAAAACT CTTAGGTCTT CGCCCATATG TGAAGAGGTA CATGATGTAC
601 CAACAAGGGT GCTTTGCAGG TGGGACGGTT CTTCGTTTGG CCAAGGATTT
651 GGCCGAGAAC AACAAAGGTG CTCGTGTGTT GGTTGTTTGC TCTGAAGTAA
701 CCGCAGTCAC ATTCCGCGGC CCCAGTGACA CTCATTTGGA CAGTCTTGTT
751 GGACAAGCAC TATTCGGAGA TGGAGCTGCT GCACTCATTG TTGGCTCAGA
801 CCCAGTACCA GAAATTGAGA AGCCAATATT TGAGATGGTT TGGACCGCAC
851 AGACAATTGC TCCAGATAGT GAAGGTGCCA TTGATGGTCA TCTTCGTGAA
901 GCTGGACTAA CATTTCATCT TCTTAAAGAT GTTCCTGGGA TTGTCTCAAA
951 GAACATTGAT AAGGCATTGG TTGAGGCATT CCAACCATTA AACATCTCTG
1001 ATTACAATTC AATCTTTTGG ATTGCTCATC CAGGTGGTCC TGCAATTCTA
1051 GACCAAGTTG AGATAAAGTT GGGCTTAAAA CCTGAAAAAA TGAAGGCCAC
1101 CAGAGATGTA CTTAGTGAAT ATGGTAACAT GTCAAGTGCA TGTGTATTGT
1151 TCATCTTAGA TGAGATGAGA AAGAAATCGG CTGAAAATGG ACTTAAAACC
1201 ACAGGAGAAG GACTTGACTG GGGTGTGTTG TTTGGATTTG GGCCCGGACT
1251 TACCATTGAA ACTGTTGTTC TACATAGTGT GGCTATATGA GAATGAGAGA
1301 CTTGATTTGT TTTTATTGTA TTGTATTGTA TTACTTTAAA TCTTGGTTGA
1351 ACCTCCATTT TAAGAATAAA TATGGAGTTC AATATGGACC ATCCTGTTAA
1401 AATAATATAT CGTTAATAGC TATTATTTTA GTGTCTGTTT CTTTTTACTA
1451 AACTATTTTA TTTTAGTATT TGTTTTTGAC CAAAAAAAAA AAAAAAAAAA
1501 AAAAAAAGTA CTCTGCGTTG TTACCACTGC TTAATCACTA GT**GAATTC**

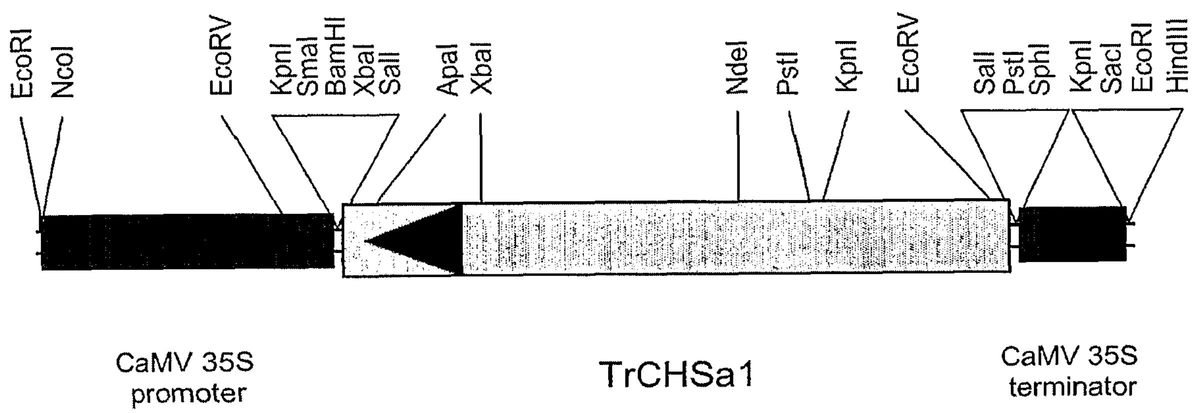
FIGURE 137

```
  1 MVSVSEIRKA QRAEGPATIL AIGTANPANR VDQSTYPDFY FKITNSEHKV
 51 ELKEKFQRMC DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSLV GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNID KALVEAFQPL NISDYNSIFW
301 IAHPGGPAIL DQVEIKLGLK PEKMKATRDV LSEYGNMSSA CVLFILDEMR
351 KKSAENGLKT TGEGLDWGVL FGFGPGLTIE TVVLHSVAI
```

FIGURE 138

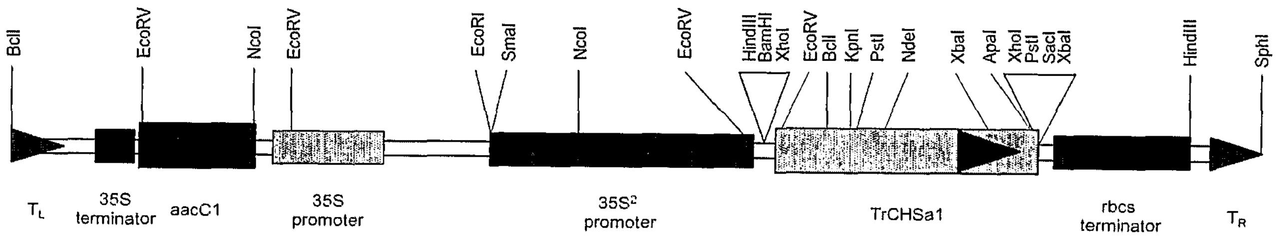


pDH51TrCHSa1 sense

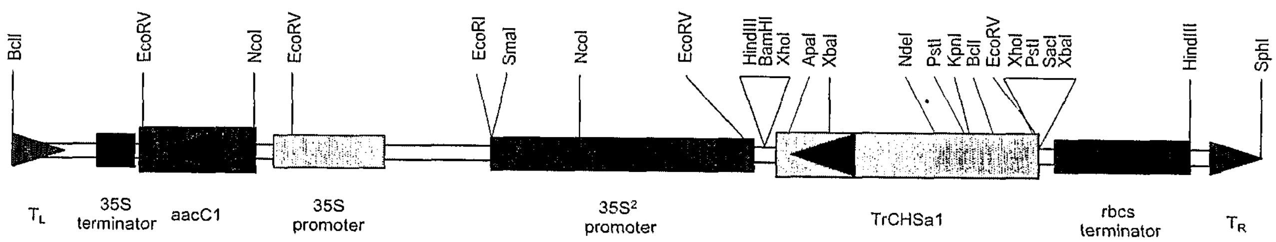


pDH51TrCHSa1 anti

FIGURE 139



pPZP221:35S²TrCHSa1 sense



pPZP221:35S²TrCHSa1 anti

FIGURE 140

TrCHSa3

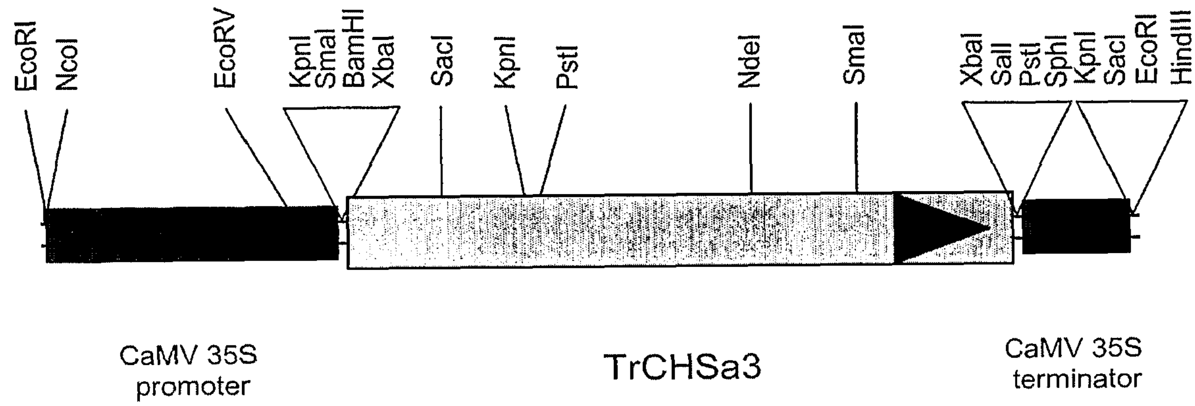
FIGURE 141

```
   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAAC
  51 AAAAACAACT ACGCATATTA TATATATATA TATATAGTCT ATAATTGAAA
 101 GAAACTGCTA AAGATATTAT TAAGATATGG TGAGTGTAGC TGAAATTCGC
 151 AAGGCTCAGA GGGCTGAAGG CCCTGCAACC ATTTTGGCCA TTGGCACTGC
 201 AAATCCACCA AACCGTGTTG AGCAGAGCAC ATATCCTGAT TTCTACTTCA
 251 AAATTACAAA CAGTGAGCAC AAGACTGAGC TCAAAGAGAA GTTCCAACGC
 301 ATGTGTGACA AATCCATGAT CAAGAGCAGA TACATGTATC TAACAGAAGA
 351 GATTTTGAAA GAAAATCCTA GTCTTTGTGA ATACATGGCA CCTTCATTGG
 401 ATGCTAGGCA AGACATGGTG GTGGTTGAGG TACCTAGACT TGGGAAGGAG
 451 GCTGCAGTCA AGGCCATTAA AGAATGGGGT CAACCAAAGT CAAAGATTAC
 501 TCACTTAATC TTTTGCACCA CAAGTGGTGT TGACATGCCT GGTGCTGATT
 551 ACCAACTCAC AAAACTCTTA GGTCTTCGCC CATATGTGAA AAGGTATATG
 601 ATGTACCAAC AAGGTTGTTT TGCAGGAGGC ACGGTGCTTC GTTTGGCAAA
 651 AGATTTGGCC GAGAACAACA AAGGTGCTCG TGTGCTAGTT GTTTGTTCTG
 701 AAGTCACCGC AGTCACATTT CGCGGCCCCA GTGATACTCA CTTGGACAGT
 751 CTTGTTGGAC AAGCATTGTT TGGAGATGGA GCCGCTGCAC TAATTGTTGG
 801 TTCTGATCCA GTGCCTGAAA TTGAGAAACC AATATTTGAG ATGGTTTGGA
 851 CTGCACAAAC AATTGCTCCA GACAGTGAAG GTGCCATTGA TGGTCATCTT
 901 CGTGAAGCTG GGCTAACATT TCATCTTCTT AAAGATGTTC CTGGGATTGT
 951 ATCAAAGAAC ATTAATAAAG CATTGGTTGA GGCTTTCCAA CCATTAGGAA
1001 TTTCTGACTA CAACTCAATC TTTTGGATTG CACACCCGGG TGGACCTGCA
1051 ATTCTTGATC AAGTAGAACA AAAGCTAGCC TTGAAGCCCG AAAAGATGAG
1101 GGCCACGAGG GAAGTTCTAA GTGAATATGG AAACATGTCA AGCGCATGTG
1151 TATTGTTCAT CTTAGATGAG ATGCGGAAGA AATCGGCTCA AAATGGACTT
1201 AAGACAACTG GAGAAGGACT TGATTGGGGT GTGTTGTTCG GCTTCGGACC
1251 AGGACTTACC ATTGAAACCG TTGTTCTTCG TAGCGTGGCT ATATAAGATG
1301 TGTGATTGTT TTTATTTTAA TGTATTACTT TTAATCTTGC TGCCTTGAAT
1351 TTCGATTTAA GAATAAATAA ATATATCTTT TGATAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CGAATTC
```

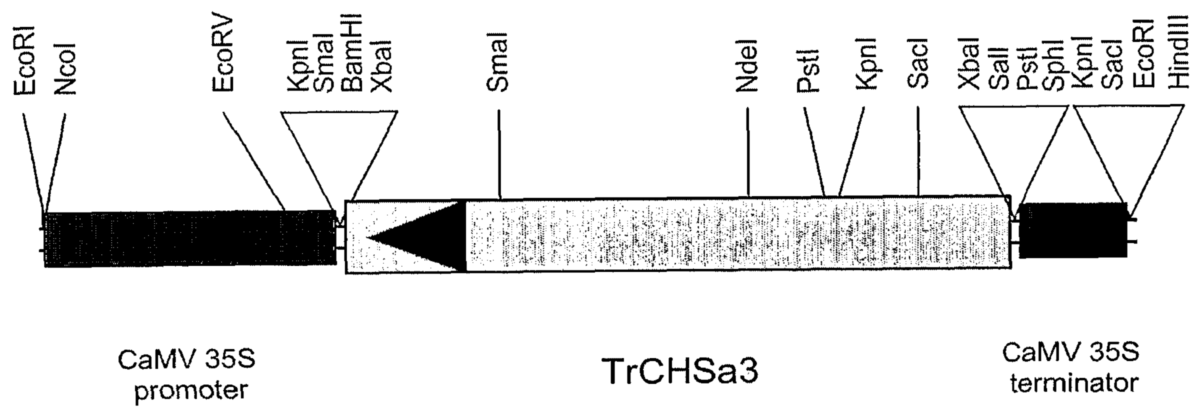
FIGURE 142

```
  1 MVSVAEIRKA QRAEGPATIL AIGTANPPNR VEQSTYPDFY FKITNSEHKT
 51 ELKEKFQRMC DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSLV GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNIN KALVEAFQPL GISDYNSIFW
301 IAHPGGPAIL DQVEQKLALK PEKMRATREV LSEYGNMSSA CVLFILDEMR
351 KKSAQNGLKT TGEGLDWGVL FGFGPGLTIE TVVLRSVAI
```

FIGURE 143

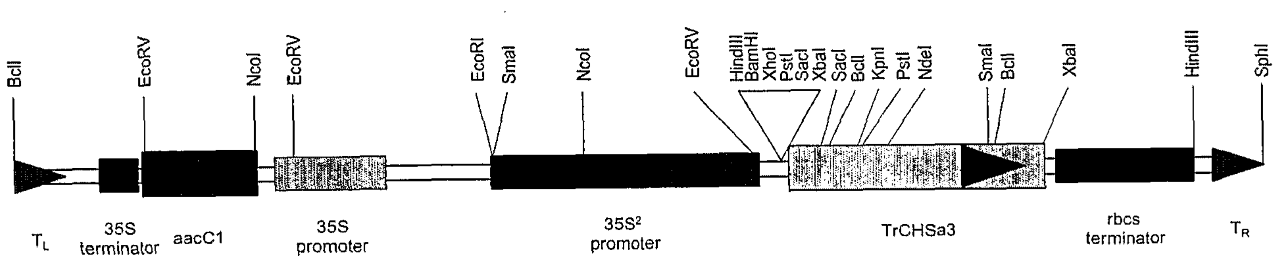


pDH51TrCHSa3 sense

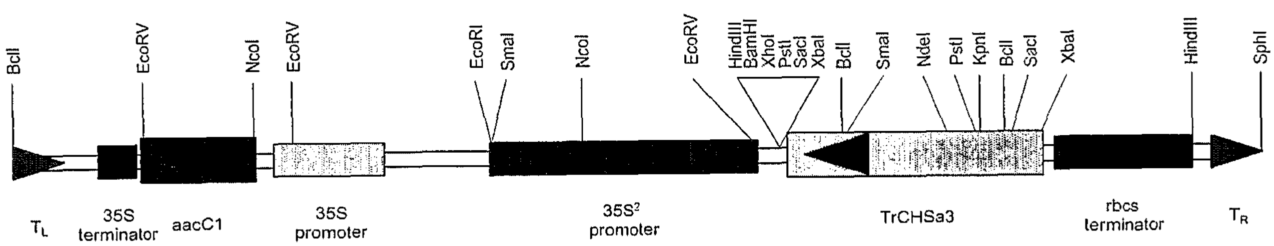


pDH51TrCHSa3 anti

FIGURE 144



pPZP221:35S^{2}TrCHSa3 sense



pPZP221:35S^{2}TrCHSa3 anti

FIGURE 145

TrCHSc

FIGURE 146

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```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATTCAATCT
  51 GTTGTGCATA AAATTCACTC ATTGCATAGA AAACCATACA CATTTGATCT
 101 TGCAAAGAAG AAATATGGGA GACGAAGGTA TAGTGAGAGG TGTCACAAAG
 151 CAGACAACCC CTGGGAAGGC TACTATATTG GCTCTTGGCA AGGCATTCCC
 201 TCACCAACTT GTGATGCAAG AGTGTTTAGT TGATGGTTAT TTTAGGGACA
 251 CTAATTGTGA CAATCCTGAA CTTAAGCAGA AACTTGCTAG ACTTTGTAAG
 301 ACAACCACGG TAAAAACAAG GTATGTTGTT ATGAATGAGG AGATACTAAA
 351 GAAATATCCA GAACTTGTTG TCGAAGGCGC CTCAACTGTA AAACAACGTT
 401 TAGAGATATG TAATGAGGCA GTAACACAAA TGGCAATTGA AGCTTCCCAA
 451 GTTTGCCTAA AGAATTGGGG TAGATCCTTA TCGGACATAA CTCATGTGGT
 501 TTATGTTTCA TCTAGTGAAG CTAGATTACC CGGTGGTGAC CTATACTTGT
 551 CAAAAGGACT AGGACTAAAC CCTAAAATTC AAAGAACCAT GCTCTATTTC
 601 TCTGGATGCT CGGGAGGCGT AGCCGGCCTT CGCGTTGCGA AAGACGTAGC
 651 TGAGAACAAC CCTGGAAGTA GAGTTTTGCT TGCTACTTCG GAAACTACAA
 701 TTATTGGATT CAAGCCACCA AGTGTTGATA GACCTTATGA TCTTGTTGGT
 751 GTGGCACTCT TTGGAGATGG TGCTGGTGCA ATGATAATTG GCTCAGACCC
 801 GGTATTTGAA ACTGAGACAC CATTGTTTGA GCTGCATACT TCAGCTCAGG
 851 AGTTTATACC AGACACCGAG AAGAAAATTG ATGGGCGGCT GACGGAGGAG
 901 GGCATAAGTT TCACACTAGC AAGGGAACTT CCGCAGATAA TCGAAGACAA
 951 TGTTGAGGGA TTCTGTAATA AACTAATTGA TGTTGTTGGG TTGGAGAATA
1001 AGGAGTACAA TAAGTTGTTT TGGGCTGTGC ATCCAGGTGG GCCTGCGATA
1051 TTGAATCGCG TGGAGAAGCG GCTTGAGTTG TCGCCGCAGA AGCTGAATGC
1101 TAGTAGAAAA GCTCTAATGG ATTATGGAAA TGCTAGCAGC AATACTATTG
1151 TTTATGTGCT GGAATATATG CTAGAAGAGG AAAAGAAGAT TAAAAAGGCG
1201 GGTGGAGGAG ATTCTGAATG GGGATTGATA CTTGCTTTTG GACCTGGAAT
1251 TACTTTTGAG GGGATTCTAG CAAGGAACTT GTGTGCATGA AGTCTTATAC
1301 AATTGTGATG CATGACTTAT ACTCTTATTT CTACTAATTA TTATATTAAG
1351 CAAATTCAGA ACTTTTAAGT AATGATTTAA TGAAGAATAC TTATAGTATA
1401 TTGACTTTAT TCACTTTCAA AGCAAGTTTA TGATCCTAAG ACATGGTAGA
1451 ACTTGAGCAT GTGGAATAGT TGTAACAAAA ACTCTAAGCA AATAGAGACT
1501 TTATGTAGTA TAAAGCATTT CCAGACATGA TAAATAATGG TACCTCAGAA
1551 CATAAAATAT ATTTAGCTAT CTTTCATCCC CAACTTTACA CATCCACCAA
1601 GGTACAGAAT AAGCATATGT CAACACAAAA TGTACTCTAA GTCTAACATG
1651 AGTAACCAAA CATGATGCCT GATTAAGTTA AAAGAAAAGA AAATCTGAGG
1701 GCATAGATCT TCAATCACAC CACTCCAGAG GGAAGGCGTA GAACAAGCTG
1751 TCCGCCGAAA ACACTGCAAT TCAATAAATA TCATTAGGAC AACAGTGCAG
1801 AGTCATGCGG GAAATGTCTT AAGTCACTGT ACTAAAAATA TAGGATTATA
1851 TTATGAACTA TACTAACCTT TTCACATAAT AGTAACAGAA ATCAGCTAAG
1901 ATGAATGTCT GGACAATTTC TGAGATAAGA ACCATGACGG CCATAAGCCA
1951 TACCCCAAGG CAACCAATAA ATGTCCACGG GTATCTAACA CCTGTTGCAA
2001 GAAATAGTAA GTTATTAGGA GATGTGCGGT TACGAAATTC AAGCTACACA
2051 ACAAAAGGAG GCCAGAACAA CAGCAATCTT GTAACCAGAT GACAACAATA
2101 AAATGTAAAC TTAAAGAGAC CGAACACACA AACATTGCAA CTCAGATGGA
2151 ATTGCTGCCA TGTAACTAGT AGGAGATTTG GGACGTCAAA TCAGTATATT
2201 ATGCAAATAC AAGGTATGAC CGCCTTGTCT ATTGTAGCAT ACAACAAACG
2251 TACAGTGGGT TTGTCCCTCT CAAAATGGCA GGATCTTTAC AGCACAATAT
2301 TTGGTTTTGT CATACTTATA CCATAAAAAA AAAAAAAAAA AAAAAAAAAA
2351 AAAGTACTCT GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC
```

FIGURE 147

```
  1 MGDEGIVRGV TKQTTPGKAT ILALGKAFPH QLVMQECLVD GYFRDTNCDN
 51 PELKQKLARL CKTTTVKTRY VVMNEEILKK YPELVVEGAS TVKQRLEICN
101 EAVTQMAIEA SQVCLKNWGR SLSDITHVVY VSSSEARLPG GDLYLSKGLG
151 LNPKIQRTML YFSGCSGGVA GLRVAKDVAE NNPGSRVLLA TSETTIIGFK
201 PPSVDRPYDL VGVALFGDGA GAMIIGSDPV FETETPLFEL HTSAQEFIPD
251 TEKKIDGRLT EEGISFTLAR ELPQIIEDNV EGFCNKLIDV VGLENKEYNK
301 LFWAVHPGGP AILNRVEKRL ELSPQKLNAS RKALMDYGNA SSNTIVYVLE
351 YMLEEEKKIK KAGGGDSEWG LILAFGPGIT FEGILARNLC A
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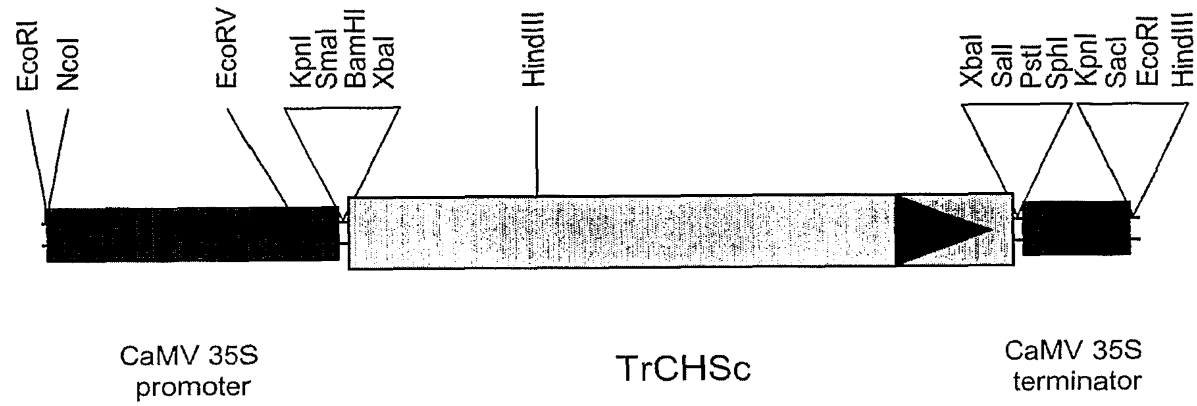
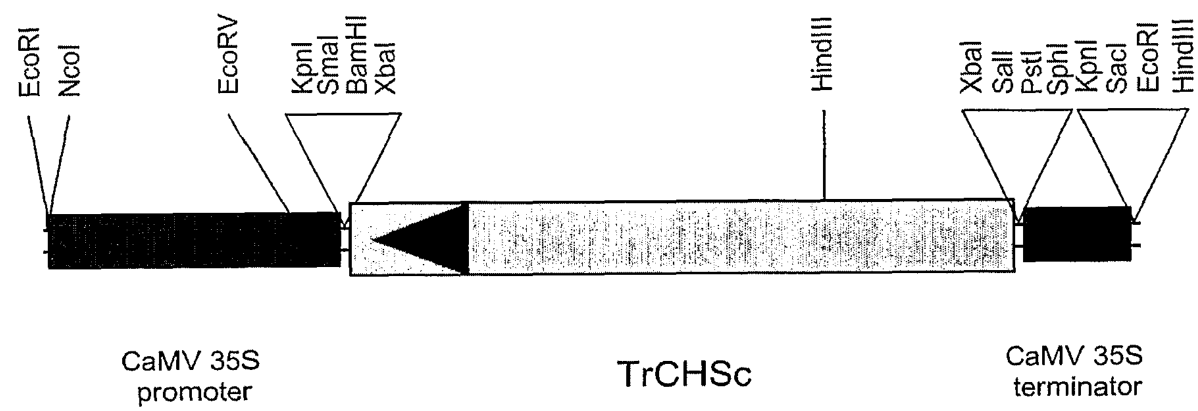
FIGURE 148

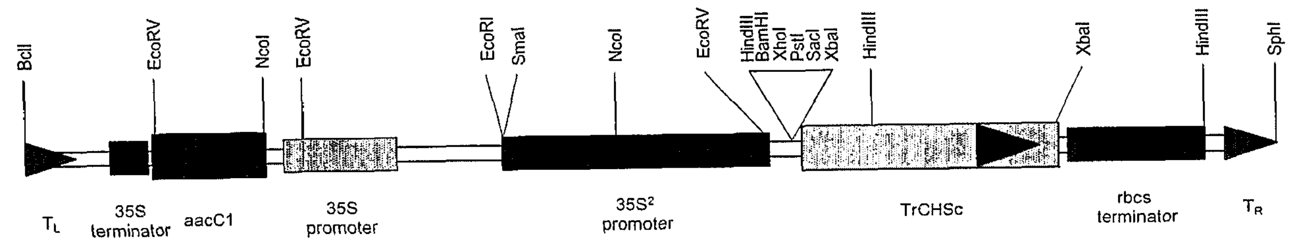


pDH51TrCHSc sense

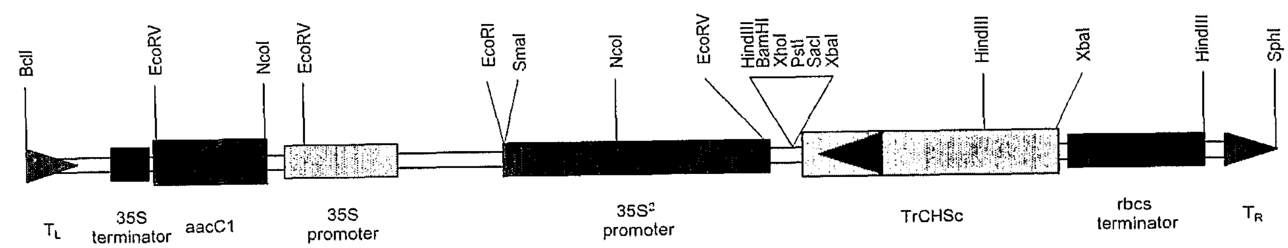


pDH51TrCHSc anti

FIGURE 149

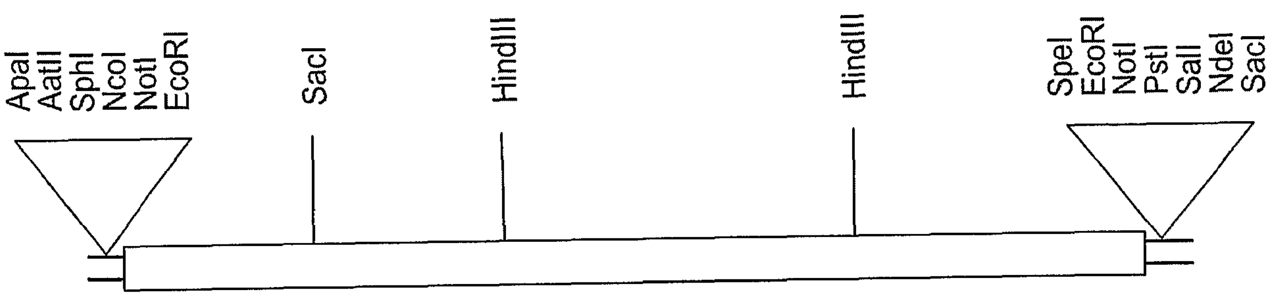


pPZP221:35S^{2}TrCHSc sense



pPZP221:35S^{2}TrCHSc anti

FIGURE 150



TrCHSd2

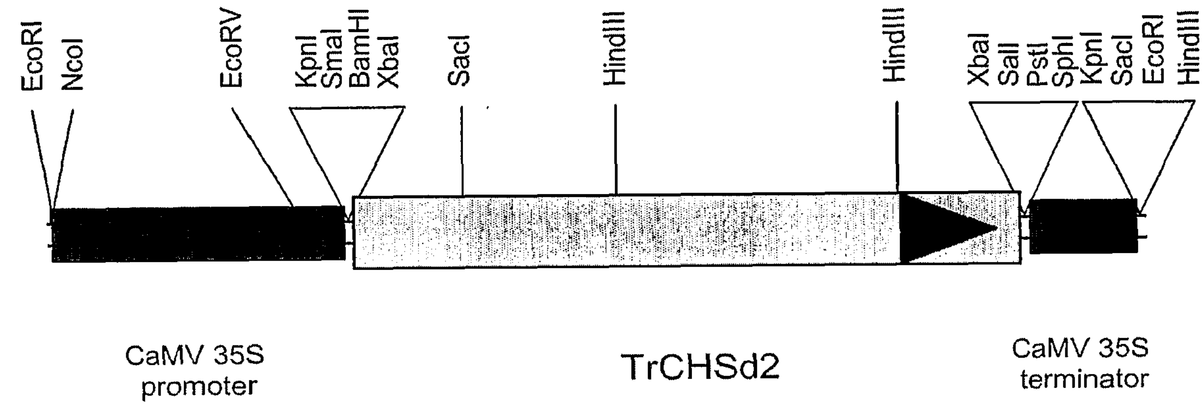
FIGURE 151

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATAGCAACA
  51 CACACTTTGA TTTCTTTTTG AGTCCTTGCT ACGTGGCTTT ACCAAAAAAC
 101 GTTGCTAAGT CATCAACCAT TCCAATTCCT TAATATAACC TATCAGTACT
 151 CACCATCTTT TCTTCCTCCC TGCTAACTTT AGACTCAGAG AAGATGGTGA
 201 ATGTTAATGA GATCCGCCAG GCACAGAGAG CTGAAGGCCC TGCCACCGTG
 251 TTGGCAATCG GCACTGCAAC TCCTCCAAAC TGTGTCGATC AGAGTACATA
 301 CCCAGACTAC TACTTCCGCA TCACAAACAG TGAGCACAAG ACAGAGCTCA
 351 AAGAAAAATT CCAGCGCATG TGTGACAAAT CTATGATTAA GAAGAGATAC
 401 ATGCATTTGA CAGAAGAGAT TTTGAAGGAG AATCCAAGTT TATGTGAGTA
 451 CATGGCACCT TCATTGGATG CAAGACAAGA CATGGTGGTT GTGGAAGTAC
 501 CAAGGCTAGG AAAAGAGGCT GCAACAAAGG CTATCAAGGA ATGGGGTCAA
 551 CCTAAGTCCA AGATTACTCA CCTCATCTTT TGCACCACAA GTGGTGTGGA
 601 CATGCCTGGC GCCGACTATC AGCTTACAAA GCTTTTAGGC CTTCGTCCGC
 651 ATGTGAAGCG TTATATGATG TACCAACAAG GTTGTTTCGC TGGTGGTACG
 701 GTGCTTCGTT TGGCTAAAGA CTTGGCTGAA AACAACAAAG GTGCCCGTGT
 751 GTTGGTGGTT TGTTCAGAGA TCACTGCGGT TACTTTCCGT GGACCCAGTG
 801 ACACTCATCT TGATAGCCTT GTGGGGCAAG CATTGTTTGG AGATGGTGCA
 851 GCAGCTGTGA TTGTAGGTTC AGACCCATTA CCACAAGTTG AGAAGCCCTT
 901 GTTTGAATTG GTATGGACTG CTCAAACAAT CCTTCCAGAC AGTGAAGGAG
 951 CCATTGATGG GCACCTTCGT GAAGTCGGGC TGACATTCCA TCTCCTCAAG
1001 GATGTTCCTG GACTCATCTC AAAGAACATT GAGAAAGCTC TTGTTGAGGC
1051 CTTTCAACCT TTAGGTATCT CTGATTACAA TTCTATATTT TGGATCGCAC
1101 ATCCTGGTGG ACCTGCAATT CTGGACCAAG TGGAAGCCAA ATTAAGCTTA
1151 AAGCCAGAGA AAATGCAAGC CACCCGGCAT GTGCTTAGCG AGTATGGTAA
1201 CATGTCAAGT GCATGTGTGT TATTTATCTT GGATGAGATG AGGAGGAAGT
1251 CAAAAGAAGA TGGACTTGCC ACAACAGGCG AGGGGCTGGA ATGGGGTGTA
1301 CTATTCGGTT TTGGACCCGG ACTCACTGTT GAGACTGTAT TGCTCCATAG
1351 TGTTGCCACT TAAATTGCCT AGATATGCTA TAACTATATG CTTATTTAAT
1401 TCTTTGTTTC TGGGGGATTT TATCTTCACT TACTTCACTG AGCATTTGAA
1451 TAAAGTTTGT TTTAATTATT CATAATGTAA TATGGTGTTG CTTAATGTAC
1501 CCATCCATAT AATATTTGTA ATACATATAT TAATCAACTT GCAATTTCAT
1551 GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAGGAAAAAA
1601 AAAAAAAAAA AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT
1651 CACTAGTGAA TTC
```

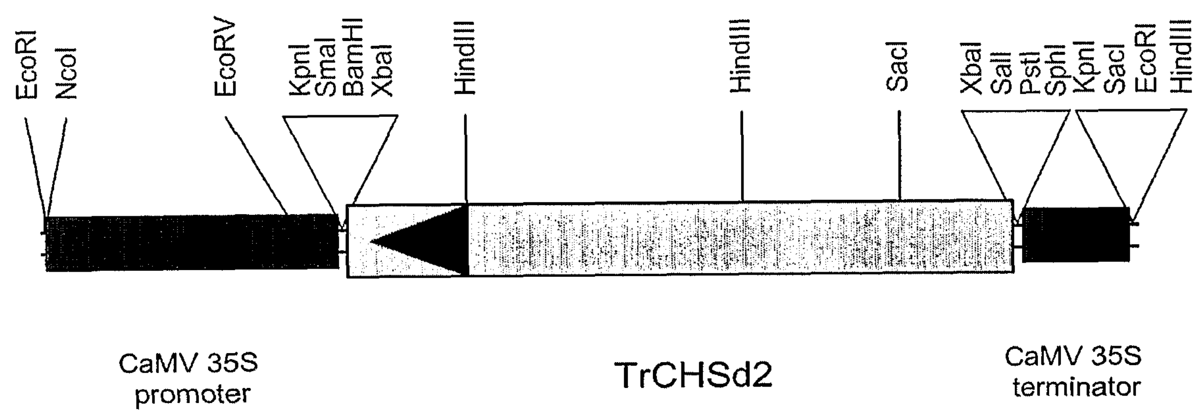
FIGURE 152

```
  1 MVNVNEIRQA QRAEGPATVL AIGTATPPNC VDQSTYPDYY FRITNSEHKT
 51 ELKEKFQRMC DKSMIKKRYM HLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA TKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPHVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEITAVTFRG
201 PSDTHLDSLV GQALFGDGAA AVIVGSDPLP QVEKPLFELV WTAQTILPDS
251 EGAIDGHLRE VGLTFHLLKD VPGLISKNIE KALVEAFQPL GISDYNSIFW
301 IAHPGGPAIL DQVEAKLSLK PEKMQATRHV LSEYGNMSSA CVLFILDEMR
351 RKSKEDGLAT TGEGLEWGVL FGFGPGLTVE TVLLHSVAT
```

FIGURE 153

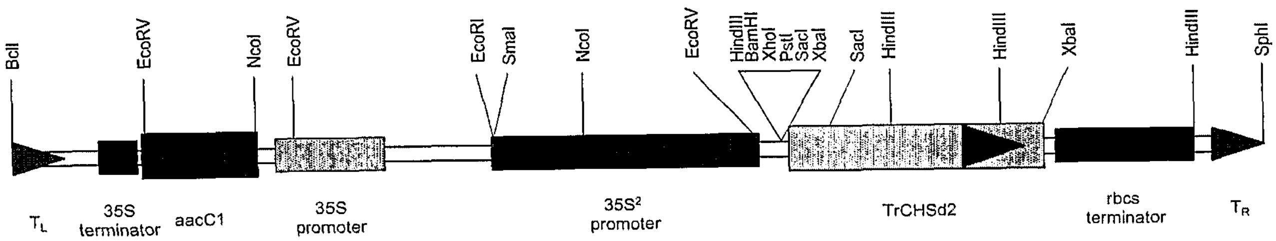


pDH51TrCHSd2 sense

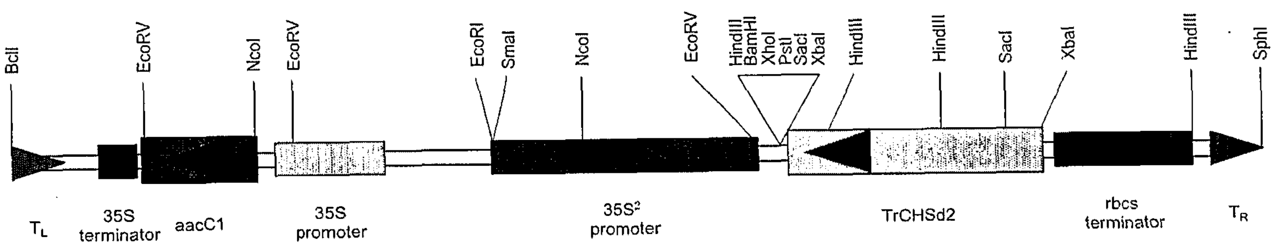


pDH51TrCHSd2 anti

FIGURE 154

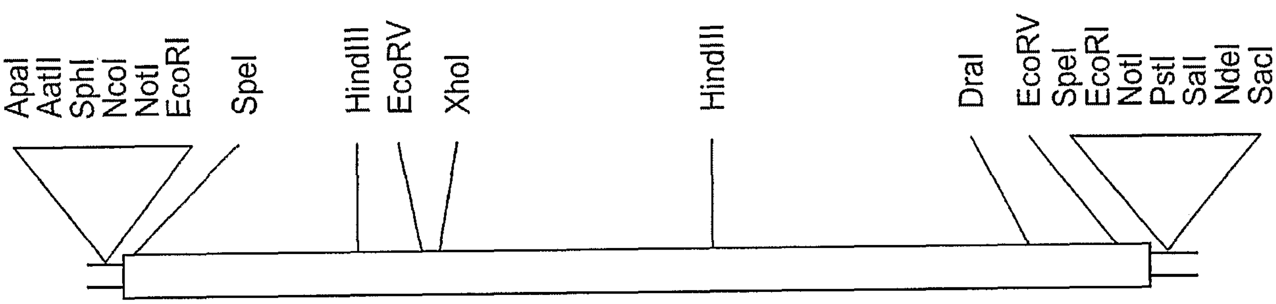


pPZP221:35S^{2}TrCHSd2 sense



pPZP221:35S^{2}TrCHSd2 anti

FIGURE 155



TrCHSf

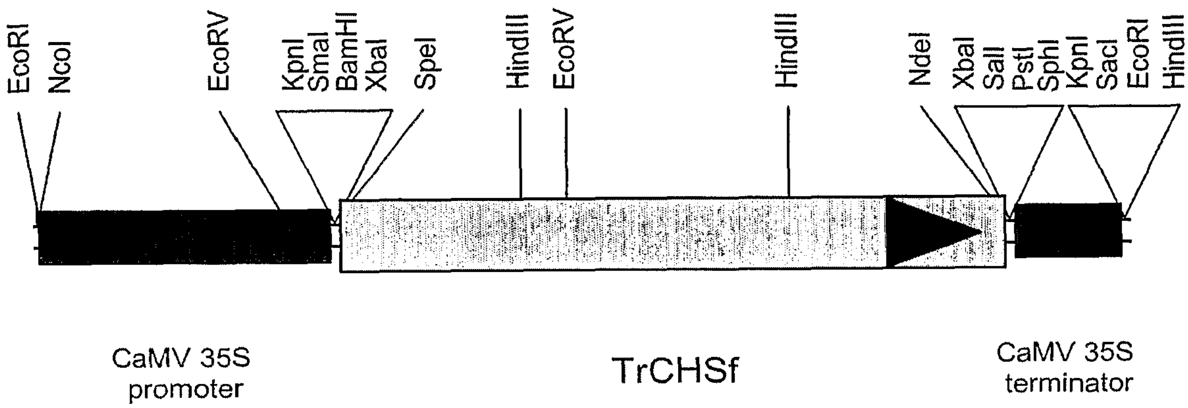
FIGURE 156

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG ACTAAGCCTT
  51 GATTCATTGT TTGTTTCCAT AACACAAGAA CTAGTGTTTG CTTGAATCTT
 101 AAGAAAAAAT GCCTCAAGGT GATTTGAATG GAAGTTCCTC GGTGAATGGA
 151 GCACGTGCTA GACGTGCTCC TACTCAGGGA AAGGCAACGA TACTTGCATT
 201 AGGAAAGGCT TTCCCCGCCC AGGTCCTCCC TCAAGAGTGC TTGGTGGAAG
 251 GATTCATTCG CGACACTAAG TGTGACGATA CTTATATTAA GGAGAAATTG
 301 GAGCGTCTTT GCAAAAACAC AACTGTGAAA ACAAGATACA CAGTAATGTC
 351 AAAGGAGATC TTAGACAACT ATCCAGAGCT AGCCATAGAT GGAACACCAA
 401 CAATAAGGCA AAAGCTTGAA ATAGCAAATC CAGCAGTAGT TGAAATGGCA
 451 ACAAGAGCAA GCAAAGATTG CATCAAAGAA TGGGGAAGGT CACCTCAAGA
 501 TATCACACAC ATAGTCTATG TTTCCTCGAG CGAAATTCGT CTACCCGGTG
 551 GTGACCTTTA TCTTGCAAAT GAACTCGGCT TAAACAGCGA TGTTAATCGC
 601 GTAATGCTCT ATTTCCTCGG TTGCTACGGC GGTGTCACTG GCTTACGTGT
 651 CGCCAAAGAC ATCGCCGAAA ATAACCCTGG TAGTAGGGTG TTACTCACAA
 701 CATCCGAGAC CACTATTCTC GGTTTTCGAC CACCGAGTAA AGCTAGACCT
 751 TATGACCTCG TTGGCGCTGC ACTTTTCGGT GATGGCGCCG CTGCTGCAAT
 801 AATTGGAACA GACCCTATAT TGAATCAAGA ATCACCTTTC ATGGAATTGA
 851 ACCATGCAGT CCAAAAATTC TTGCCTGATA CACAAAATGT GATTGATGGT
 901 AGAATCACTG AAGAGGGTAT TAATTTTAAG CTTGGAAGAG ACCTTCCTCA
 951 AAAAATTGAA GACAATATTG AAGAATTTTG CAAGAAAATT ATGGCTAAAA
1001 GTGATGTTAA GGAATTTAAT GACTTATTTT GGGCTGTTCA TCCTGGTGGG
1051 CCAGCTATAC TCAATAAGCT AGAAAATATA CTCAAATTGA AAAGTGATAA
1101 ATTGGATTGT AGTAGGAAGG CATTAATGGA TTATGGAAAT GTTAGTAGCA
1151 ATACTATATT CTATGTGATG GAGTATATGA GAGATTATTT GAAGGAAGAT
1201 GGAAGTGAAG AATGGGGATT AGGATTGGCT TTTGGACCAG GGATTACTTT
1251 TGAAGGGGTT CTCCTCCGTA GCCTTTAATC TTGAAATAAT AATTCATATG
1301 AAATTACTTG TCTTAAGATT GTGATAGGAA GATGAATATG TATTGGATTA
1351 ATATTGATAT GGTGTTATTT TAAGTTGATT TTAAAAAAAG TTTATTAATA
1401 AAGTATGATG TAACAATTGT TGTTTGAATG TTAAAAGGGA AGTATACTAT
1451 TTTAAGTTCT TGACCATACT GATTTTTTCT TTACACATTT TCATATCTAA
1501 AATTGTTCTA TGATATCTTC ATTGTTGATA CTGTAATAAT ATAATATCTA
1551 ATTTGGCTGG CAAAATGAAA GATTTTTCAC CGAAAAAAAA AAAAAAAAAA
1601 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CACTAGTGAA
1651 TTC
```

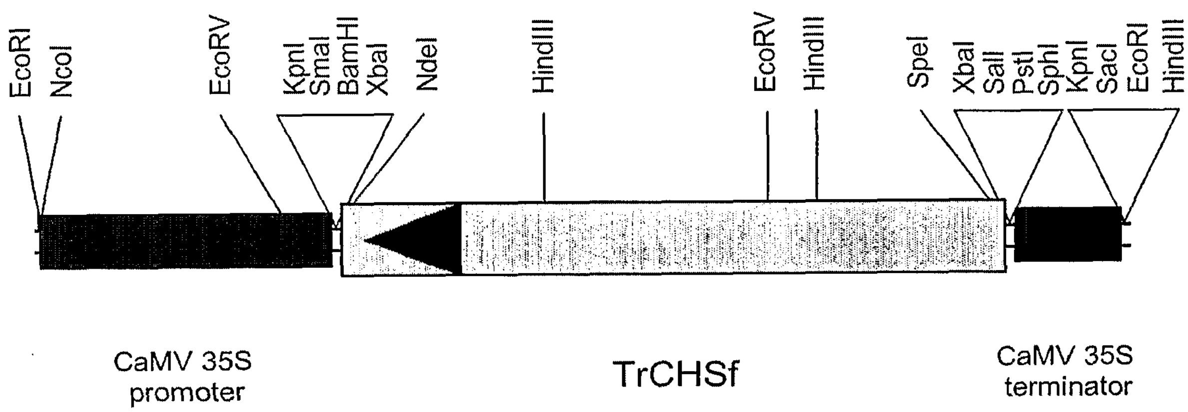
FIGURE 157

```
  1 MPQGDLNGSS SVNGARARRA PTQGKATILA LGKAFPAQVL PQECLVEGFI
 51 RDTKCDDTYI KEKLERLCKN TTVKTRYTVM SKEILDNYPE LAIDGTPTIR
101 QKLEIANPAV VEMATRASKD CIKEWGRSPQ DITHIVYVSS SEIRLPGGDL
151 YLANELGLNS DVNRVMLYFL GCYGGVTGLR VAKDIAENNP GSRVLLTTSE
201 TTILGFRPPS KARPYDLVGA ALFGDGAAAA IIGTDPILNQ ESPFMELNHA
251 VQKFLPDTQN VIDGRITEEG INFKLGRDLP QKIEDNIEEF CKKIMAKSDV
301 KEFNDLFWAV HPGGPAILNK LENILKLKSD KLDCSRKALM DYGNVSSNTI
351 FYVMEYMRDY LKEDGSEEWG LGLAFGPGIT FEGVLLRSL
```

FIGURE 158

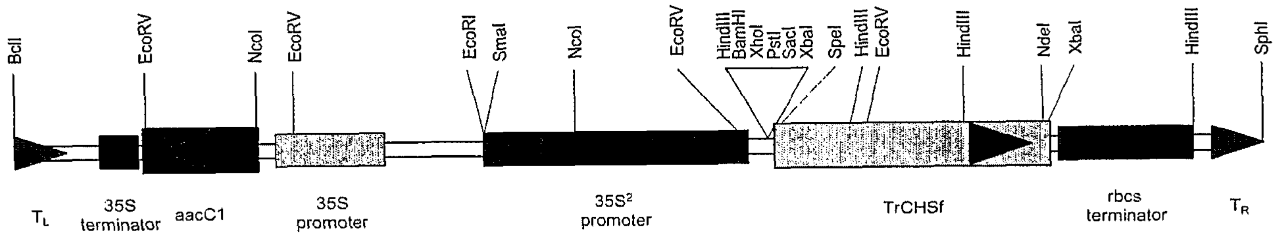


pDH51TrCHSf sense

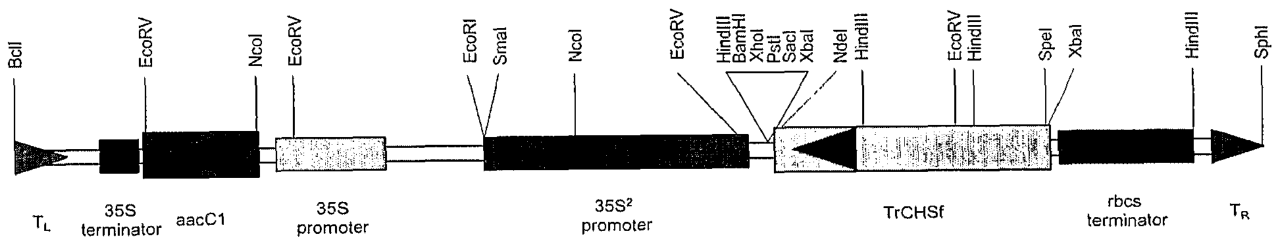


pDH51TrCHSf anti

FIGURE 159



pPZP221:35S²TrCHSf sense



pPZP221:35S²TrCHSf anti

FIGURE 160

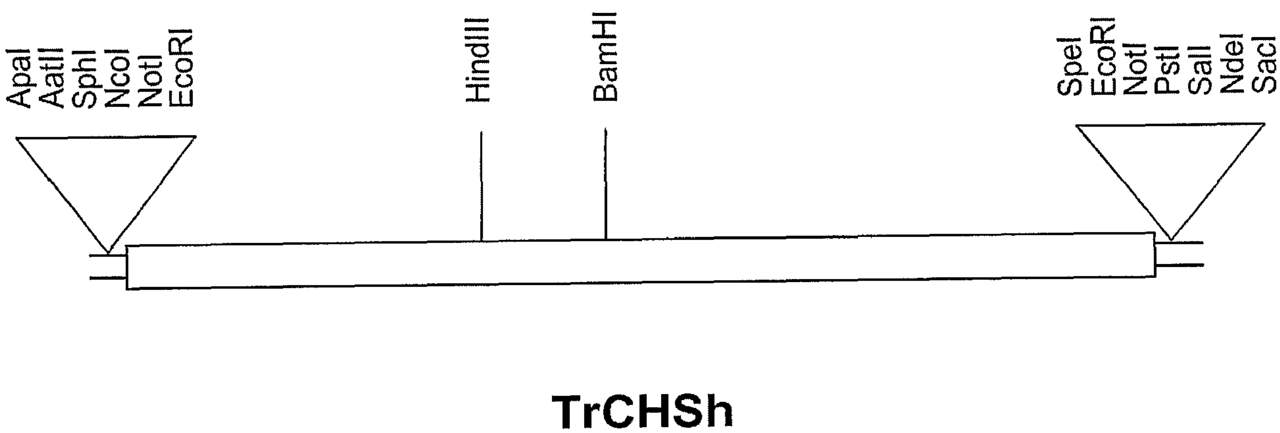

ApaI
AatII
SphI
NcoI
NotI
EcoRI
HindIII
BamHI
SpeI
EcoRI
NotI
PstI
SalI
NdeI
SacI
TrCHSh

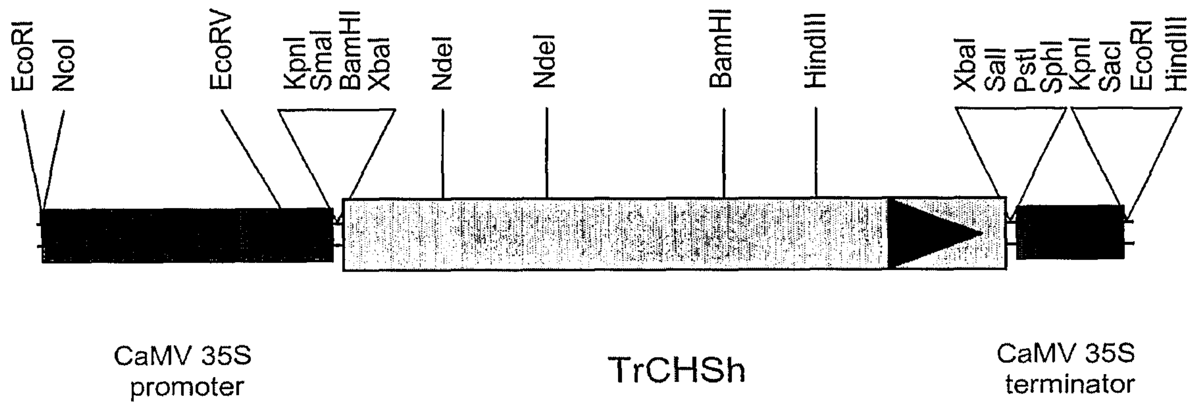
FIGURE 161

```
   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGAA
  51 TCCACCAAAT CAACACCATT AATAACCTTC CAAATTCTCG TTACCTCACC
 101 AAATCTCATT TTTCATTATA TATCTTGGGT ACATCTTTTG TTACCTCCAA
 151 CAAAAAAATG GTGACCGTAG AAGAGATTCG TAACGCCCAA CGTTCAAATG
 201 GCCCTGCCAC TATCTTAGCT TTTGGCACAG CCACTCCTTC TAACTGTGTC
 251 ACTCAAGCTG ATTATCCTGA TTACTACTTT CGTATCACCA ACAGCGAACA
 301 TATGACTGAT CTTAAGGAAA AATTCAAGCG GATGTGTGAT AGATCAATGA
 351 TAAAGAAACG TTACATGCAC CTAACAGAAG ACTTTCTGAA GGAGAATCCA
 401 AATATGTGTG AATACATGGC ACCATCACTA GATGTAAGAC GAGACATAGT
 451 GGTTGTTGAA GTACCAAAGC TAGGTAAAGA AGCAGCAAAA AAAGCCATAT
 501 GTGAATGGGG ACAACCAAAA TCCAAAATCA CACATCTTGT TTTCTGCACC
 551 ACTTCCGGTG TTGACATGCC GGGAGCCGAT TACCAACTCA CCAAACTTTT
 601 AGGCTTAAAA CCTTCTGTCA AGCGTCTCAT GATGTATCAA CAAGGTTGTT
 651 TCGCTGGCGG CACAGTTCTC CGCTTAGCAA AAGACCTTGT TGAGAATAAC
 701 AAAAATGCAA GAGTTCTTGT TGTTTGTTCT GAAATTACTG CGGTTACTTT
 751 TCGTGGACCA TCGGATACTC ATCTTGATTC GCTCGTGGGA CAGGCGCTTT
 801 TTGGTGATGG AGCCGCAGCA ATGATTATTG GTGCGGATCC TGATTTAACC
 851 GTGGAGCGTC CGATTTTCGA GATTGTTTCG GCTGCTCAGA CTATTCTTCC
 901 TGATTCTGAT GGCGCAATTG ATGGACATCT TCGTGAAGTG GGGCTCACTT
 951 TTCATTTATT GAAAGATGTT CCGGGGATTA TTTCAAAGAA CATTGAAAAA
1001 AGTTTAGTTG AAGCTTTTGC GCCTATTGGG ATTAATGATT GGAACTCAAT
1051 ATTTTGGGTT GCACATCCAG GTGGACCGGC TATTTTAGAC CAGGTTGAAG
1101 AGAAACTCCA TCTTAAAGAG GAGAAACTCC GGTCCACCCG GCATGTGCTT
1151 AGTGAATATG GAAATATGTC AAGTGCATGT GTTTTATTTA TTTTGGATGA
1201 AATGAGAAAG AGGTCTAAAG AGGAAGGGAT GATTACAACT GGTGAAGGGT
1251 TGGAATGGGG TGTGTTGTTT GGGTTTGGAC CGGGTTTAAC TGTTGAAACC
1301 GTTGTGCTTC ATAGTGTTCC GGTTCAGGGT TGAATTTATT ATACATAGAT
1351 TGGAAAATAA AATTTGCCTG CCGAGAGATG TGAACTAACT TTGTAGGCAA
1401 GCTCAAATTA AAGTTTGAGA TAATATTGTG CTTTAGTTAT TATGGTATGT
1451 AATGTAATGT TTTTACTTTT TTCGAAATTC ATGTAATTTG ATATGTAAAG
1501 TAATATGTTT GGGTTGGAAT ATAATTATTT GTTAACTAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT AATCGAATTC
```

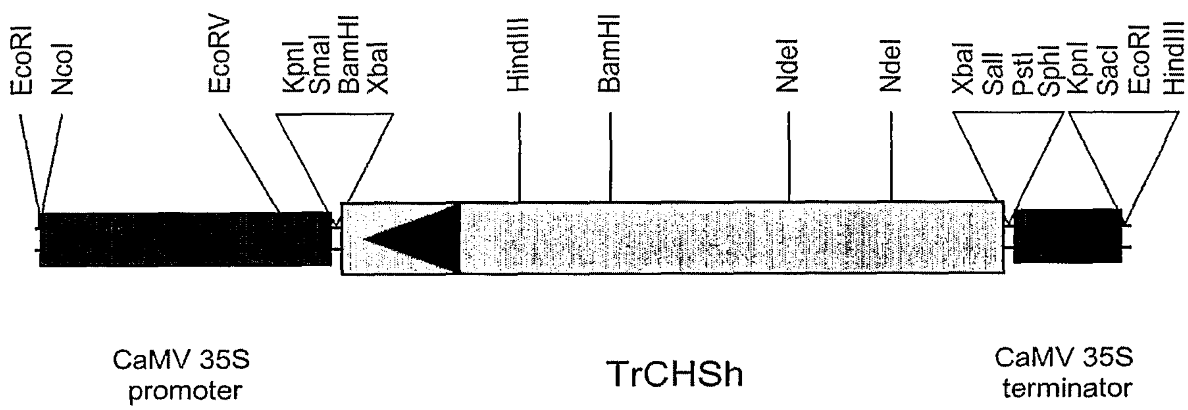
FIGURE 162

```
  1 MVTVEEIRNA QRSNGPATIL AFGTATPSNC VTQADYPDYY FRITNSEHMT
 51 DLKEKFKRMC DRSMIKKRYM HLTEDFLKEN PNMCEYMAPS LDVRRDIVVV
101 EVPKLGKEAA KKAICEWGQP KSKITHLVFC TTSGVDMPGA DYQLTKLLGL
151 KPSVKRLMMY QQGCFAGGTV LRLAKDLVEN NKNARVLVVC SEITAVTFRG
201 PSDTHLDSLV GQALFGDGAA AMIIGADPDL TVERPIFEIV SAAQTILPDS
251 DGAIDGHLRE VGLTFHLLKD VPGIISKNIE KSLVEAFAPI GINDWNSIFW
301 VAHPGGPAIL DQVEEKLHLK EEKLRSTRHV LSEYGNMSSA CVLFILDEMR
351 KRSKEEGMIT TGEGLEWGVL FGFGPGLTVE TVVLHSVPVQ G
```

FIGURE 163

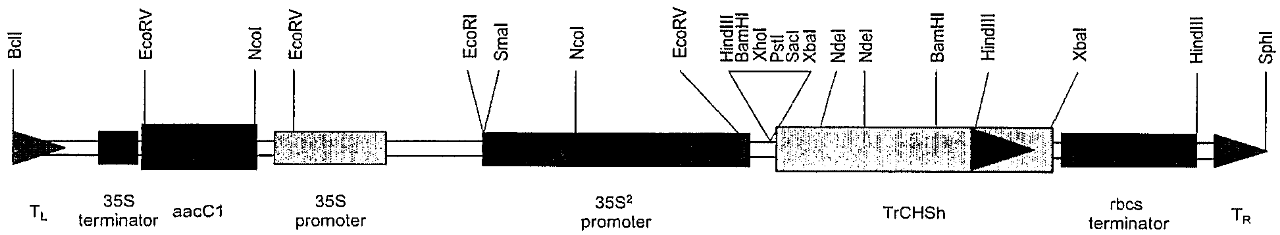


pDH51TrCHSh sense

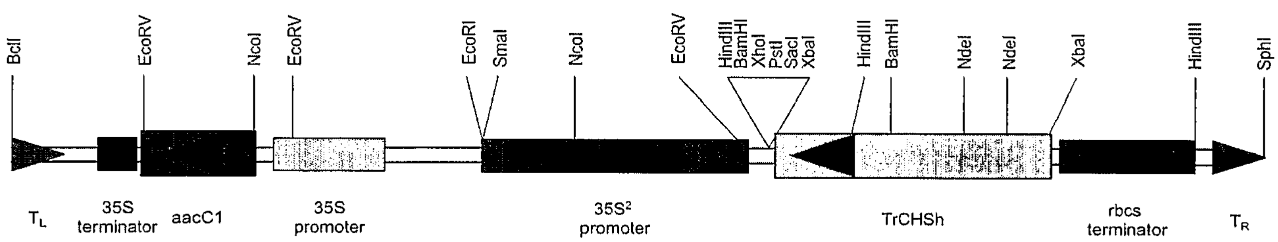


pDH51TrCHSh anti

FIGURE 164

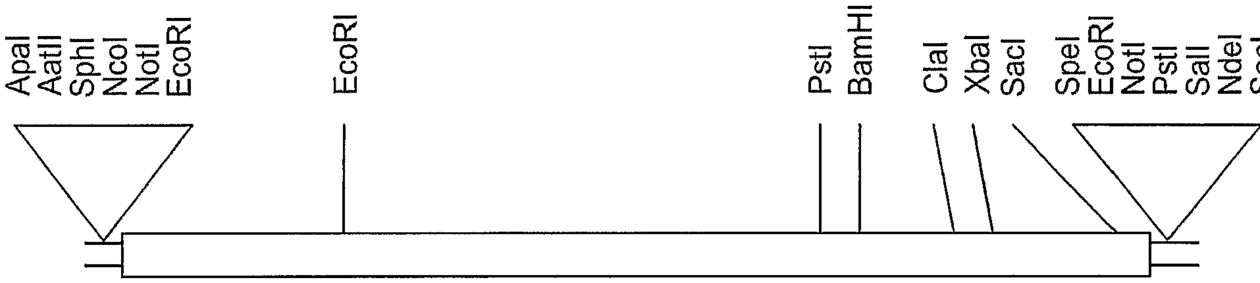


pPZP221:35S^{2}TrCHSh sense



pPZP221:35S^{2}TrCHSh anti

FIGURE 165



TrDFRd

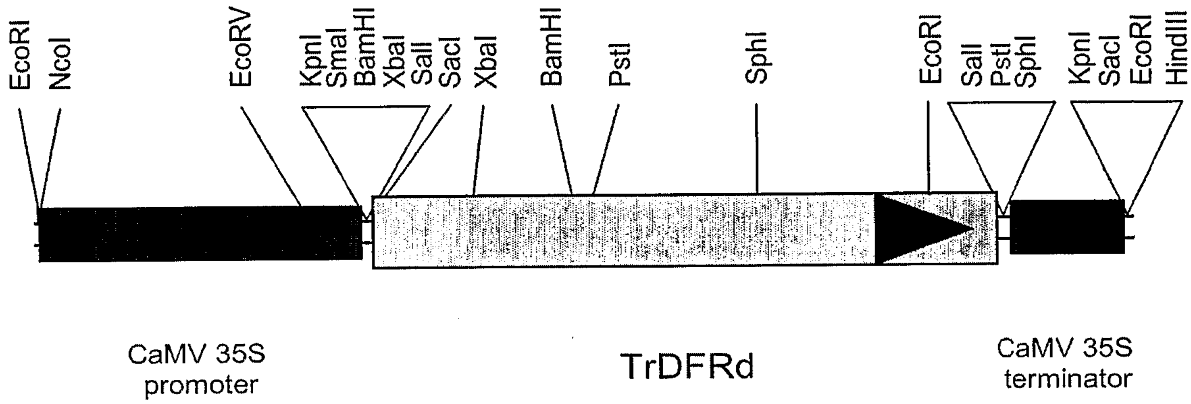
FIGURE 166

```
   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGTG
  51 ACTTGATCTA GCAGTTATCA AACACAACAG TCTTCCACTT GAGCTCTGTT
 101 TCTCCACATG TCGAAGCTAG TTTGCGTCAC CGGCGGCAGC GGATGCATCG
 151 GTTCATGGCT AGTCCATCTC CTTCTCCTCC GCGGCTACAC TGTTCACGCC
 201 ACCGTCCAAA ATCTCAATGA TGAGAACGAA ACGAAGCATC TAGAAGCTCT
 251 CGAAGGAGCA CAAACTAATC TCCGTCTCTT CCAGATCGAT CTCCTTAACT
 301 ACGACACAAT CCTCGCTGCT GTCCGCGGTT GCGTCGGAAT TTTCCACCTC
 351 GCTTCACCTT GCACTGTAGA CAAAGTTCAT GATCCTCAGA AGGAGCTTTT
 401 GGATCCTGCA ATTAAAGGGA CTTTGAATGT GCTTACTGCA GCTAAGGAAG
 451 TAGGGGTGAA GCGTGTGGTT GTTACCTCGT CTGTCTCGGC GATTACTCCT
 501 AGTCCTGATT GGCCTTCTGA TGTTGTTAAA AGAGAGGATT GTTGGACTGA
 551 TGTTGAATAT TGCAAGAAAA AAGAGTTGTG GTATCCGTTG TCCAAAACAT
 601 TGGCTGAGAA AGCTGCGTGG GATTTTTCCA AAGAAAATGG TTTGGATGTT
 651 GTTGTGGTGA ATCCCGGTAC TGTGATGGGT CCTGTTATTC CACCACGGCA
 701 TAATGCAAGC ATGCTCATGC TTGTGAGACT TCTTGAAGGC TGCGCTGAAA
 751 CATTTGAAGA CTATTTTATG GGATTGGTCC ACTTCAAAGA TGTAGCATTG
 801 GCGCATATTT TGGTGTATGA GAACAAAGAA GCATCTGGTA GACATGTGTG
 851 TGTTGAAACT ATCTCTCACT ACGGTGATTT TGTGGCAAAA GTTGCTGAAC
 901 TTTATCCAGA ATATAGTGTT CCTAGGATGC AGCGAGATAC GCAACCTGGA
 951 TTGTTGAGAG CGAATGATGG ATCAAAGAAG CTCATAGATT TGGGTTTGGA
1001 ATTCATTCCA ATGGAGCAAA TTATCAAGGA TGCTGTAGAG AGTTTGAAGA
1051 ACAAAGGATT CATTTCTTGA ATGATGTTAC TGTTCTTTGG AGAACCCTAT
1101 AGTTACCAGA GTATAGACTA AATAATATAT AGGTGATGGG TCAGAGAATG
1151 AGTACTTATG TCATGAGTTG TGTCTGTATA ATATGTTTTC TCAATTCTTA
1201 TATGTTAAAT TGCTAATGTT AACTTCAATA TTTATCAGCC AGTATTGTTT
1251 TTTTAATAAA ATATTGAAGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAGT
1301 ACTCTGCGTT GTTACCACTG CTTAATCGAA TTC
```

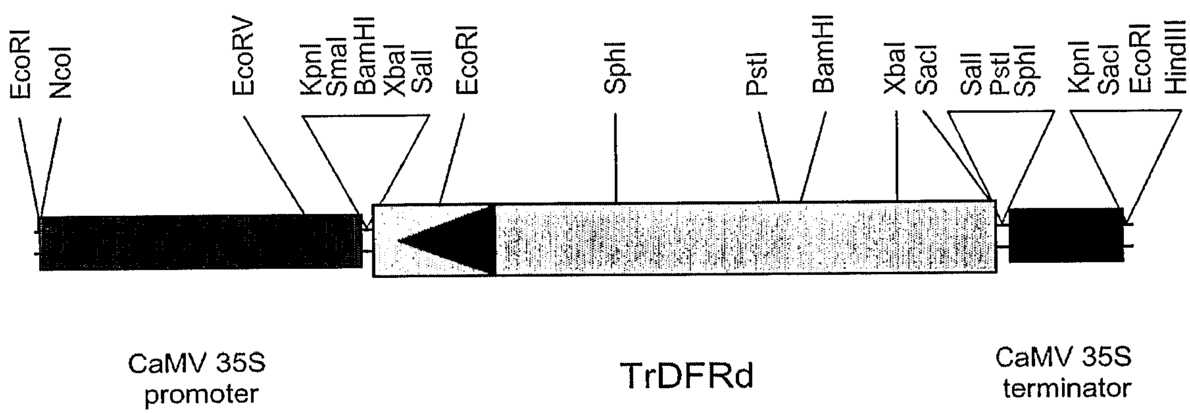
FIGURE 167

```
  1  MSKLVCVTGG SGCIGSWLVH LLLLRGYTVH ATVQNLNDEN ETKHLEALEG
 51  AQTNLRLFQI DLLNYDTILA AVRGCVGIFH LASPCTVDKV HDPQKELLDP
101  AIKGTLNVLT AAKEVGVKRV VVTSSVSAIT PSPDWPSDVV KREDCWTDVE
151  YCKKKELWYP LSKTLAEKAA WDFSKENGLD VVVVNPGTVM GPVIPPRHNA
201  SMLMLVRLLE GCAETFEDYF MGLVHFKDVA LAHILVYENK EASGRHVCVE
251  TISHYGDFVA KVAELYPEYS VPRMQRDTQP GLLRANDGSK KLIDLGLEFI
301  PMEQIIKDAV ESLKNKGFIS
```

FIGURE 168

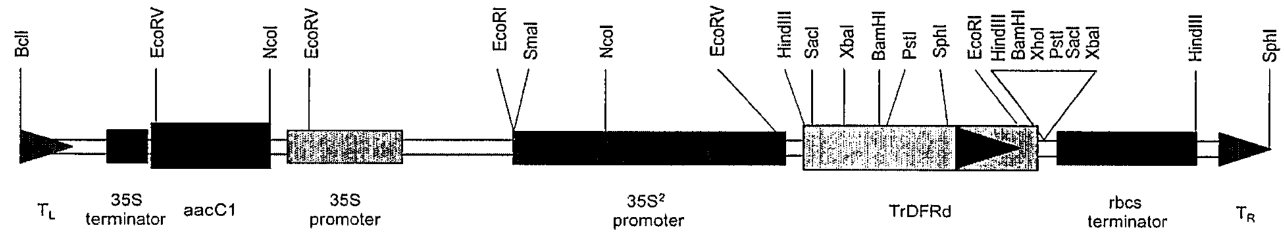


pDH51TrDFRd sense

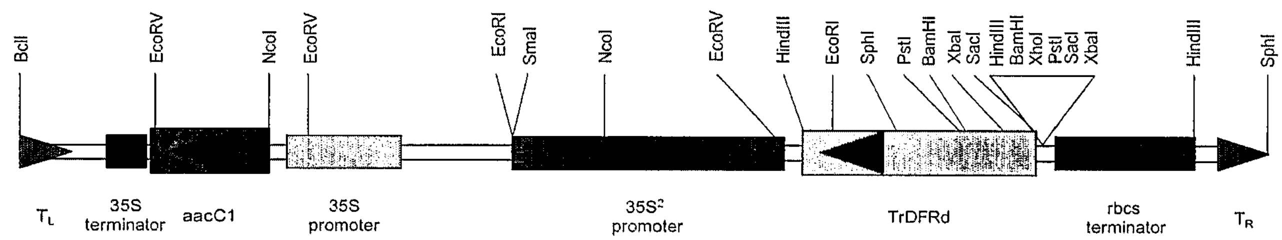


pDH51TrDFRd anti

FIGURE 169

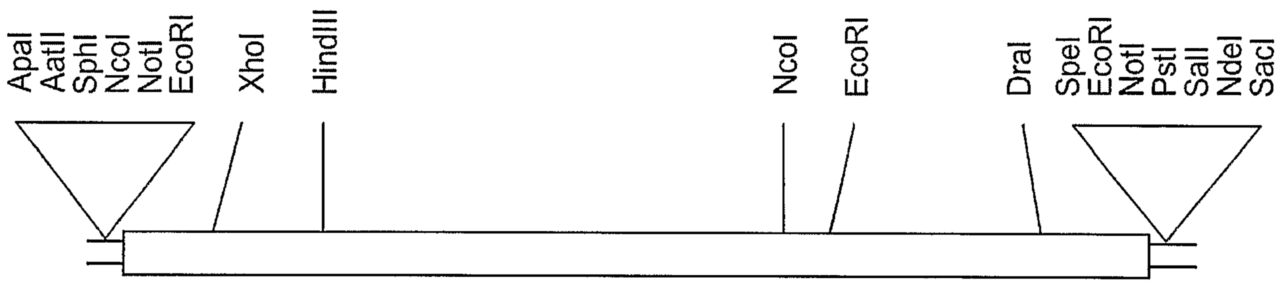


pPZP221:35S²TrDFRd sense



pPZP221:35S²TrDFRd anti

FIGURE 170



TrF3Ha

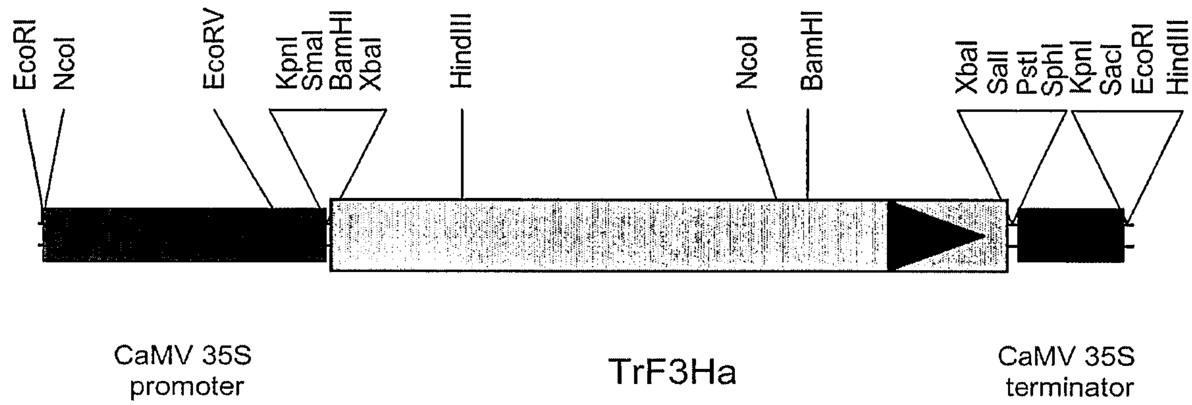
FIGURE 171

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GACCACTCTA
  51 TTTATTTCTA CTTAAACCTC ACAAAAAATA AACCACACAA CACACAAACA
 101 CCAAAAACAG AGCACCGTTT CCATCATCAA ACAATGGCAC CAGCCAAAAC
 151 TCTAAGTTAT CTCTCACAAC AAAACACTCT CGAGTCAAGT TTCGTTAGGG
 201 AAGAAGATGA GCGTCCAAAA GTTGCCTACA ATAACTTCAG CAACGAGATT
 251 CCAATCATTT CTCTTGCTGG AATTGATGAG GTTGATGGTC GTAGAACAGA
 301 GATATGTAAC AAGATTGTTG AAGCTTGTGA GAATTGGGGT ATTTTTCAGG
 351 TTGTTGATCA TGGTGTTGAT ACAAAACTTG TTTCTGAGAT GACCCGTTTT
 401 GCTAGAGAGT TTTTTGCTTT GCCACCGGAA GAGAAGCTCC GGTTTGACAT
 451 GTCCGGTGGT AAAAAGGGTG GTTTCATTGT CTCTAGTCAT CTTCAAGGAG
 501 AAGCAGTGAA GGATTGGAGA GAGCTAGTGA CATATTTTTC ATACCCAATT
 551 AAACAAAGAG ATTATTCAAG GTGGCCAGAC AAGCCAGAAG GATGGAAAGA
 601 GGTAACAGAA AAATACAGTG AAAACCTAAT GAATTTAGCT TGCAAGCTAT
 651 TGGAAGTTTT ATCAGAAGCA ATGGGTTTAG AAAAAGAAGC TCTAACAAAA
 701 GCATGTGTTG ATATGGATCA AAAAGTTGTT ATAAATTATT ACCCAAAATG
 751 CCCTGAACCT GACCTCACAC TTGGCCTTAA ACGTCACACT GACCCTGGCA
 801 CAATTACTCT TTTGCTTCAA GATCAAGTTG GTGGTCTTCA AGCTACCAAA
 851 GATAATGGTA AGACGTGGAT TACAGTTCAA CCAGTTGAAG GTGCTTTTGT
 901 TGTTAATCTT GGAGACCATG GTCACTATCT AAGTAATGGA CGGTTCAAAA
 951 ATGCTGACCA TCAAGCAGTG GTGAATTCGA ACTACAGCCG TTTATCAATA
1001 GCAACATTTC AAAATCCAGC TCCAGATGCA ACTGTGTACC CTTTGAAGAT
1051 TAGAGATGGT GAAAAATCTG TGTTGGAAGA ACCAATCACT TTTGCTGAAA
1101 TGTATAGAAG GAAGATGACC AAAGACCTTG AAATTGCTAG GATGAAGAAG
1151 TTGGCTAAGG AACAACAACT TAGGGACTTG GAGGAGAACA AGACTAAATA
1201 TGAGGCCAAA CCTTTGAATG AGATCTTTGC TTAATTAATT AGTCTTAATT
1251 TAAATAATAA ATTTTAGACT TAATTTACAT ATAATAATTT TAATTTTTTG
1301 TTCAATTAAT CTATGTTTAA TTTGTCGTTA TTGTCCACGT GTATTAAGCT
1351 GCTTGGTTGT GTGTGCCTTG GAGAATAATC AATAATATTA CATCTATGTT
1401 TAATTATAAA AAAAAAAAAA AAAAAAAAAA GTATCTGCGT TGTTACCACT
1451 GCTTAATCAC TAGTGAATTC
```

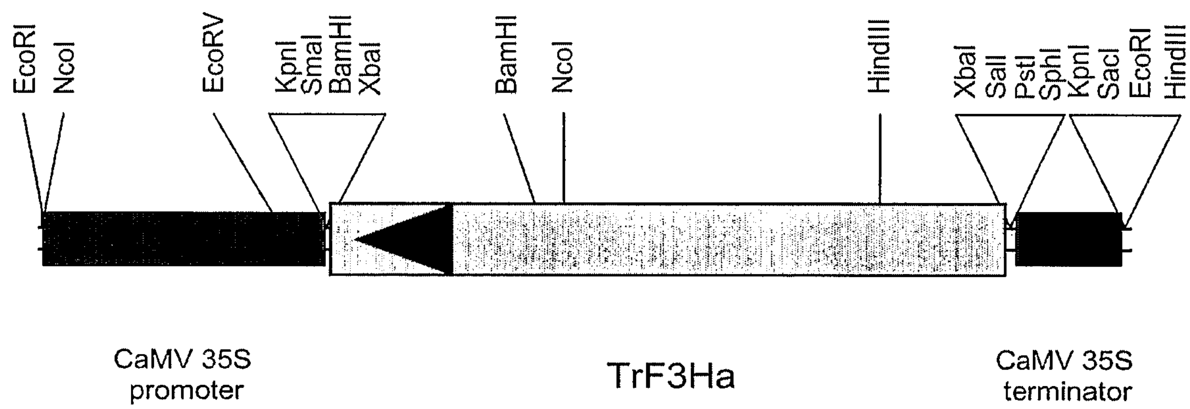
FIGURE 172

```
  1 MAPAKTLSYL SQQNTLESSF VREEDERPKV AYNNFSNEIP IISLAGIDEV
 51 DGRRTEICNK IVEACENWGI FQVVDHGVDT KLVSEMTRFA REFFALPPEE
101 KLRFDMSGGK KGGFIVSSHL QGEAVKDWRE LVTYFSYPIK QRDYSRWPDK
151 PEGWKEVTEK YSENLMNLAC KLLEVLSEAM GLEKEALTKA CVDMDQKVVI
201 NYYPKCPEPD LTLGLKRHTD PGTITLLLQD QVGGLQATKD NGKTWITVQP
251 VEGAFVVNLG DHGHYLSNGR FKNADHQAVV NSNYSRLSIA TFQNPAPDAT
301 VYPLKIRDGE KSVLEEPITF AEMYRRKMTK DLEIARMKKL AKEQQLRDLE
351 ENKTKYEAKP LNEIFA
```

FIGURE 173

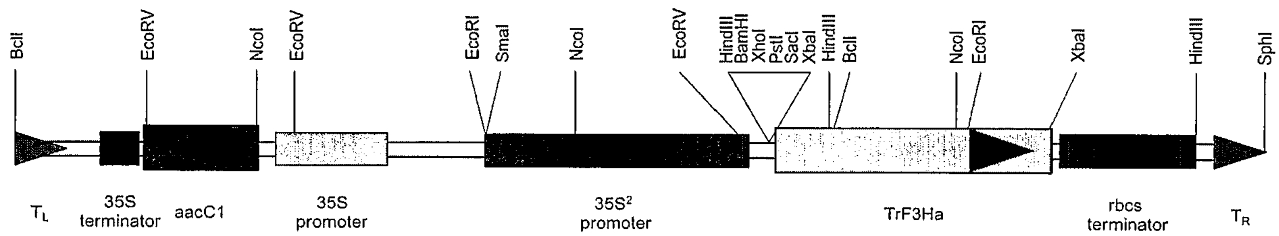


pDH51TrF3Ha sense

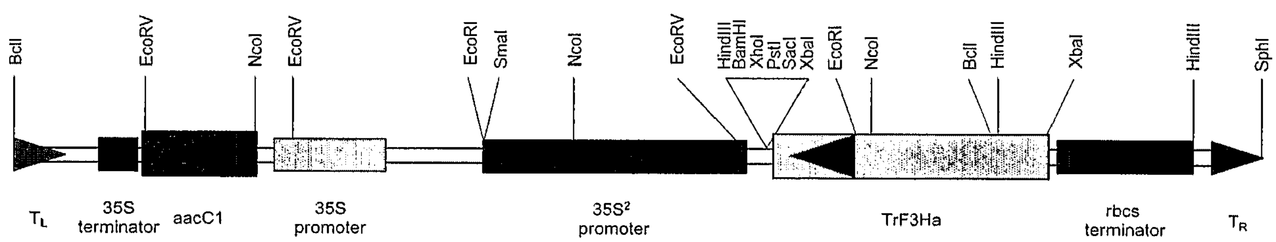


pDH51TrF3Ha anti

FIGURE 174

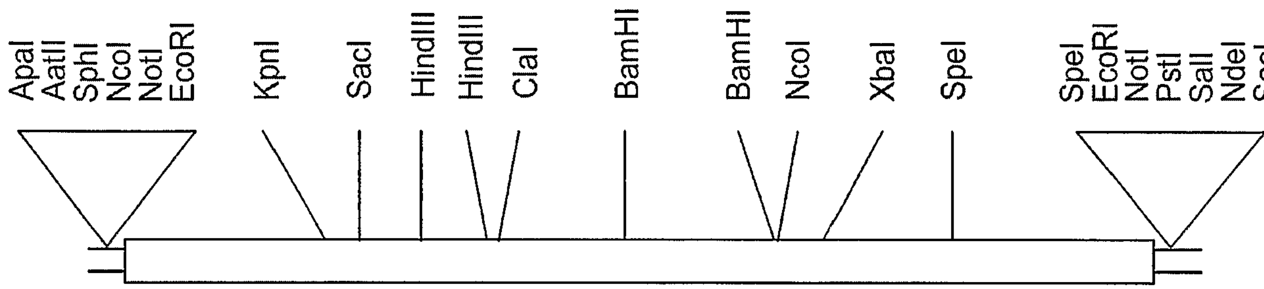


pPZP221:35S^{2}TrF3Ha sense



pPZP221:35S^{2}TrF3Ha anti

FIGURE 175



TrPALa

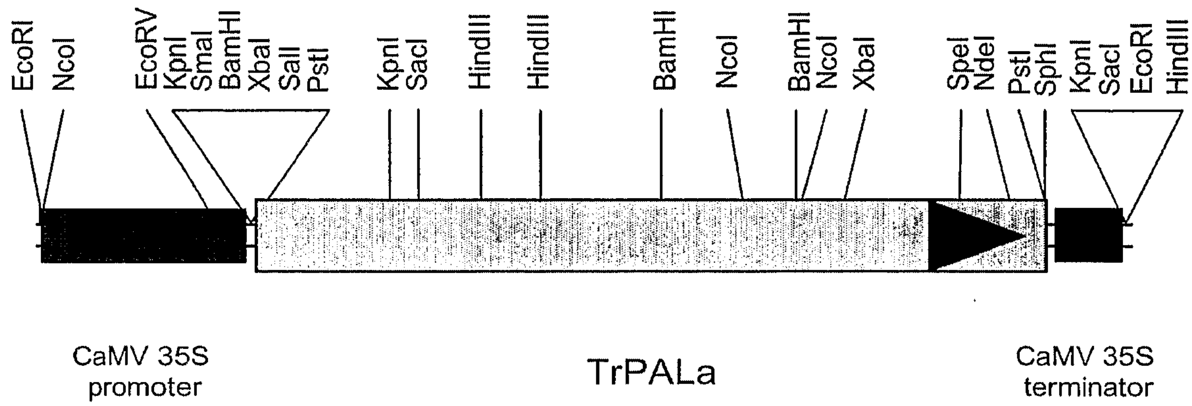
FIGURE 176

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GAGGAAATTC
  51 ACAACTCAAA TATTCCTTTA ATTCTTTCAT ATAATCATTT GAATTTCCAT
 101 TCTCCCTAAA AATTCTATAG CTACCACATC ACACAACATA ACAAATTAAG
 151 AAATATTTAT TACTATATTA AGATATGGAA GTAGTAGCAG CAGCAATCAC
 201 AAAAAACAAT GGCAAGATTG ATTCATTTTG CTTGAATCAT GCTAATGCTA
 251 ATAACATGAA AGTGAATGGT GCTGATCCTT TGAATTGGGG TGTGGCTGCT
 301 GAGGCAATGA AGGGAAGTCA CTTGGATGAG GTGAAGCGTA TGGTGGAGGA
 351 ATACCGGAAA CCGGTTGTCC GTCTTGGTGG CGAGACACTA ACCATTTCTC
 401 AGGTGGCTGC CATTGCTGCA CACGATGGTG CAACGGTGGA GCTATCGGAA
 451 TCTGCTAGAG CCGGCGTTAA GGCAAGCAGT GACTGGGTTA TGGAGAGTAT
 501 GAACAAAGGT ACCGACAGCT ACGGTGTCCC AACAGGGTTC GGCGCTACCT
 551 CGCACCGCCG AACCAAACAA GGTGGTGCTT TGCAGAAAGA GCTCATAAGG
 601 TTTTTGAATG CTGGAATATT TGGAAATGGA ACTGAGTCAA GCCACACACT
 651 ACCACACACA GCCACAAGAG CTGCCATGCT AGTGAGAATC AACACACTTC
 701 TCCAAGGCTA TTCAGGAATT AGATTTGAAA TCTTAGAAGC TATCACCAAG
 751 CTTCTTAACA ACAATGTCAC CCCATGTTTA CCGCTTCGCG GTACAATCAC
 801 AGCTTCAGGA GATTTAGTCC CTCTTTCTTA CATTGCTGGT TTACTAACCG
 851 GACGACCAAA TTCCAAGGCT CATGGACCTT CTGGAGAAGT ACTTAATGCA
 901 AAACAAGCTT TTCAATCAGC TGGAATCGAT GCCGAGTTCT TTGAATTACA
 951 ACCAAAAGAA GGCCTTGCCC TTGTTAACGG AACCGCTGTT GGTTCTGGTT
1001 TAGCTTCTAT TGTTCTTTTT GAGGCTAATA TATTGGCGGT GTTGTCTGAA
1051 GTTCTATCTG CAATTTTCGC TGAAGTTATG CAAGGGAAGC CCGAATTTAC
1101 CGATCATTTG ACACATAAGT TGAAACATCA CCCTGGTCAA ATTGAGGCTG
1151 CTGCTATTAT GGAACACATT TTGGATGGGA GTGCTTATGT TAAAGACGCT
1201 AAGAAGTTGC ATGAGATGGA TCCTTTACAG AAGCCAAAAC AAGATAGATA
1251 TGCACTTAGG ACTTCGCCAC AATGGCTTGG TCCTTTGATT GAAGTGATTA
1301 GATTCTCTAC CAAGTCAATT GAGAGAGAGA TCAACTCTGT CAATGACAAT
1351 CCTTTGATTG ATGTTTCAAG GAACAAGGCT TTGCATGGTG GAAATTTTCA
1401 AGGAACACCT ATCGGAGTAT CCATGGATAA TACACGTTTG GCTCTTGCAT
1451 CAATTGGCAA ACTTATGTTT GCTCAATTCT CTGAGCTTGT CAATGATTTT
1501 TACAACAATG GATTGCCATC AAATCTCTCT GCTAGTAGAA ATCCGAGCTT
1551 GGATTATGGG TTCAAGGGAT CCGAAATTGC CATGGCTTCT TATTGTTCCG
1601 AGTTGCAATA TCTTGCAAAT CCGGTTACAA CTCATGTCCA AAGTGCGGAA
1651 CAACACAACC AAGATGTCAA CTCTTTGGGT TTGATTTCTT CTAGAAAAAC
1701 TTATGAAGCA ATTGAGATCC TTCAATTGAT GTCTTCCACA TTCTTGATTG
1751 CACTTTGTCA AGCAATTGAT TTAAGACATT TGGAGGAGAA TTTGAAAAAC
1801 TCGGTCAAAA ATACCGTAAG CCAAGTGGCC AAAAAGACAC TAACCATAGG
1851 TGTCAATGGA GAACTTCATC CTTCAAGATT TTGTGAAAAA GACTTATTGA
1901 AAGTGGTTGA TAGGGAACAT GTCTTTGCCT ACATTGATGA TCCTTGTAGT
1951 GCTACATACC CATTGATGCA AAAACTCAGG CAAGTACTAG TGGATCATGC
2001 ATTAGTTAAT GGAGAAAGTG AGAAGAATTT GAACACATCA ATCTTCCAAA
2051 AGATTGCAAC TTTTGAGGAA GAGTTGAAAA ACCTTTGCCA AAAGAGGTTG
2101 AAAGTGCAAG GATTGCATAT GAAAGTGGAA ATTCAACAAT TCCAAACAAG
2151 ATCAATGGAT GCAGATCTTA TCCACTCTAC AATTTTGTGA GAAAGGAGTT
2201 GGGAACTGGT TTGCTAACTG GAGAAAATGT CATTTCACCG GGTGAAGAGT
2251 GTGACAAACT ATTCACAGCT ATGTGTCAAG GAAAAATCAT TGATCCTCTT
2301 CTTGAATGCT TGGGAGAGTG GAACGGTGCT CCTCTTCCAA TTTGTTAACT
2351 TTGATTGTTA GTTCATAAAA TGTTTTATTT GTATTTATCA TTTGTATTTA
2401 TGCGAGTGTA GTAATAATGA TTAGGTGTTT TGTGCCTTTA ATGAAAAAAA
2451 AAAAAAAAAA AAAAAAAAAA AAAAGTACTC TGCGTTGTTA CCACTGCTTA
2501 ATCACTAGTG AATTC
```

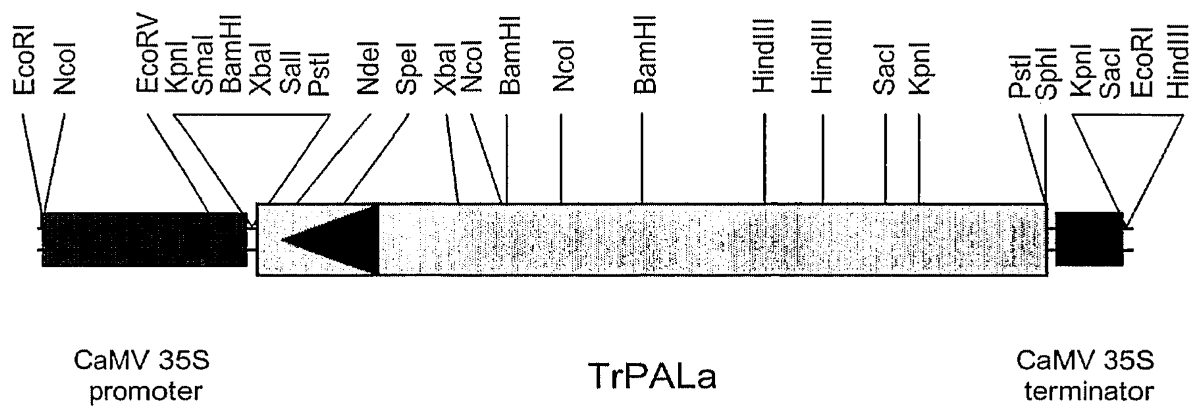
FIGURE 177

```
  1 MEVVAAAITK NNGKIDSFCL NHANANNMKV NGADPLNWGV AAEAMKGSHL
 51 DEVKRMVEEY RKPVVRLGGE TLTISQVAAI AAHDGATVEL SESARAGVKA
101 SSDWVMESMN KGTDSYGVPT GFGATSHRRT KQGGALQKEL IRFLNAGIFG
151 NGTESSHTLP HTATRAAMLV RINTLLQGYS GIRFEILEAI TKLLNNNVTP
201 CLPLRGTITA SGDLVPLSYI AGLLTGRPNS KAHGPSGEVL NAKQAFQSAG
251 IDAEFFELQP KEGLALVNGT AVGSGLASIV LFEANILAVL SEVLSAIFAE
301 VMQGKPEFTD HLTHKLKHHP GQIEAAAIME HILDGSAYVK DAKKLHEMDP
351 LQKPKQDRYA LRTSPQWLGP LIEVIRFSTK SIEREINSVN DNPLIDVSRN
401 KALHGGNFQG TPIGVSMDNT RLALASIGKL MFAQFSELVN DFYNNGLPSN
451 LSASRNPSLD YGFKGSEIAM ASYCSELQYL ANPVTTHVQS AEQHNQDVNS
501 LGLISSRKTY EAIEILQLMS STFLIALCQA IDLRHLEENL KNSVKNTVSQ
551 VAKKTLTIGV NGELHPSRFC EKDLLKVVDR EHVFAYIDDP CSATYPLMQK
601 LRQVLVDHAL VNGESEKNLN TSIFQKIATF EEELKNLCQK RLKVQGLHMK
651 VEIQQFQTRS MDADLIHSTI L
```

FIGURE 178

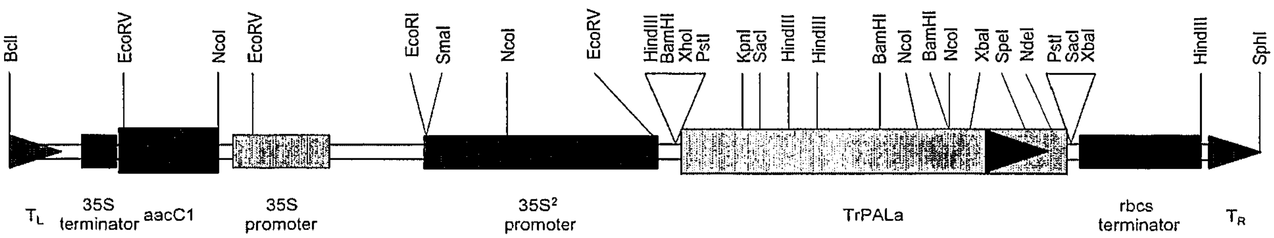


pDH51TrPALa sense



pDH51TrPALa anti

FIGURE 179



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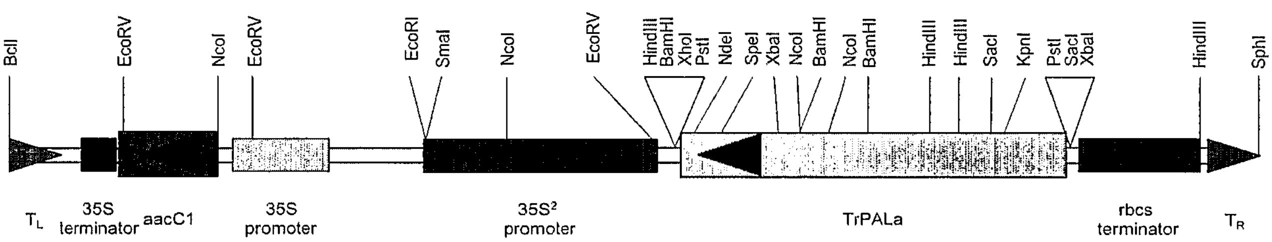
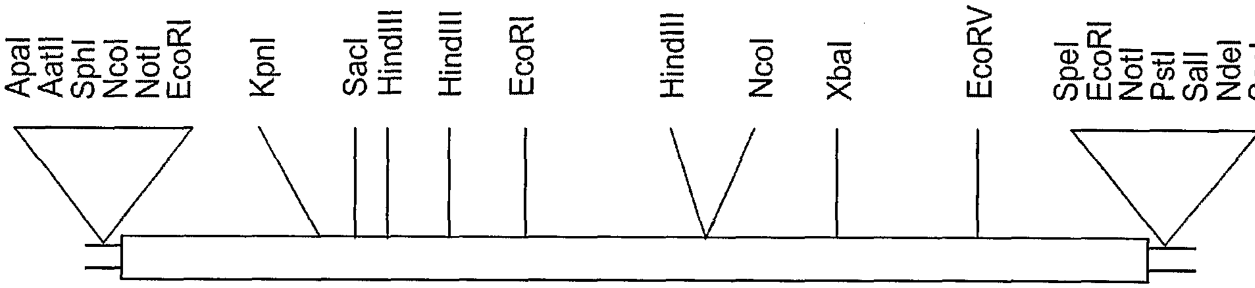


pPZP221:$35S^2$TrPALa anti

FIGURE 180



TrPALb

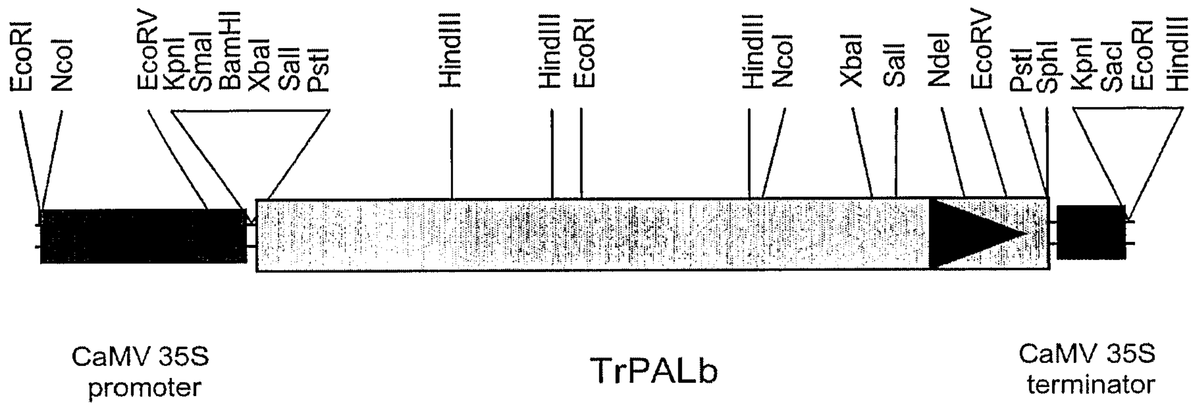
FIGURE 181

1 **GAATTC**GATT AAGCAGTGGT AACAACGCAG AGTACGCGGG AGGAAATAAA
51 TTCATCATTG TTCCTTATTT CCCACCCAAC ACAACATAAC AAATACATTT
101 CCTCTCCTCT CATCACAATT ATTACTTTCT ACACCCCCCC CTCTCAACTA
151 TTATTAACTA ACATAATGGA GGGAATTACC AATGGCCATG CTGAAGCAAC
201 TTTTTGCGTG ACCAAAAGTG TTGGTGATCC ACTCAACTGG GGTGCAGCCG
251 CGGAGTCGTT GATGGGGAGT CATTTGGATG AGGTGAAGCG TATGGTGGAG
301 GAATACCGTA ATCCATTGGT TAAAATTGGC GGCGAGACGC TTACCATTGC
351 TCAGGTGGCT GGAATTGCTT CTCATGATAG TGGTGTGAGG GTGGAGCTGT
401 CTGAGTCCGC CAGGGCCGGC GTTAAGGCGA GTAGTGGTTG GGTGATGGAC
451 AGCATGAACA ATGGGACTGA TAGTTATGGT GTTACCACTG GTTTCGGCGC
501 CACCTCTCAC CGGAGAACCA AGCAGGGTGG TGCCTTGCAG AAGGAGCTAA
551 TTAGGTTTTT GAATGCCGGA ATATTTGGCA ATGGTACAGA ATCTAACTGT
601 ACACTACCAC ACACAGCAAC CAGAGCTGCA ATGCTTGTGA GAATCAACAC
651 TCTTCTTCAA GGATATTCTG GAATTAGATT TGAAATTTTG GAAGCTATCA
701 CAAAGCTTCT AAACAACAAC ATTACCCCAT GTTTACCACT TCGTGGTACA
751 ATCACGGCTT CCGGTGATCT CGTTCCGCTT TCCTACATTG CCGGTTTGTT
801 AACCGGTAGA CCGAACTCCA AAGCCGTTGG ACCCTCCGGA GAAATTCTCA
851 ATGCAAAAGA AGCTTTTCAA CTTGCCGGCA TTGGTTCTGA GTTTTTTGAA
901 TTGCAGCCAA AAGAAGGTCT TGCTCTTGTT AATGGTACTG CTGTTGGTTC
951 TGGTTTAGCT TCTATTGTTC TGTTTGAAGC AAATGTACTA GCTGTTTTGT
1001 CTGAAGTTAT GTCGGCGATT TTCGCTGAAG TTATGCAAGG GAAACCAGAA
1051 TTCACTGATC ATTTGACTCA TAAGTTGAAA CATCACCCTG GTCAAATTGA
1101 AGCTGCTGCA ATTATGGAAC ATATTTTGGA TGGAAGTGCT TATGTTAAAG
1151 CAGCTAAGAA ATTACACGAA ACCGATCCTT TACAAAAGCC GAAACAAGAT
1201 CGTTATGCAC TTAGAACTTC ACCTCAATGG CTTGGTCCTT TGATTGAAGT
1251 GATAAGATTT TCAACTAAGT CAATTGAGAG AGAAATTAAC TCTGTCAATG
1301 ATAACCCTTT GATTGATGTT TCAAGGAACA AGGCCATTCA CGGTGGTAAT
1351 TTTCAAGGAA CACCTATTGG AGTTTCAATG GATAACACAC GTTTAGCTCT
1401 TGCTTCAATT GGTAAACTCA TGTTTGCTCA ATTCTCTGAA CTTGTTAATG
1451 ATTTTTACAA CAACGGGTTA CCTTCGAATC TTACTGCTAG TAGGAACCCA
1501 AGCTTGGATT ACGGTTTCAA GGGATCGGAA ATTGCCATGG CTTCTTATTG
1551 TTCTGAGTTA CAATATCTTG CTAATCCTGT CACCACCCAT GTCCAAAGTG
1601 CGGAGCAACA CAATCAAGAT GTTAACTCTT TGGGTTTGAT TTCTTCAAGA
1651 AAAACAAATG AAGCTATTGA GATCCTAAAG CTCATGTCTT CGACATTTCT
1701 GATTGCACTT TGTCAAGCAA TTGATTTAAG GCATTTGGAG GAAAATCTGA
1751 GGAACACTGT CAAGAACACG GTAAGCCAAG TAGCGAAGAG AACACTCACC
1801 ACCGGTGTTA ATGGAGAACT TCATCCTTCT AGATTTTGTG AGAAAGATTT
1851 GCTCAAAGTT GTTGATAGGG AGTATGTATT TGCCTATGTC GACGATCCTT
1901 GTCTAGCTAC ATACCCTTTG ATGCAAAAGT TGAGACAAGT GCTTGTGGAT
1951 CATGCATTGG TAAATGCTGA TGGAGAGAAG AATTTGAACA CATCAATCTT
2001 TCAAAAGATT GCAACTTTTG AGGATGAATT GAAAGCTATC TTGCCAAAGG
2051 AAGTTGAAAG TACAAGAACT GCATATGAAA ATGGACAATG TGGAATTTCA
2101 AACAAGATTA AGGAATGCAG GTCTTATCCA TTGTACAAGT TTGTTAGAGA
2151 GGAGTTAGGA ACCGCGTTGC TAACCGGAGA AAAAACGATA TCGCTGGGCG
2201 AAGAGTGTGA CAAATTGTTC ACAGCTATGT GCCAAGGTAA AATTGTTGAT
2251 CCTCTTTTGG AATGCCTTGG AGAGTGGAAT GGTGCTCCTC TACCAATATG
2301 TTAATTAGCA GAATTAATAT GTTTCTTTGA GAAGTGATTT CTTTATATAT
2351 TTGTAGTATA CTATAGTAGT TGCATTGAGA AGCAATTGGT TTGTCTATAA
2401 GCCTATGGAA AATGGCAAAA CAATTTTCTG CTCAAAGCAT CGTTTATTAA
2451 GTTTTCCTTA AAGTGTTAAG GAACTTTTAA TTGTTTTTGT AATAGAATTT
2501 CATTTGTTTG CCACAACTTT GGGTGCAAAT ATCACGTGAT ACATGTGGTG
2551 TTTGATGTAA ATGGTGTTTT CTCAATTAAT AAATAGTGTT TCAGCCATGA
2601 AAAAAAAAAA AAAAAAAAAA AAAAAAGTAC TCTGCGTTGT TACCACTGCT
2651 TAATCACTAG T**GAATTC**

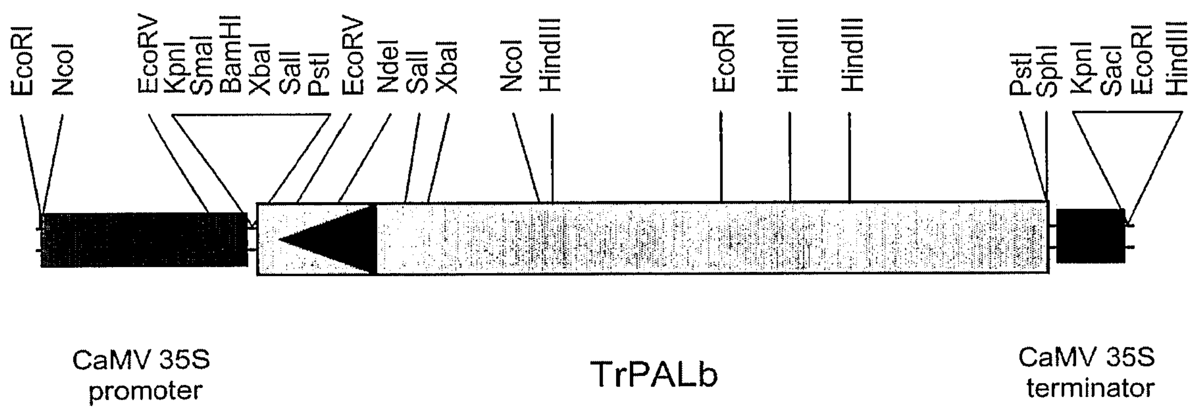
FIGURE 182

```
  1 MEGITNGHAE ATFCVTKSVG DPLNWGAAAE SLMGSHLDEV KRMVEEYRNP
 51 LVKIGGETLT IAQVAGIASH DSGVRVELSE SARAGVKASS GWVMDSMNNG
101 TDSYGVTTGF GATSHRRTKQ GGALQKELIR FLNAGIFGNG TESNCTLPHT
151 ATRAAMLVRI NTLLQGYSGI RFEILEAITK LLNNNITPCL PLRGTITASG
201 DLVPLSYIAG LLTGRPNSKA VGPSGEILNA KEAFQLAGIG SEFFELQPKE
251 GLALVNGTAV GSGLASIVLF EANVLAVLSE VMSAIFAEVM QGKPEFTDHL
301 THKLKHHPGQ IEAAAIMEHI LDGSAYVKAA KKLHETDPLQ KPKQDRYALR
351 TSPQWLGPLI EVIRFSTKSI EREINSVNDN PLIDVSRNKA IHGGNFQGTP
401 IGVSMDNTRL ALASIGKLMF AQFSELVNDF YNNGLPSNLT ASRNPSLDYG
451 FKGSEIAMAS YCSELQYLAN PVTTHVQSAE QHNQDVNSLG LISSRKTNEA
501 IEILKLMSST FLIALCQAID LRHLEENLRN TVKNTVSQVA KRTLTTGVNG
551 ELHPSRFCEK DLLKVVDREY VFAYVDDPCL ATYPLMQKLR QVLVDHALVN
601 ADGEKNLNTS IFQKIATFED ELKAILPKEV ESTRTAYENG QCGISNKIKE
651 CRSYPLYKFV REELGTALLT GEKTISLGEE CDKLFTAMCQ GKIVDPLLEC
701 LGEWNGAPLP IC
```

FIGURE 183

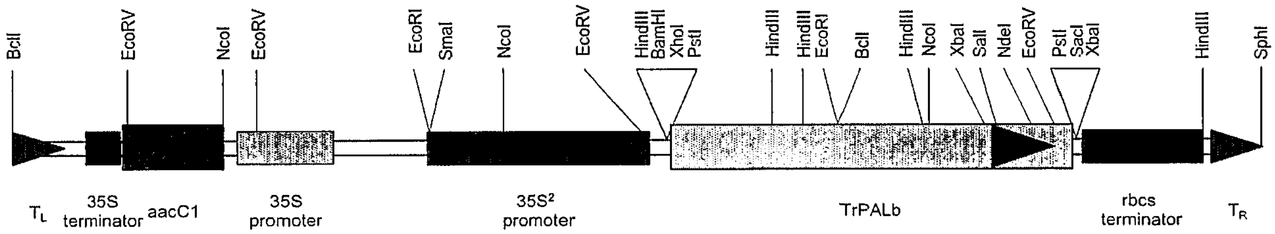


pDH51TrPALb sense



pDH51TrPALb anti

FIGURE 184



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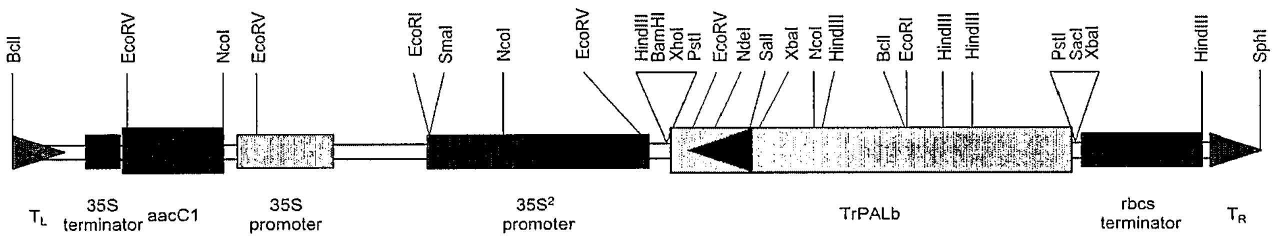
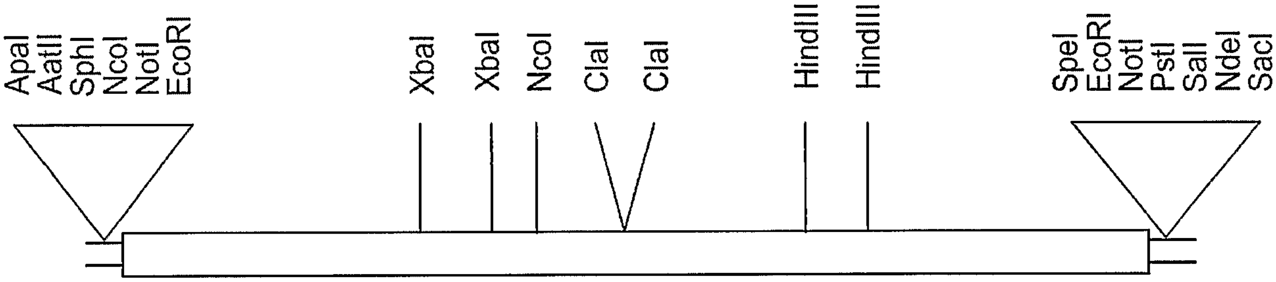


pPZP221:35S^{2}TrPALb anti

FIGURE 185



TrPALf

FIGURE 186

```
   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAGG
  51 AAATAAATTC ATCATTGTTC ATTATTTCCC ACCCAACACA ACATAACAAA
 101 TACATTATTC TCTCCTCTGA TCACAATTAT TACTTTCTAC ACCCTCCTCT
 151 CAACTATTAT TAACTAGCAT AATGGAGGGA ATTACCAATG GCCATGCTGA
 201 AACAACTTTT TGCGTGACCA AAAGTGTTGG TGATCCACTC AACTGGGGTG
 251 CAGCCGCGGA GTCGTTGACG GGGAGTCATT TGGATGAGGT GAAGCGTATG
 301 GTGGAGGAGT ACCGTAATCC GTTGGCTAAA ATTGGCGGCG AGACGCTTAC
 351 CATTGCTCAG GTGGCTGGAA TTGCTTCTCA TGATAGTGGT GTGAGGGTGG
 401 AGCTGTCCGA GTCCGCAAGG GCCGGCGTTA AGGCGAGTAG TGATTGGGTG
 451 ATGGATAGCA TGAACAATGG GACTGATAGT TACGGTGTTA CCACCGGTTT
 501 TGGTGCCACC TCTCACCGGA GAACCAAGCA GGGTGGTGCT TTGCAGAAGG
 551 AGCTAATTAG GTTTTTGAAT GCTGGAATAT TTGGCAATGG TACAGAATCT
 601 AACTGTACAC TACCACACAC AGCAACTAGA GCTGCAATGC TTGTGAGAAT
 651 CAACACTCTT CTTCAAGGGT ACTCTGGTAT TAGATTTGAA ATTTTGGAAG
 701 CTATCACAAA GCTTCCAAAC AACAACATTA CCCCATGTTT ACCACTTCGT
 751 GGTACAATCA CGGCTTCCGG TGATCTTGTT CCGCTTTCCT ACATTGCCGG
 801 TTTGTTAACC GGAAGACCCA ACTCCAAAGC AGTTGGACCT TCCGGAGAAA
 851 TTTTGAGTGC TAAAGAAGCT TTTCAACTCG CCGGCATTGG TTCTGAGTTT
 901 TTTGAATTGC AACCAAAAGA AGGTCTTGCT CTTGTTAATG GTACTGCTGT
 951 TGGCTCTGGT TTAGCTTCTA TTGTTCTGTT TGAAGCAAAT GTACTAGCTG
1001 TTTTATCCGA AGTTATGTCG GCGATTTTCG CTGAAGTTAT GCAAGGGAAA
1051 CCGGAATTTA CCGATCATTT GACTCATAAG TTGAAACATC ACCCTGGTCA
1101 AATTGAAGCT GCTGCAATTA TGGAACATAT TTTGGATGGA AGTGCTTATG
1151 TTAAAGCAGC TAAGAAGTTA CACGAAACCG ATCCTTTACA AAAACCGAAA
1201 CAAGATCGTT ATGCACTTAG AACTTCACCT CAATGGCTTG GTCCTTTGAT
1251 TGAAGTGATA AGATTTTCAA CCAAATCGAT TGAAAGAGAA ATTAACTCGG
1301 TCAACGACAA CCCTTTGATC GATGTTTCAA GGAACAAGGC CATTCATGGT
1351 GGTAACTTTC AAGGAACACC TATTGGAGTT TCAATGGATA ACACACGTTT
1401 AGCTCTTGCT TCAATTGGTA AACTCATGTT TGCTCAATTC TCTGAACTTG
1451 TTAATGATTT TTACAACAAC GGGTTGCCTT CGTATCTTAC TGCTAGTAGG
1501 AACCCGAGCT TGGACTATGG TTTCAAGGGA TCGGAAATTG CCATGGCTTC
1551 GTATTGTTCC GAGTTACAAT ATCTTGCTAA TCCTGTCACC ACCCATGTCC
1601 AAAGTGCCGA GCAACACAAC CAAGATGTTA ACTCTTTGGG TTTGATTTCT
1651 TCTAGAAAAA CAAATGAAGC TATTGAGATT CTCAAGCTCA TGTCTTCCAC
1701 TTTCTTGATT GCATTATGTC AAGCAATCGA CTTAAGGCAC TTGGAGGAAA
1751 ATCTCAGGAA CACCGTCAAG AACACGGTAA GCCAAGTAGC GAAGAGAACA
1801 CTCACCACCG GCGTCAACGG AGAACTTCAT TCTTCTAGAT TTTGTGAGAA
1851 AGATTTGCTT AAAGTTGTTG ATAGGGAGTA TGTATTTGCC TATGCCGACG
1901 ATCCTTGTCT AGCTACATAC CCTTTGATGC AAAAGTTGAG ACAAGTGCTT
1951 GTGGATCATG CATTGGTAAA TGTTGATGGA GAGAAGAATT TGAACACATC
2001 AATCTTTCAA AAGATTGCAA CTTTTGAGGA TGAGTTGAAA GCTATTTTGC
2051 CAAAGGAGGT TGAAAGTACA AGAACTGCAT ATGAAAATGG ACAATGTGGA
2101 ATTTCAAACA AGATTAAGGA ATGCAGGTCT TATCCATTGT ACAAGTTTGT
2151 TAGAGAGGAG TTAGGAACCG CGTTGCTAAC CGGAGAAAAA ACTATATCGC
2201 CGGGCGAAGA GTGCGATAAA TTGTTCACAG CTATGTGCCA AGGTAAAATT
2251 GTTGATCCTC TTATGGAATG CCTCGGAGAG TGGAATGGTG CTCCTCTACC
2301 AATATGTTAA TTAGCATAAT ATGTTTTCTT TGAGAAGTGA TTACTTTATA
2351 TATTTGTAGT ATACTATAGT AGTTGCATTG AGAAGAAATT GGTTTGTTTA
2401 TAAGCCTATG GAAAATGGCA AATCAATTTT CTGCTCAAAG CATCGTTTAT
2451 TAAGTTTTCC TTAAAGTGTT AAGGAACTTT TAATTGTTTT TGTAATAGAA
2501 TTTCATTTGT TTGCCACAAC TTTGGGTGCA AATATCACAT GATACATGTG
2551 GTGTTTGATG TAAATGGTGT TTTTTCAATA AATAAATAGT GTTTCAACTA
2601 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAG TACTCTGCGT TGTTACCACT
2651 GCTTAATCGA ATTC
```

FIGURE 187

```
  1 MEGITNGHAE TTFCVTKSVG DPLNWGAAAE SLTGSHLDEV KRMVEEYRNP
 51 LAKIGGETLT IAQVAGIASH DSGVRVELSE SARAGVKASS DWVMDSMNNG
101 TDSYGVTTGF GATSHRRTKQ GGALQKELIR FLNAGIFGNG TESNCTLPHT
151 ATRAAMLVRI NTLLQGYSGI RFEILEAITK LPNNNITPCL PLRGTITASG
201 DLVPLSYIAG LLTGRPNSKA VGPSGEILSA KEAFQLAGIG SEFFELQPKE
251 GLALVNGTAV GSGLASIVLF EANVLAVLSE VMSAIFAEVM QGKPEFTDHL
301 THKLKHHPGQ IEAAAIMEHI LDGSAYVKAA KKLHETDPLQ KPKQDRYALR
351 TSPQWLGPLI EVIRFSTKSI EREINSVNDN PLIDVSRNKA IHGGNFQGTP
401 IGVSMDNTRL ALASIGKLMF AQFSELVNDF YNNGLPSYLT ASRNPSLDYG
451 FKGSEIAMAS YCSELQYLAN PVTTHVQSAE QHNQDVNSLG LISSRKTNEA
501 IEILKLMSST FLIALCQAID LRHLEENLRN TVKNTVSQVA KRTLTTGVNG
551 ELHSSRFCEK DLLKVVDREY VFAYADDPCL ATYPLMQKLR QVLVDHALVN
601 VDGEKNLNTS IFQKIATFED ELKAILPKEV ESTRTAYENG QCGISNKIKE
651 CRSYPLYKFV REELGTALLT GEKTISPGEE CDKLFTAMCQ GKIVDPLMEC
701 LGEWNGAPLP IC
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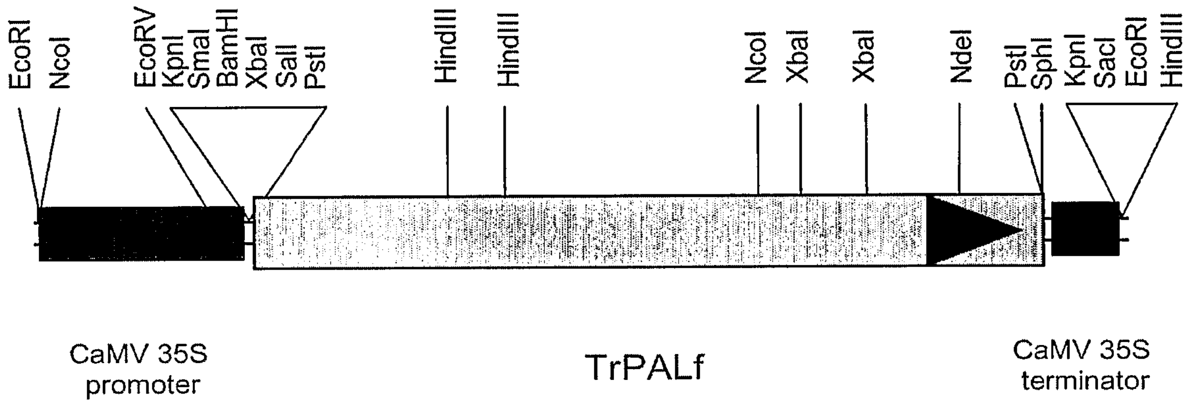
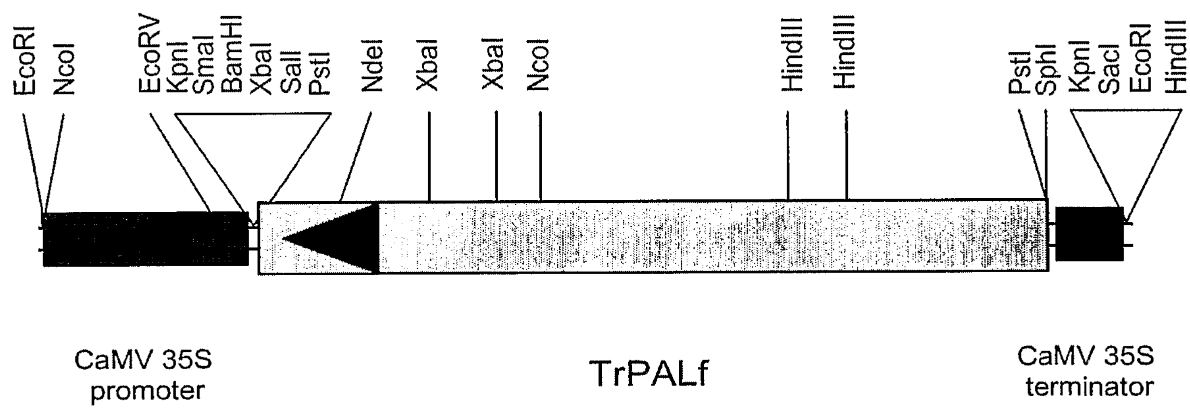
FIGURE 188

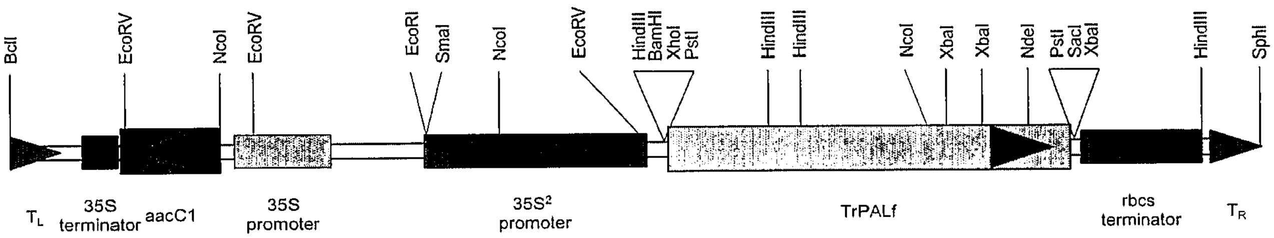


pDH51TrPALf sense

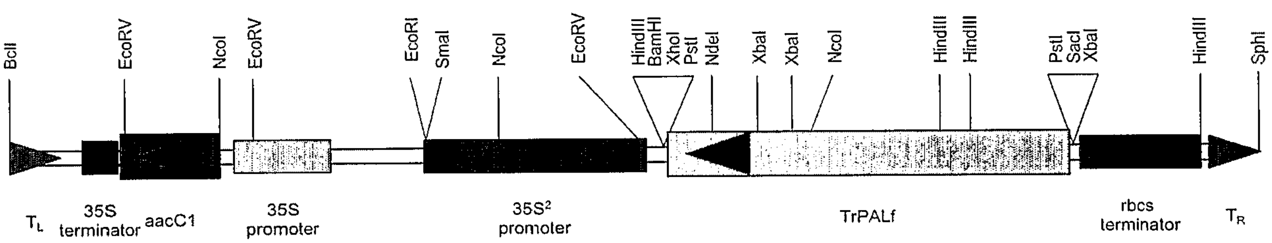


pDH51TrPALf anti

FIGURE 189

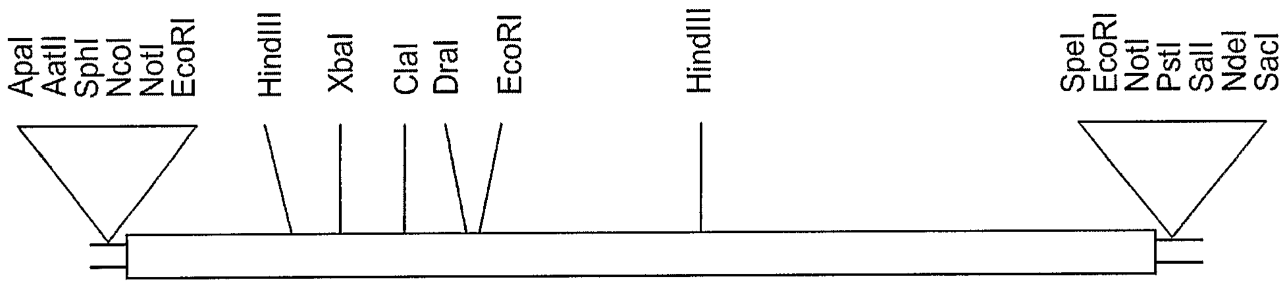


pPZP221:35S^{2}TrPALf sense



pPZP221:35S^{2}TrPALf anti

FIGURE 190



TrVRa

FIGURE 191

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG ATAGTAGTAG
  51 TTGAGAAAAA ATACACAAAT AAAGTAAACA CTATCATAGA AAGAGAGTCA
 101 AAAATGGCTG AAGGAAAAGG AAGGGTTTGT GTTACTGGAG GAACAGGTTT
 151 TCTTGGTTCA TGGATCATCA AGAGTCTTCT TGAAAATGGA TACTCTGTTA
 201 ATACCACTAT TAGAGCTGAT CCAGAACGTA AGAGGGATGT AAGCTTCCTA
 251 ACAAATCTAC CCGGCGCATC CGAAAGGCTA CATTTCTTCA ACGCCGATCT
 301 AGACGACCCA GAGAGTTTCA ACGAAGCAAT TGAAGGTTGT GTCGGGATAT
 351 TCCACACCGC TTCACCAATC GATTTCGCCG TGAGTGAGCC AGAAGAAATA
 401 GTGACAAAAA GAACAGTGGA TGGAGCATTA GGAATTTTAA AAGCATGTGT
 451 GAATTCAAAG ACAGTGAAGA GATTTATTTA CACTTCAAGT GGTTCTGCTG
 501 TTTCATTCAA TGGAAAAAAC AAAGATGTTT TGGATGAGAG TGATTGGAGT
 551 GATGTTGATT TGCTTAGAAG TGTTAAACCA TTTGGTTGGA GTTATGGTGT
 601 TTCAAAGACT TTGGCTGAGA AAGCAGTGCT TGAATTTGGT CAACAAAATG
 651 GGATTGATGT TGTTACTTTG ATTCTTCCTT TTATTGTTGG AAGTTTTGTT
 701 TGTCCTAAGC TTCCTGATTC TGTTGAGAAA GCTCTTGTTT TGGTACTAGG
 751 CAAAAAGGAA CAAATTGGTA TTATAAGTTT CCACATGGTA CATGTGGATG
 801 ATGTGGCTAG AGCACATATT TATCTACTTG AGAATCCTGT TCCAGGAGGT
 851 AGATATAATT GTTCACCATT CTTTGTATCT ATTGAAGAAA TGTCACAACT
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1051 GATTCAATGC TGCAAGGAAA AAGGCTATCT CTAAGTATGT GTTTGAAAAA
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1151 AATGAAATGT ACAAGTTTAT GCATAAAGTT ATTTGTGATG AATCAAATAA
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```

FIGURE 192

```
  1 MAEGKGRVCV TGGTGFLGSW IIKSLLENGY SVNTTIRADP ERKRDVSFLT
 51 NLPGASERLH FFNADLDDPE SFNEAIEGCV GIFHTASPID FAVSEPEEIV
101 TKRTVDGALG ILKACVNSKT VKRFIYTSSG SAVSFNGKNK DVLDESDWSD
151 VDLLRSVKPF GWSYGVSKTL AEKAVLEFGQ QNGIDVVTLI LPFIVGSFVC
201 PKLPDSVEKA LVLVLGKKEQ IGIISFHMVH VDDVARAHIY LLENPVPGGR
251 YNCSPFFVSI EEMSQLLSAK YPEYQILSVD ELKEIKGARL PDLNSKKLVD
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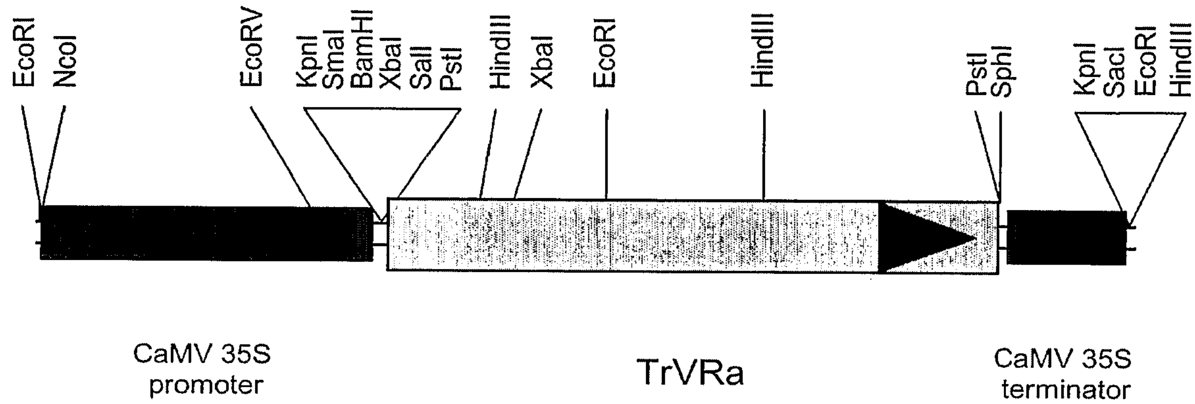
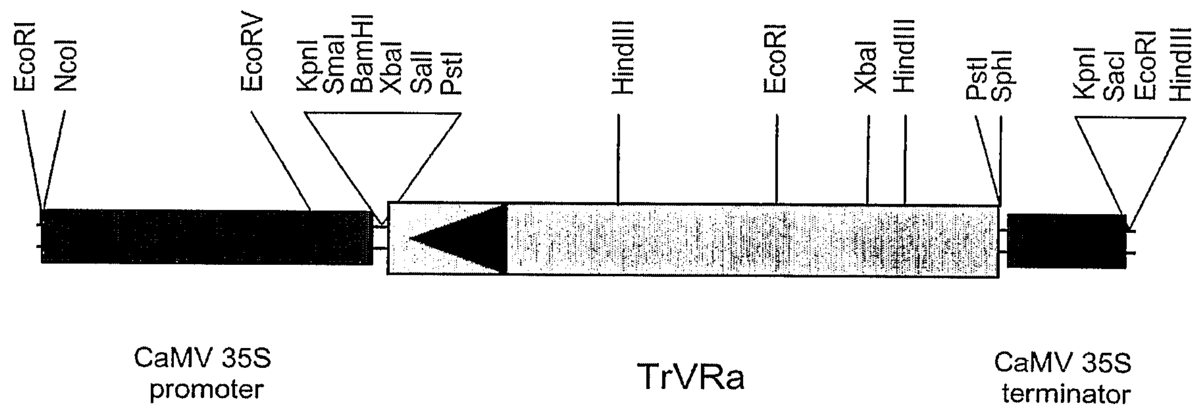
FIGURE 193

267/271

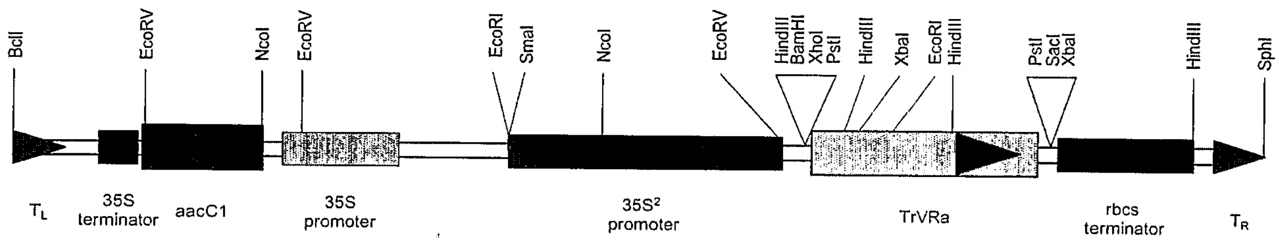


pDH51TrVRa sense

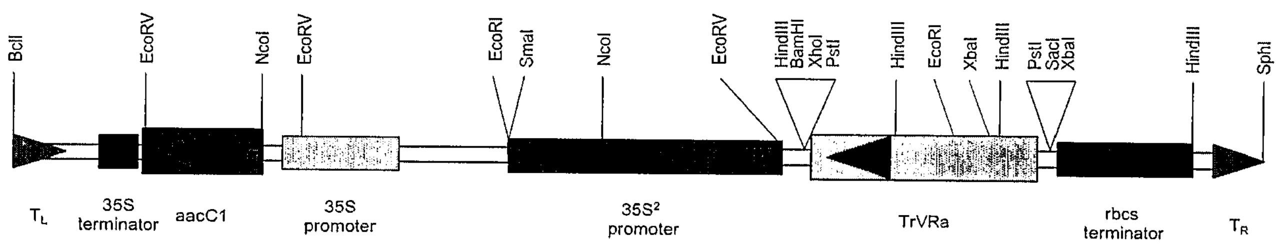


pDH51TrVRa anti

FIGURE 194



pPZP221:35S^{2}TrVRa sense



pPZP221:35S^{2}TrVRa anti

FIGURE 195

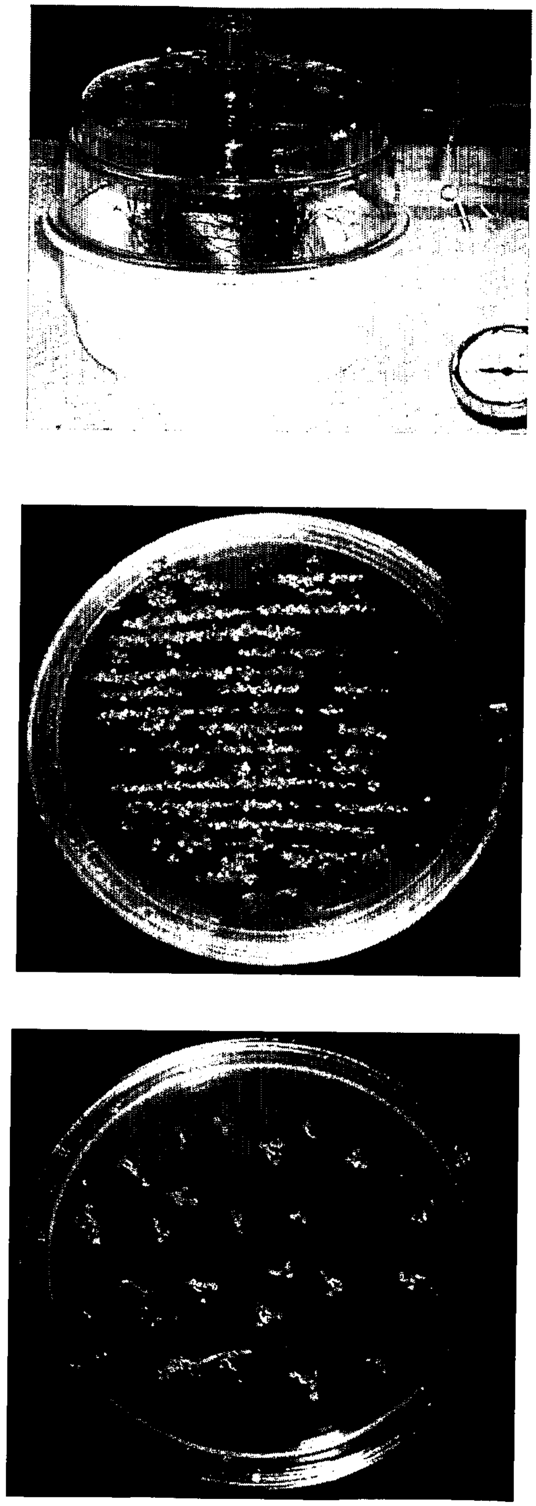
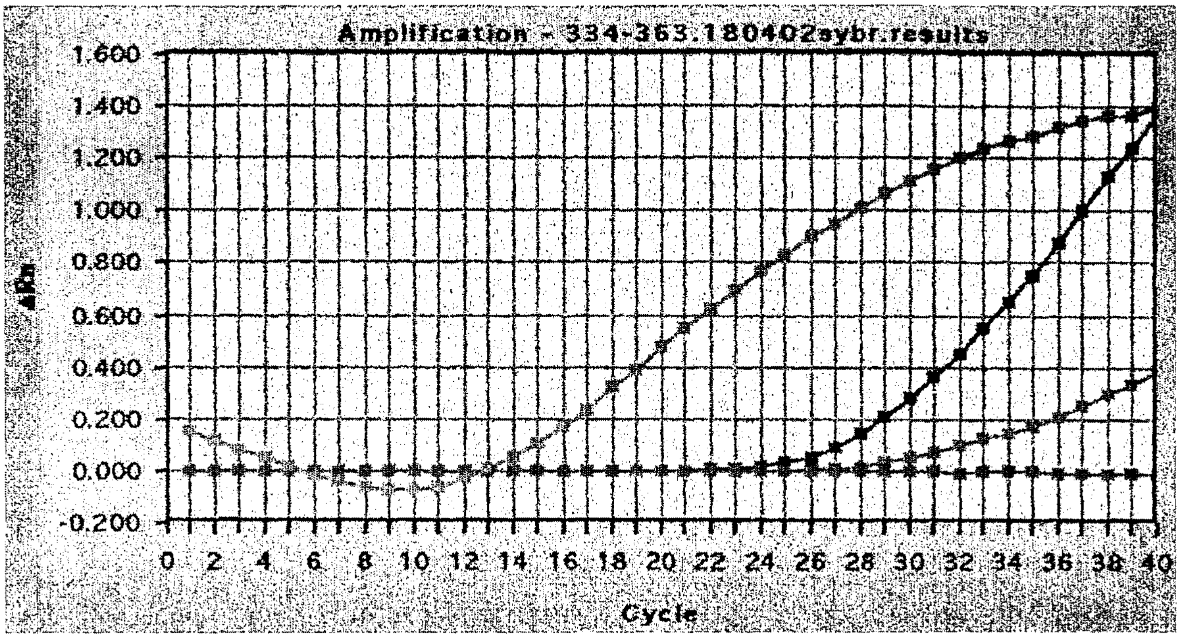


FIGURE 196

D



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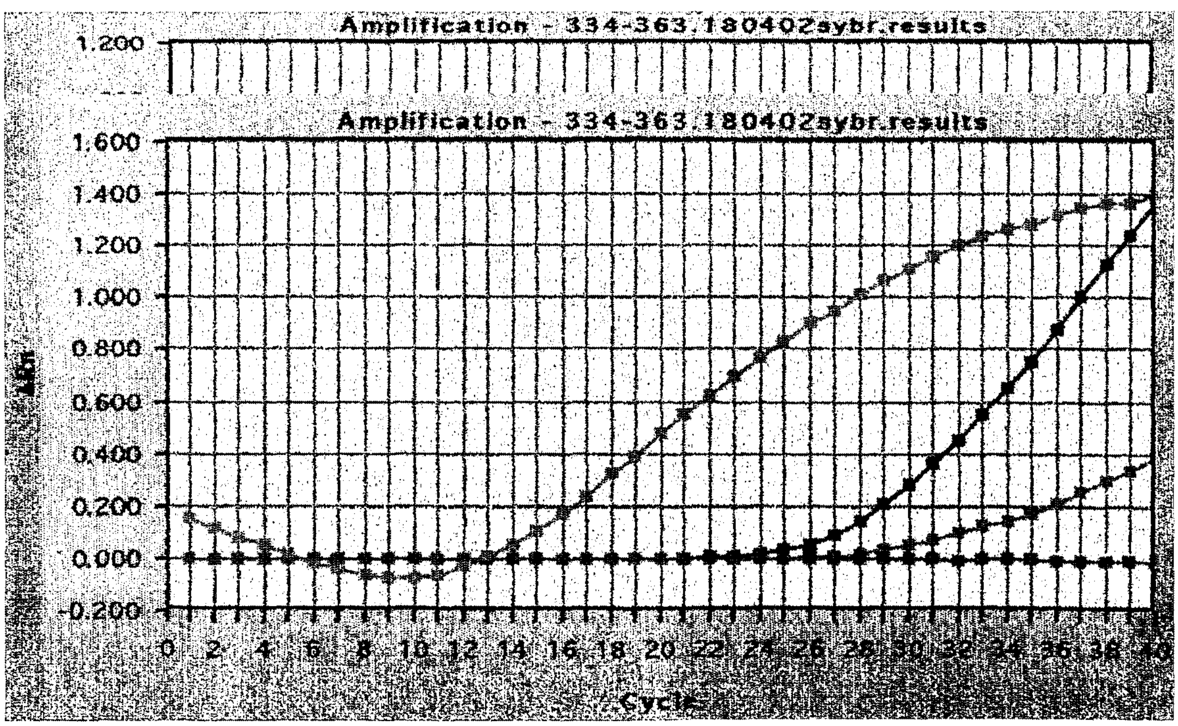

FIGURE 196 (cont)

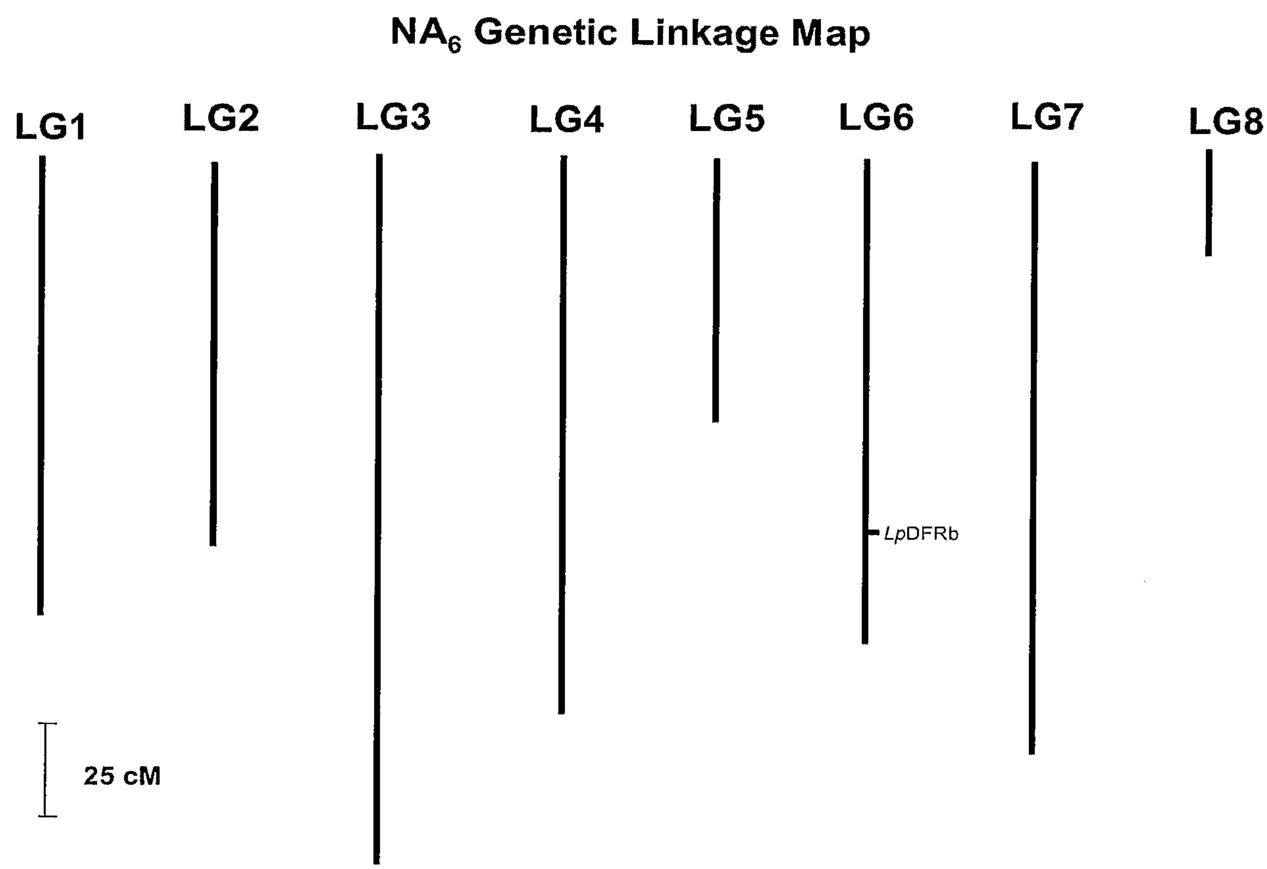
NA6 Genetic Linkage Map
LG1
LG2
LG3
LG4
LG5
LG6
LG7
LG8
LpDFRb
25 cM

FIGURE 197

SEQUENCE LISTING

<110> Agriculture Victoria Services Pty Ltd
AgResearch Limited

<120> Manipulation of flavonoid biosynthesis in plants

<130> M80393510

<150> PR8113
<151> 2001-10-05

<160> 336

<170> PatentIn version 3.1

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35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Val Ala Ser Leu Ala Thr Lys
50 55 60

Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr
65 70 75 80

Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys
85 90 95

Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Asn Glu Asn
100 105 110

Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Val
115 120 125

Glu Ala Met Gln Lys Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro
130 135 140

Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly
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120

ccggctgtgg ttacttctcc ggccaccggt aagtcatatt ttcttggtgg tgcaggggag
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gcagtggctt cacttgccac taaatggaag ggcaaatcct ctgaagagtt gcttcagacc
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cttgacttct acagagatat catttcagga ccatttgaga agttgattcg aggatccaag
360

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ttaaaatctg ttgggactta tggagatgca gaagttgaag ctatgcaaaa atttgttgaa
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gccttcaagc ctattaattt tccacctggt gcctctgttt tttacaggca atcacctgat
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gtcgagaacc ttgaattccc ggcggtgatt acttctccgg tcaacggtaa gtcatatttt
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cttggtggtg caggggagag aggttngact attgaaggaa acttcatcaa gttcactgcc
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35 40 45

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180

ttggtggtgc aggggagaga ggttngacta ttgaaggaaa cttcatcaag ttcactgcca
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tgttgggact tatggagatg cagaagctga agctatgcaa aaatttgttg aagccttcaa
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Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Ala Glu Ala Met Gln Lys
        35                  40                  45

Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro Pro Gly Ala Ser Val
    50                  55                  60

Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly Val Ser Ile Ala Asn
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120

tgttgggact tatggagatg cagaagctga agctatgcaa aaatttgttg aagccttcaa
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gcctattaat tttccacctg gtgcctctgt tttttacagg caatcacctg atggaatatt

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tatggagatg cagaagctga agctatgcaa aaatttgttg aagccttcaa gcctattaat
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Phe Phe Arg Asp Ile Val Thr Gly Pro Phe Glu Lys Phe Met Gln Val
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Gly Ala His Gly Val Ser Pro Ala Ala Lys Gln Ser Phe Gly His Gln
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tcacaccacc gggatccacc aacaatttct tcctcggcgg tgcaggagag cggggtcttc
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aaattcaaga caaatttgtn aaattgaccg ntattggtgt ttatgtacng gacgttggtg
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tcaagacaaa tttgtcaaat tcaccgctat tggtgtttat ctacaggaca ttgctgttcc
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cttcagggac atcgttacag gtccatttga gaaatttatg caggtgacaa tgatcttgcc
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attgactggg caacaatact cagagaaagt gtcagaaaat tgtgtagcta tttggaagtc
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tcttgggatt tataccgacg aagaagccaa agcaattgag aagtttgttt ctgtcttcaa
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gctaaatgga agggtaagac tgctcaagag ctaactcaaa ctgttccttt cttcagggac
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atcgttacag gtccatttga gaaatttatg caggtgacaa tgatcttgcc attgactggg
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gctaaagata nttattaaga tatggtgagt gtagctgaaa ttcgcaaggc tcagagggct
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Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
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Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
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Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
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Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
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145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
210 215 220

Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
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Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
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Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
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180

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120

gcaaggctca aagggctgaa ggccctgcaa ctattttggc cattggcact gcaaatccag
180

caaaccgtgt tgatcagagt acatatcctg atttctactt caaaatcact aacagtgagc
240

ataaagttga gctcaaagag aaattccagc gcatgtgtga taaatctatg atcaagagca
300

gatacatgta tctaacagaa gagattttga aagaaaatcc tagtctttgt gaatacatgg
360

caccttcatt ggatgctagg caagatatgg tggtggttga ggtacctaga cttggaaagg
420

aggctgcagt gaaggctatt aaagaatggg gtcaaccaaa atctaagatt acacatttga
480

tcttttgcac cacaagtggt gtagacatgc ctggtgctga ttaccagccc acaaaacttt
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575

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120

aaattcgcaa ggctcaaagg gcagaaggcc ctgcaacaat cttggccatt ggcactgcaa
180

atccagcaaa ccgtgttgat cagagcacat atcctgattt ctacttcaaa atcactaaca
240

gtgaacataa agttgagctc aaagagaaat tccagcgcat gtgtgataaa tctatgatca
300

agagcagata catgtatcta acagaagaga ttttgaaaga aaatcctagt ctttgtgagc
360

acatggcacc ttcattggat gctaggcaag acatggtggt ggttgaggta cctagacttg
420

ggaaggaggc tgcagtgaaa gctataaaag aatggggtca accaaagtca aagattactc
480

acttaatctt ttgcaccaca agtggtgttg acatgcctgg tgctgattac caactcacaa
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120

aaagggcaga aggccctgca acaatcttgg ccattggcac tgcaaatcca gcaaaccgtg
180

ttgatcagag cacatatcct gatttctact tcaaaatcac taacagtgaa cataaagttg
240

agctcaaaga gaaattccag cgcatgtgtg ataaatctat gatcaagagc agatacatgt
300

atctaacaga agagattttg aaagaaaatc ctagtctttg tgagcacatg gcaccttcat

360

tggatgctag gcaagacatg gtggtggttg aggtacctag acttgggaag gaggctgcag
420

tgaaagctat aaaagaatgg ggtcaaccaa agtcaaagat tactcactta atcttttgca
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ccacaagtgg tgttgacatg cctggtgctg attaccaact cacaaaactc ttaggtcttc
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120

caaagggcag aaggccctgc aaccatttta gccattggta ctgcaaatcc agcaaaccgt
180

gtagaccaga gcacatatcc tgatttctac ttcaaaatca ctaacagtga gcataaggtt
240

gagcttaaag agaaattcca gcgcatgtgt gataaatcta tgatcaagag cagatacatg
300

tatctaacag aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca
360

ttggatgcta ggcaagacat ggtggtggtt gaggtaccta gactaggaaa ggaggctgca
420

gtcaaggcca ttaaagaatg ggtcaacca aagtcaaaga ttactcactt aatcttttgc
480

accacaagtg gtgtagacat gcctggtgct gattaccaac tcacaaaact cttgggactt
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aaagatatta ttaagatatg gtgagtgtag ctgaaattcg caaggctcag agggctgaag
120

gccctgcaac cattttggcc attggcactg caaatccacc aaaccgtgtt gagcagagca
180

catatcctga tttctacttc aaaattacaa acagtgagca caagactgag ctcaaagaga
240

agttccaacg catgtgtgac aaatccatga tcaagagcag atacatgtat ctaacagaag
300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360

aagacatggt ggtggttgag gtacctagac ttgggaagga ggctgcagtc aaggccatta
420

aagaatgggg tcaaccaaag tcaaagatta ctcacttaat cttttgcacc acaagtggtg
480

ttgacatgcc tggtgctgat taccaactca caaaactctt aggtcttcgc ccatatgtga
540

aaaggtatat gatgtaccaa caaggttgtt ttgcaggagg cacggtgctt cgtttggcaa
600

aagatttggc cgagaacaac aaaggtgctc gtgtgctagt tgtttgttct gaagtcaccg
660

cagtcacatt tcgcggcccc agtgatactc acttggacag tcttgntg
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120

ctgaaggccc tgcaaccatt ttggccattg gcactgcaaa tccaccaaac cgtgttgagc
180

agagcacata tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca
240

aagagaagtt ccaacgcatg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa
300

cagaagagat tttgaaagaa aatcctagnc tttgtgaata catgncacct tcattggatg
360

ctagncaaga catggtgncg ccnnannnnc ccaccctccc cncgccn
407

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aaagatatta ttaagatatg gtgagtgtag ctgaaattcg caaggctcag agggctgaag 120

gccctgcaac cattttggcc attggcactg caaatccacc aaaccgtgtt gagcagagca 180

catatcctga tttctacttc aaaattacaa acagtgagca caagactgag ctcaaagaga 240

agttccaacg catgtgtgac aaatccatga tcaagagcag atacatgtat ctaacagaag 300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc 360

aagacatggt ggtggttgag gtacctanac ttgggaagga ggctgcannc aaggccatta 420

aagaatgggg tcaaccaaag tcanagatna ctnacttaat cttttgcacc acaagnggng 480

ccn 483

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120

ctgaaggccc tgcaaccatt ttggccattg gcactgcaaa tccaccaaac cgtgttgagc
180

agagcacata tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca
240

aagagaagtt ccaacgcatg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa
300

cagaagagat tttgaaagaa aatcctagtc tttgtgaata catggcacct tcattggatg
360

ctagacaaga catggtggtg gttgaggtac ctagacttgg gaaggaggct gcagtcaagg
420

ctatcaaaga atggggtcaa ccaaaatcta agattacaca tttgatcttt tgcaccacaa
480

gtggtgtaga catgcctggt gctgattacc aactcacaaa actcttagga cttcgtccat
540

atgtgaagag gtacatgatg taccaacaag ggtgctttgc aggtgg
586

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120

gaaggccctg caactatttt ggccattggc actgcaaatc cagcaaaccg tgttgatcag
180

agcacatatc ctgattttta cttcaaaatc actaacagtg agcataaggt tgagcttaaa
240

gagaaatttc agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca
300

gaagagattt tgaaagaaaa tcctagtctt tgtgaataca tggcaccttc attggatgct
360

aggcaagaca tggtggtggt tgaggtacct agacttggga aggaggctgc agtgaaagct
420

atcaaagaat ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt
480

ggtgtagaca tgcctggagc tgattaccaa ctcacaaaac tcttaggtct tcgcccatat

540

gtgaagaggt acatgatgta ccaacaaggg tgct
574

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120

gcaaccattt tggccattgg tactgcaaat ccaccaaacc gtgttgagcg gagcacatat
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cctgatttct acttcaaaat tacaaacagt gagcacaaga ctgagctcaa agagaagttc
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caacgcatgt gtgacaaatc catgatcaag agcagataca tgtatctaac agaagagatt
300

ttgaaagaaa atcctagtct ttgtgaatac atggcacctt cattggatgc taggcaagac
360

atggtggtgg ttgaggtacc tagacttggg aaggaggctg cagtgaaagc tatcaaagaa
420

tggggtcaac caaagtcaaa gattactcac ttaatctttt gcaccacaag tggtgtagac
480

atgcctggag ctgattacca actcacaaaa ctcttaggtc ttcgcccata tgtgaaaagg
540

tatatgatgt accaacaagg ttgttttgca ggaggcacgg tgcttcgttt ggcaaaagat
600

ttgg
604

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120

caactatttt ggccattggt actgcaaatc cagcaaatcg tgttgaccag agtacatatc
180

ctgatttcta cttcaaaatc actaacagtg agcataaggt tgagcttaaa gagaaatttc
240

agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca gaagagattt
300

tgaaagaaaa tcctagtctt tgtgaataca tggcaccttc attggatgct aggcaagaca
360

tggtggtggt tgaggtacct agacttggga aggaggctgc agtgaaagct atcaaagaat
420

ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt ggtgttgaca
480

tgcctggtgc cgattaccaa ctcacaaaac tcttaggtct tcgcccatat gtgaagaggt
540

acatgatgta ccaacaaggg tgctttgcag
570

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120

aaggccctgc aactattttg gccattggta ctgcaaatcc agcaaatcgt gttgaccaga
180

gtacatatcc tgatttctac ttcaaaatca ctaacagtga gcataaggtt gagcttaaag
240

agaaatttca gcgcatgtgt gataaatcta tgatcaagag cagatacatg tatctaacag
300

aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta
360

ggcaagacat ggtggtggtt gaggtaccta gacttgggaa ggaggctgca gtgaaagcta
420

tcaaagaatg ggtcaacca aagtcaaaga ttactcactt aatcttttgc accacaagtg
480

gtgtagacat gcctggagct gattaccaac tcacaaaact cttaggtctt cgcccatatg
540

tgaagaggta catgatgtac caacaagggt gctttgcagg tgggacggtt cttcgttt
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120

ggccctgcaa ccattttggc cattggcact gcaaatccac caaaccgtgt tgagcagagc
180

acatatcctg atttctactt caaaattaca aacagtgagc acaagactga gctcaaagag
240

aagttccaac gcatgtgtga caaatccatg atcaagagca gatacatgta tctaacagaa
300

gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
360

caagacatgg tggtggttga ggtacctaga cttgggaagg aggctgcagt caaggccatt
420

aaagaatggg gtcaaccaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggt
480

gttgacatgc ctggtgctga ttaccaactc acaaaactct taggtcttcg cccatatgtg
540

aaaaggtata tgatgtacca acaaggttgt tttgcaggag gcacggtgct tcgtttggca
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aaagatttg
609

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ctaaatacaa catggttagt gtttctgaaa ttcgcanggc tcaaagggct gaaggccctg 120

caactatttt ggccattggt actgcaaatc cagcaaatcg tgttgaccag agtacatatc 180

ctgatttcta cttcaaaatc actaacagtg agcataaggt tgagcttaaa gagaaatttc 240

agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca gaagagattt 300

tgaaagaaaa tcctagtctt tgtgaataca tggnaccttc attgnatgnt agncaagaca 360

tgntgntgnc ngaggnaccn agacttgccn 390

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taaagatant tattaagata tggtgagtgt agctgaaatt cgcaaggctc agagggctga
120

aggccctgca accattttgg ccattggcac tgcaaatcca ccaaaccgtg ttgagcagag
180

cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agctcaaaga
240

gaagttccaa cgcatgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
300

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
360

acaagacatg gtggtggttg aggtacctag acttgggaag gaggctgcag tcaaggctat
420

caaagaatgg ggtcaaccaa aatctaagat tacacatttg atcttttgca ccacaagtgg

480

tgtanacatg cctggtgctg attaccnact ngcaaaactn ttaggacttn gcccatatgt
540

gangaggcgc gtgntgnncc n
561

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120

ggccctgcaa ctattttggc cattggtact gcaaatccag caaatcgtgt tgaccagagt
180

acatatcctg atttctactt caaaatcact aacagtgagc ataaggttga gcttaaagag
240

aaatttcagc gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa
300

gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
360

caagacatgg tggtggttga ggtacctaga cttgggaagg aggctgcagt gaaagctatc
420

aaagaatggg gtcaaccaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggt
480

gttgacatgc ctggtgctga ttaccaactc acaaaactct taggtcttcg cccatatgtg
540

aag
543

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aacaaagata tcaacatatg gttagtgttt ctgaaattcg taaggctcaa agggcagaag
120

gccctgcaac tattttggcc attggtactg caaatccagc aaaccgtgtt gatcagagta
180

catatcctga tttctacttc aaaatcacta acagtgagca taaagttgag ctcaaagaga
240

aattccagcg catgtgtgat aaatctatga tcaagagcag atacatgtat ctaacagaag
300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360

aagatatggt ggncgttgag gtacctanac ttgnaaagga ggctgcnntg aaggctatta
420

aagaatgggg ccanccn
437

<210> 43
<211> 607
<212> DNA
<213> Trifolium repens

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120

ccctgcaacc attttggcca ttggcactgc aaatccacca aaccgtgttg agcagagcac
180

atatcctgat ttctacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa
240

gttccaacgc atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga
300

gattttgaaa gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca
360

agacatggtg gtggttgagg tacctagact tgggaaggag gctgcagtga aagctatcaa
420

agaatggggt caaccaaagt caaagattac tcacttaatc ttttgcacca caagtggtgt
480

agacatgcct ggagctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa
540

aaggtatatg atgtaccaac aaggttgttt tgcaggaggc acggtgcttc gtttggcaaa
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agatttg
607

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atanttatta agatatggtg agtgtagctg aaattcgcaa ggctcagagg gctgaaggcc
120

ctgcaaccat tttggccatt ggcactgcaa atccaccaaa ccgtgttgag cagagcacat
180

atcctgattt ctacttcaaa attacaaaca gtgagcacaa gactgagctc aaagagaagt
240

tccaacgcat gtgtgacaaa tccatgatca agagcagata catgtatcta acagaagaga
300

ttttgaaaga aaatcctagt ctttgtgaat acatggcacc ttcattggat gctaggcaag
360

acatggtggt ggttgaggta cctagacttg ggaaggaggc tgcagtcaag gccattaaag
420

aatggggtca accaaagtca aagattactc acttaatctt ttgcaccaca agtggtgttg
480

acatgcctgg tgctgattac caactcacaa aactcttagg tcttcgccca tatgtgaaaa
540

ggtatatgat gtaccaacaa ggttgttttg caggaggcac g
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120

tgcaaccatt ttggccattg gcactgcaaa tccaccaaac cgcgttgagc agagcacata
180

tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca aagagaagtt
240

ccaacgcatg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa cagaagagat
300

tttgaaagaa aatcctagtc tttgtgaata catggcacct tcattggatg ctaggcaaga
360

catggtggtg gttgaggtac ctagacttgg gaaggaggct gcagtcaagg ctatcaaaga
420

atggggtcaa ccaaaatcta agattacaca tttgatcttt tgcaccacaa gtggtgtaga
480

catgcctggt gctgattacc aactcacaaa actcttggga cttcgtccat atgtgaagag
540

attcatgatg taccaacaag gctgctttgc aggtgggacg gttcttcg
588

<210> 46
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120

aaccattttg gccattggca ctgcaaatcc accaaaccgt gttgagcaga gcacatatcc

180

tgatttctac ttcaaaatta caaacagtga gcacaagact gagctcaaag agaagttcca
240

acgcatgtgt gacaaatcca tgatcaagag cagatacatg tatctaacag aagagatttt
300

gaaagaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta ggcaagacat
360

ggtggtggtt gaggtaccta gacttgggaa ggaagctgca gtcaaggcca ttaaagaatg
420

gggtcagcca aagtcaaaga ttactcactt aatcttttgc accacaagtg gtgttgacat
480

gcctggagct gattaccaac tcacaaaact cttaggtctt cgcccatatg tgaaaaggta
540

tatgatgtac caacaaggtt gttttgcagg aggcacggtg cttcgtttgg caaaagattt
600

ggccgagaac aac
613

<210> 47
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120

tttggccatt ggtactgcaa atccagcaaa ccgtgttgat cagagtacat atcctgattt
180

ctacttcaaa atcactaaca gtgagcataa ggttgagctc aaggagaaat tccagcgcat
240

gtgtgacaaa tctatgatca agagcagata catgtatcta acagaagaga ttttgaaaga
300

aaatcctagt ctttgtgaat acatggcacc ttcattggat gctaggcaag atatggtggt
360

cgttgaggta cctagactgg gaaaggaagc tgcagtgaag gctattaaag aatggggtca
420

accaaagtca aagattactc acttaatctt ttgcactaca agtggtgtag acatgcctgg
480

tgctgattac cagctcacaa aactcttagg tcttcgccca tatgtgaaga ggtatatgat
540

gtat
544

<210> 48
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atcaacatat ggttactgtt tctgaaattc gcaaggctca aagggctgaa ggccctgcaa
120

ccattttggc cattggtact gcaaatccag caaaccgtgt tgatcagagt acatatcctg
180

atttctactt caaaatcact aacagtgagc ataaggttga gctcaaggag aaattccagc
240

gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa gagattttga
300

aagaaaatcc tagtctgtgt gagtacatgg caccttcatt ggatgctagg caagacatgg
360

ttgtggttga ggtacctaga cttggaaagg aggctgcagt caaggccatt aaagaatggg
420

gtcaaccaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggt gtagacatgc
480

ctggtgctga ttaccaactc acaaaactct tangtcttcg tccatacgtg aagagggaca
540

tgatgtacca acaag
555

<210> 49
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<212> DNA
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120

ccattttggc cattggcact gcaaatccac caaaccgtgt tgagcagagc acatatcctg
180

atttctactt caaaattaca aacagtgagc acaagactga gctcaaagag aagttccaac
240

gcatgtgtga caaatccatg atcaagagca gatacatgta tctaacagaa gagattttga

300

aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg caagacatgg
360

tggtggttga ggtacctaga cttgggaagg aggctgcagt caaggccatt aaagaatggg
420

gtcaaccaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggt gttgacatgc
480

ctggtgctga ttaccaactc acaaaactct taggtcttcg cccatatgtg aaaaggtata
540

tgatgtacca acaaggttgt tttgcaggag
570

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120

ccattggtac tgcaaatcca gcaaaccgtg ttgatcagag tacatatcct gatttctact
180

tcaaaatcac taacagtgag cataaggttg agctcaagga gaaattccag cgcatgtgtg
240

ataaatctat gatcaagagc agatacatgt atctaacaga agagattttg aaagaaaatc
300

ctagtctgtg tgagtacatg gcaccttcat tggatgctag gcaagacatg gttgtggttg
360

aggtacctag acttggaaag gaggctgcag tcaaggccat taaagaatgg ggtcaaccaa
420

agtcaaagat tactcactta atcttttgca ccacaagtgg tgtagacatg cctggtgctg
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attaccaact cacaaaactc ttaggtcttc gtccatacgt gaagaggtac atgatgtacc
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546

<210> 51
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120

ttggtactgc aaatccagca aaccgtgttg atcaaagtac atatcctgat ttctacttca
180

aaatcactaa cagtgagcat aaggttgagc tcaaagagaa attccagcgc atgtgtgata
240

aatctatgat caagagcaga tacatgtatc caacagaaga gattttgaaa gaaaatccta
300

gtctttgtga atacatggca ccttcattgg atgctagaca agacatggtg gtggttgagg
360

tacctagact tggaaaggag gctgcagtga aggccattaa agaatggggt caaccaaaat
420

ctaagattac acatttgatc ttttgcacca caagtggtgt agacatgcct ggtgctgatt
480

accagctcac aaaactctta ggtcttcgtc catatgtgaa aaggtatatg atgtaccaac
540

aagggtgctt tgcaggtggg acggtgcttc gtttggccaa gg
582

<210> 52
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<212> DNA
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120

ttggccattg gtactgcaaa tccagcaaac cgtgttgatc aaagtacata tcctgatttc
180

tacttcaaaa tcactaacag tgagcataag gttgagctca aagagaaatt ccagcgcnng
240

tgtgataaat ctatgatcaa gagcagatac atgtatctaa cagaagagat tttgaaagaa
300

aatcctagtc tttgtgaata catggcacct tcattggatg ctagacaaga catggtggtg
360

gttgaggtac ctagacttgg aaaggaggct gcagtgaagg ccattaaaga atggggtcaa
420

ccaaaatcta agattacaca tttgatcttt tgcaccacaa gtggtgtana catgcctggt
480

gctgattacc agctcacaaa actcttaggt cttcgtccat atgtgaaaag ggatatgatg
540

taccaacaag ggtgctttgc aggtgggacc gtgcttcntt tggccaanga tttggcccan
600

aacaacaaan gngctcgngn gttggntggt tggtctnaan tcaccgcan
649

<210> 53
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<400> 53
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120

caaaccgtgt tgagcagagc acatatcctg atttctactt caaaattaca aacagtgagc
180

acaagactga gctcaaagag aagttccaac gcatgtgtga caaatccatg atcaagagca
240

gatacatgta tctaacagaa gagattttga aagaaaatcc tagtctttgt gaatacatgg
300

caccttcatt ggatgctagg caagacatgg tggtggttga ggtacctaga cttgggaagg
360

aggctgcagt gaaagctatc aaagaatggg gtcaaccaaa gtcaaagatt actcacttaa
420

tcttttgcac cacaagtggt gtagacatgc ctggagctga ttaccaactc acaaaactct
480

taggtcttcg cccatatgtg aaaaggtata tgatgtacca a
521

<210> 54
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<400> 54
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tgaaggccct gcaaccattt tggccattgg cactgcaaat ccaccaaacc gtgttgagca
120

gagcacatat cctgatttct acttcaaaat tacaaacagt gagcacaaga ctgagctcaa
180

agagaagttc caacgcatgt gtgacaaatc catgatcaag agcagataca tgtatctaac
240

agaagagatt ttgaaagaaa atcctagtct ttgtgaatac atggcacctt cattggatgc
300

taggcaagac atggtggtgg ttgaggtacc tagacttggg aaggaggctg cagncnaggc
360

cattaaanaa tggggncnac caaagncaaa gattactcac ttaatctttt gcaccacaag
420

tggtgctgac atgnctggtg ctgattacca actcacaaaa ctcttaggnc ttcccccata
480

tgtnaaaagg natatgatgc ccncan
506

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<223> Any nucleotide

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120

cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agctcaaaga
180

gaagttccaa cgcatgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
240

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300

gcaagacatg gtggtggttg aggtacctag acttgggaag gaggctgcag tcaaggccat
360

taaagaatgg ggtnaaccaa agtgaaagat tactnactta atcttttgca ccacaagtgg
420

tgttgacatg nctggtgctg attaccaact cacaaaactc ttaggnnttg gcncatatgt
480

gaaaaggtct atgatgcacc aacn
504

<210> 56
<211> 782
<212> DNA
<213> Trifolium repens

<400> 56
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aggccctgca accattttgg ccattggcac tgcaaatcca ccaaaccgtg ttgagcagag
120

cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agctcaaaga
180

gaagttccaa cgcatgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
240

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300

gcaagacatg gtggtggttg aggtacctag acttgggaag gaggctgcag tgaaagctat
360

caaagaatgg ggtcaaccaa agtcaaagat tactcactta atcttttgca ccacaagtgg
420

tgtagacatg cctggagctg attaccaact cacaaaactc ttaggtcttc gcccatatgt
480

gaaaaggtat atgatgtacc aacaaggttg ttttgcagga ggcacggtgc ttcgtttggc
540

aaaagatttg gccgagaaca acaaaggtgc tcgtgtgttg gttgtttgtt ctgaagtcac
600

tgcagttaca ttccgtggcc cgagtgacac tcacttggac agtcttgttg gacaagcatt
660

gtttggagat ggagcagctg cacttatcgt tggttctgat ccagtgccag aaattgagaa
720

accaatattt gagatggttt ggactgcaca aacaattgct ccagacagtg aaggtgccat
780

tg
782

<210> 57
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<400> 57
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aggccctgca accattttgg ccattggcac tgcaaatcca ccaaaccgtg ttgagcagag
120

cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agctcaaaga
180

gaagttccaa cgcatgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
240

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300

acaagacatg gtggtggttg aggtacctag acttgggaag gaggctgcag tcaaggctat
360

caaagaatgg ggtcaaccaa aatctaagat tacacatttg atcttttgca ccacaagtgg
420

tgtagacatg cctggtgctg attaccaact cacaaaactc ttaggacttc gtccatatgt
480

gaagaggtac atgatgtacc aacaagggtg ctttgcaggt ggggcggttc ttcgtttggc
540

taaagatttg gccgagaaca acaaaggtgc tcgtgtgttg gttgtttgtt ctgaagt
597

<210> 58
<211> 590
<212> DNA
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120

ctgagctcaa agagaagttc caacgcatgt gtgacaaatc catgatcaag agcagataca
180

tgtatctaac agaagagatt ttgaaagaaa atcctagtct ttgtgaatac atggcacctt
240

cattggatgc tagacaagac atggtggtgg ttgaggtacc tagacttggg aaggaggccg
300

cagtcaaggc tatcaaagaa tggggtcaac caaaatctaa gattacacat ttgatctttt
360

gcaccacaag tggtgtagac atgcctggtg ctgattacca actcacaaaa ctcttaggac
420

ttcgtccata tgtgaagagg tacatgatgt accaacaagg gtgctttgca ggtgggacgg
480

ttcttcgttt ggctaaagat ttggccgaga acaacaaagg tgctcgtgtg ttggttgttt
540

gttctgaagt aactgcagtc acattccgtg gcccgagtga cactcacttg
590

<210> 59
<211> 618
<212> DNA

<213> Trifolium repens

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gtacatatcc tgatttctac ttcaaaatca ctaacagtga gcataagatt gagcttaaag
120

agaaatttca gcgcatgtgt gataaatcta tgatcaagag cagatacatg tatctaacag
180

aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta
240

ggcaagacat ggtggtggtt gaggtaccta gacttgggaa ggaggctgca gtgaaagcta
300

tcaaagaatg gggtcaacca aagtcaaaga ttactcactt aatcttttgc accacaagtg
360

gtgttgacat gcctggtgct gattaccaac tcacaaaact cttaggtctt cgcccatatg
420

tgaagaggta catgatgtac caacaagggt gctttgcagg tgggacggtt cttcgtttgg
480

ccaaggattt ggccgagaac aacaaaggtg ctcgtgtgtt ggttgtttgc tctgaagtaa
540

ccgcagtcac attccgcggc cccagtgaca ctcatttgga cagccttgtt ggacaagcac
600

tatttggaga tggagctg
618

<210> 60
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<212> DNA
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acatatcctg atttctactt caaaatcact aacagtgagc ataaggttga gcttaaagag
120

aaatttcagc gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa
180

gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
240

caagacatgg tggtggttga ggtacctaga cttgggaagg aggctgcagt gaaagctatc
300

aaagaatggg gtcaaccaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggt
360

gttgacatgc ctggtgctga ttaccaactc acaaaactct taggtcttcg cccatatgtg
420

aagaggtaca tgatgtacca acaagggtgc tttgcaggtg ggacggttct tcgtttggcc
480

aaggatttgg ccgagaacaa caaaggtgct cgtgtgttgg ttgtttgctc tgaagtaacc
540

gcagtcacat tccgcggccc cagtgacact catttggaca gccttgttgg acaagcacta
600

tttggagatg gagctgctg
619

<210> 61
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120

caccttcatt ggatgctagg caagacatgg tggtggttga ggtacctaga cttgggaagg
180

aggctgcagt gaaagctatc aaagaatggg gtcaaccaaa gtcaaagatt actcacttaa
240

tcttttgcac cacaagtggt gtagacatgc ctggagctga ttaccaactc acaaaactct
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taggtcttcg cccatatgtg aagaggtaca tgatgtacca acaagggtgc tttgcaggtg
360

ggacggttct tcgtttggcc aaggatttgg ccgagaacaa caaaggtgct cgtgtgttgg
420

ttgtttgctc tgaagtaacc gcagtcacat tccgcggccc cagtgacact catttggaca
480

gtcttgttgg acaagcacta ttcggagatg gagctgctgc actcattgtt ggctcagacc
540

cagtaccaga aattgagan
559

<210> 62
<211> 553
<212> DNA
<213> Trifolium repens

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gagtacatgg caccttcatt ggatgctagg caagacatgg ttgtggttga ggtacctaga
120

cttggaaagg aggctgcagt caaggccatt aaagaatggg gtcaaccaaa gtcaaagatt
180

actcacttaa tctttttgcac cacaagtggt gtagacatgc ctggtgctga ttaccaactc
240

acaaaactct taggtcttcg tccatacgtg aagaggtaca tgatgtacca acaagggtgc
300

tttgcaggtg ggacggtgct tcgtttggcc aaggatttgg ccgagaacaa caaaggtgct
360

cgtgtgttgg ttgtttgttc tgaagtcacc gcagtcacat tccgtggccc tagtgacact
420

catttggaca gtcttgttgg acaagcacta tttggagatg gagctgctgc tctcattgtt
480

ggttctgatc cagtaccaga aattgagaag ccaatatttg agatggtatg gaccgcacag
540

acaattgctc cag
553

<210> 63
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tggtgtagac atgcctggtg ctgattacca gctcacaaaa ctcttaggtc ttcgcccata
120

tgtgaagagg tatatgatgt atcaacaagg ttgctttgca ggaggcacgg tgcttcgttt
180

ggctaaagat ttggccgaga acaacaaagg tgctcgtgtg ctagttgttt gttctgaagt
240

aacagcagtc acattccgcg gtccaagtga cactcacttg gacagtcttg ttggacaagc
300

actattcgga gatggagctg ctgctctcat tgttggctca gaccctgtac cagaaatcga
360

gaaacctata tttgagatgg tatggaccgc acagacaatt gctccggaca gtgaaggtgc
420

cattgatggt caccttcgtg aagctggact aacatttcat cttcttaaag atgttcctgg
480

gattgtatca aagaacatta ataaagcatt ggtcgaggct ttccaaccat taggaatttc
540

tgattacaac tcaatctttt ggattgcaca cccgggtgga cctgcaattc t
591

<210> 64
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<223> Any nucleotide

<400> 64
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gaacattgat aaggcattgg ttgaggcatt ccaaccatta aacatctctg attacaattc
120

aatcttttgg attgctcatc caggtggtcc tgcaattcta gaccaagttg agataaagtt
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gggcttaaaa cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat
240

gtcaagtgca tgtgtattgt tcatcttaga tgagatgcaa aagaaatcgg ctgaaaatgg
300

actgaaaacc acaggagaag gacttgactg gggtgtgttg tttggatttg gaccaggact
360

taccattgaa actgttgttc tacatagtgt ggctatatga gaatgcgaga cttgattgtt
420

ttgtattgta ttgtattgta ttgtattact tttaatcttg cttgaatttc catttaacaa
480

taaatatgga gttcaataag taccatcagt gttaaaataa tatatcgtta atagctatta
540

ttttagtgtc tgtttctttt tactaaacta tattttattt tagtatttgc tattgatttg
600

aaataaatat tgtcctctta actgaaaaaa aaaa
634

<210> 65
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<213> Trifolium repens

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<220>
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<223> Any amino acid

<400> 65

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Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln Pro
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Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro Gly
        35   40   45

Gly Pro Ala Ile Leu Asp Gln Val Glu Ile Lys Leu Gly Leu Lys Pro
    50   55   60

Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Glu Tyr Gly Asn Met
65   70   75   80

Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Gln Lys Lys Ser
                85   90   95

Ala Glu Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly Val
            100   105   110

Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu His
        115   120   125

Ser Val Ala Ile
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<210> 66
<211> 491
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gaacattgat aaggcattgg ttgaggcatt ccaaccatta aacatctctg attacaattc
120

aatcttttgg attgctcatc caggtggtcc tgcaattcta gaccaagttg agataaagtt
180

gggcttaaaa cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat
240

gtcaagtgca tgtgtattgt tcatcttaga tgagatgaga aagaaatcgg ctgaaaatgg
300

acttaaaacc acaggagaag gacttgactg gggtgtgttg tttggatttg ggcccggact
360

taccattgaa actgttgttc tacatagtgt ggctatatga gaatgagaga cttgatttgt
420

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gntcantntg n
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<210> 67
<211> 363
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<213> Trifolium repens

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<400> 67
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ggtgtgttgt ttggatttgg accaggactt accattgaaa ctgttgttct acatagtgtg
120

gctatatgag aatgcgagac ttgattgttt tgtattgtat tgtattgtat tgtattactt
180

ttaatcttgc ttgaatttcc atttaacaat aaatatggag ttcaataagt accatcagtg
240

ttaaaataat atatcgttaa tagctattat tttagtgtct gtttcttttt actaaactat
300

attttatttt agtatttgct attgatttga aataaatatt gtcctcttaa ctgaaaaaaa
360

aaa

363

<210> 68
<211> 363
<212> DNA
<213> Trifolium repens

<400> 68
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ggtgtgttgt ttggatttgg accaggactt accattgaaa ctgttgttct acatagtgtg
120

gctatatgag aatgcgagac ttgattgttt tgtattgtat tgtattgtat tgtattactt
180

ttaatcttgc ttgaatttcc atttaacaat aaatatggag ttcaataagt accatcagtg
240

ttaaaataat atatcgttaa tagctattat tttagtgtct gtttcttttt actaaactat
300

attttatttt agtatttgct attgatttga aataaatatt gtcctcttaa ctgaaaaaaa
360

aaa
363

<210> 69
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<223> Any nucleotide

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<223> Any nucleotide

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<222> (33)..(33)
<223> Any nucleotide

<400> 69
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60

caaagaagaa atatgggaga cgaaggtata gtgagaggtg tcacaaagca gacaacccct
120

gggaaggcta ctatattggc tcttggcaag gcattccctc accaacttgt gatgcaagag
180

tatttagttg atggttattt tagggacact aattgtgaca atcctgaact taagcagaaa
240

cttgctagac tttgtaagac aaccacggta aaaacaaggt atgttgttat gaatgaggag 300

atactaaaga aatatccaga acttgttgtc gaaggcgcct caactgtaaa acaacgttta 360

gagatatgta atgaggcagt aacacaaatg gcaattgaag cttcccaagt ttgcctaaag 420

aattggggta gatccttatc ggacataact catgtggttt atgtttcatc tagtgaagct 480

agattacccg gtggtgacct atacttgtca aaaggactag gactaaaccc taaaattcaa 540

agaaccatgc tctatttctc tggatgctcg ggaggcgtag ccggccttcg cgttgcgaaa 600

gacatagctg agaacaaccc tggaagtaga gttttgcttg ctacttctga aactacaatt 660

attggattca agccaccaag tgttgataga ccttatgatc ttgttggtgt ggcactcttt 720

ggagatggtg ctggtgctat gataattggc tcagacccaa tacttgaaac tgagactcca 780

ttgtttgagc ttcatacttc agctcaggag tttataccag acacagagaa gaaaatagat 840

gggcggctga cggaggaggg cataagtttc acgctagcga gggaactgcc gcagata 897

<210> 70
<211> 275
<212> PRT
<213> Trifolium repens

<400> 70

Met Gly Asp Glu Gly Ile Val Arg Gly Val Thr Lys Gln Thr Thr Pro
1 5 10 15

Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
20 25 30

Val Met Gln Glu Tyr Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
35 40 45

Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
50 55 60

Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
65 70 75 80

Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
85 90 95

Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
100 105 110

Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
115 120 125

Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
130 135 140

Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
145 150 155 160

Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
165 170 175

Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
180 185 190

Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
195 200 205

Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
210 215 220

Ile Gly Ser Asp Pro Ile Leu Glu Thr Glu Thr Pro Leu Phe Glu Leu
225 230 235 240

His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
245 250 255

Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
260 265 270

Pro Gln Ile
275

<210> 71
<211> 577
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

<220>
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<222> (26)..(26)
<223> Any nucleotide

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<221> misc_feature
<222> (33)..(33)
<223> Any nucleotide

<220>
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<222> (43)..(43)
<223> Any nucleotide

<400> 71
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caaagaagaa atatgggaga cgaaggtata gtgagaggtg tcacaaagca gacaacccct
120

gggaaggcta ctatattggc tcttggcaag gcattccctc accaacttgt gatgcaagag
180

tgtttagttg atggttattt tagggacact aattgtgaca atcctgaact taagcagaaa
240

cttgctagac tttgtaagac aaccacggta aaaacaaggt atgttgttat gaatgaggag
300

atactaaaga aatatccaga acttgttgtc gaaggcgcct caactgtaaa acaacgttta
360

gagatatgta atgaggcagt aacacaaatg gcaattgaag cttcccaagt ttgcctaaag
420

aattggggta gatccttatc ggacataact catgtggttt atgtttcatc tagtgaagct
480

agattacccg gtggtgacct atacttgtca aaaggactag gactaaaccc taaaattcaa
540

agaaccatgc tctatttctc tggatgctcg ggaggcg
577

<210> 72
<211> 599
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (12)..(12)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (20)..(20)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (23)..(23)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (30)..(30)
<223> Any nucleotide

<400> 72
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agaagaaata tgggagacga aggtatagtg agaggtgtca caaagcagac aacccctggg 120

aaggctacta tattggctct tggcaaggca ttccctcacc aacttgtgat gcaagagtgt 180

ttagttgatg gttattttag ggacactaat tgtgacaatc ctgaacttaa gcagaaactt 240

gctagacttt gtaagacaac cacggtaaaa acaaggtatg ttgttatgaa tgaggagata 300

ctaaagaaat atccagaact tgttgtcgaa ggcgcctcaa ctgtaaaaca acgtttagag 360

atatgtaatg aggcagtaac acaaatggca attgaagctt cccaagtttg cctaaagaat 420

tggggtagat ccttatcgga cataactcat gtggtttatg tttcatctag tgaagctaga 480

ttacccggtg gtgacctata cttgtcaaaa ggactaggac taaaccctaa aattcaaaga 540

accatgctct atttctctgg atgctcggga ggcgtagccg gccttcgcgt tgcgaaaga 599

<210> 73
<211> 581
<212> DNA
<213> Trifolium repens

<220>
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<222> (10)..(11)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (19)..(19)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (26)..(26)
<223> Any nucleotide

<400> 73
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gaaatatggg agacgaaggt atagtgagag gtgtcacaaa gcagacaacc cctgggaagg

120

ctactatatt ggctcttggc aaggcattcc ctcaccaact tgtgatgcaa gagtatttag
180

ttgatggtta ttttagggac actaattgtg acaatcctga acttaagcag aaacttgcta
240

gactttgtaa gacaaccacg gtaaaaacaa ggtatgttgt tatgaatgag gagatactaa
300

agaaatatcc agaacttgtt gtcgaaggcg cctcaactgt aaaacaacgt ttagagatat
360

gtaatgaggc agtaacacaa atggcaattg aagcttccca agtttgccta aagaattggg
420

gtagatcctt atcggacata actcatgtgg tttatgtttc atctagtgaa gctagattac
480

ccggtggtga cctatacttg tcaaaaggac taggactaaa ccctaaaatt caaagaacca
540

tgctctattt ctctggatgc tcgggaggcg tagccggcct t
581

<210> 74
<211> 588
<212> DNA
<213> Trifolium repens

<220>
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<222> (11)..(11)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (13)..(13)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (25)..(27)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (36)..(36)
<223> Any nucleotide

<400> 74
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60

gaaatatggg agacgaaggt atagtgagag gtgtcacaaa gcagacaacc cctgggaagg
120

ctactatatt ggctcttggc aaggcattcc ctcaccaact tgtgatgcaa gagtgtttag
180

ttgatggtta ttttagggac actaattgtg acaatcctga acttaagcag aaacttgcta
240

gactttgtaa gacaaccacg gtaaaaacaa ggtatgttgt tatgaatgag gagatactaa
300

agaaatatcc agaacttgtt gtcgaaggcg cctcaactgt aaaacaacgt ttagagatat
360

gtaatgaggc agtaacacaa atggcaattg aagcttccca agtttgccta aagaattggg
420

gtagatcctt atcggacata actcatgtgg tttatgtttc atctagtgaa gctagattac
480

ccggtggtga cctatacttg tcaaaaggac taggactaaa ccctaaaatt caaagaacca
540

tgctctattt ctctggatgc tcgggaggcg tagccggcct tcgcgttg
588

<210> 75
<211> 563
<212> DNA
<213> Trifolium repens

<400> 75
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60

cgaaggtata gtgagaggtg tcacaaggca gccaacccct gggaaggcta ctatattggc
120

tcttggcaag gcattccctc accaacttgt gatgcaagag tatttagttg atggttattt
180

tagggacact aattgtgaca atcctaagct taagcagaaa cttgctagac tttgcaagac
240

aaccacagtg aaaacaaggt atgttgttat gaatgaagag atactaaaga aatatccaga
300

acttactatc ggaggcacct cgacggtaaa acaacattta gagatatgta atgaggcagt
360

aacacaaatg gcaattgaag cttcccaagt ttgcctaaag aattggggta gacccatatc
420

agacataact catgtggttt atgtttcatc tagtgaagct agattacctg gtggtgacct
480

atacttgtca aaaggactag gactaaaccc taaaattcaa agaaccatgc tctatttctc
540

gggatgctcg ggaggcgtag ccg
563

<210> 76
<211> 603
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature

<222> (4)..(4)
<223> Any nucleotide

<400> 76
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gtgagaggtg tcacaaagca gacaacccct gggaaggcta ctatattggc tcttggcaag 120

gcattccctc accaacttgt gatgcaagag tatttagttg atggttattt tagggacact 180

aattgtgaca atcctgacct taagcagaaa cttgctagac tttgtaagac aaccacggta 240

aaaacaaggt atgttgttat gaatgaggag atactaaaga aatatccaga acttgttgtc 300

gaaggcgcct caactgtaaa acaacgttta gagatatgta atgaggcagt aacacaaatg 360

gcaattgaag cttcccaagt ttgcctaaag aattggggta gatccttatc ggacataact 420

catgtggttt atgtttcatc tagtgaagct agattacccg gtggtgacct atacttgtca 480

aaaggactag gactaaaccc taaaattcaa agaaccatgc tctatttctc tggatgctcg 540

ggaggcgtag ccggccttcg cgttgcgaaa gacatagctg agaacaaccc tggaagtaga 600

gtt 603

<210> 77
<211> 584
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (1)..(1)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (5)..(5)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (40)..(40)
<223> Any nucleotide

<400> 77
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aggcagtaac acaaatggca attgaagctt cccaagtttg cctaaagaat tggggtagac
120

ccttatcaga cataactcat gtggtttatg tttcctctag tgaagctaga ttacccggtg
180

gtgacctata tttgtcaaaa ggactaggac taaatcctaa aattcaaaga accatgctct
240

atttctctgg atgctcagga ggcgtagccg gccttcgcgt tgcgaaagac atagctgaga
300

acaaccctgg aagtagagtt ttgcttgcta cttctgaaac tacaattatt ggattcaagc
360

caccaagtgt tgatagacct tatgatcttg ttggtgtggc actctttgga gatggtgctg
420

gtgctatgat aattggctca gacccaatac ttgaaactga gactccattg tttgagcttc
480

atacttcagc tcaggagttt ataccagaca cagagaagaa aatagatggg cggctgacgg
540

aggagggcat aagtttcacg ctagcgaggg aactgccgca gata
584

<210> 78
<211> 735
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (47)..(47)
<223> Any nucleotide

<400> 78
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60

ttgctaagtc atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120

cttcctccct gctaacttta tacttagaga agatggtgaa agttaatgag atccgccagg
180

cacagagagc tgaaggccct gccactgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgttgatca gagtacatac cccgactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagataca
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga aaagaggcag
480

caacaaaggc aatcaaggaa tggggtcaac ctaagtccaa gattacccac ctcatctttt
540

gcaccacaag tggtgtggac atgcccggtg ccgactatca gcttacaaag cttttaggcc
600

ttcgtccgca tgtgaagcgt tacatgatgt accaacaagg ttgttttgct ggtggcacgg
660

tgcttcgttt ggctaaagac ttggctgaaa acaacaaagg tgcccgtgta ttggtggttt
720

gttcagagat aactg
735

<210> 79
<211> 194
<212> PRT
<213> Trifolium repens

<400> 79

Met Val Lys Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Thr Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro His Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu

180 185 190

Ile Thr

<210> 80
<211> 574
<212> DNA
<213> Trifolium repens

<220>
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<222> (47)..(47)
<223> Any nucleotide

<400> 80
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ttgctcactc atcaaccatt ccaattcctt aatataacct atcagtactt accatctttt 120

cttcctccct gctaacttta gaatcagaga agatggtgaa tgttaatgag atccgccagg 180

cacagagagc tgaaggccct gccactgtgt tggcaatcgg cactgcaact cctccaaact 240

gtgtcgatca gagtacatac ccggactact acttccgcat cacaaacagt gagcacaaga 300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagataca 360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt 420

cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga aaagaggcag 480

caacaaaggc aattaaggaa tggggtcaac ctaagtccaa gattacccac ctcatctttt 540

gcaccaccag tggtgtcgac atgcccggtg ccgc 574

<210> 81
<211> 597
<212> DNA
<213> Trifolium repens

<400> 81
gtagcaacac acactttgat ttctttttga gtccttgcta cgtggcttta ccaaaaaacg 60

ttgctaagtc atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt 120

cttcctccct gctaacttta gactcagaga agatggtgaa tgttaatgag atccgccagg 180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact

240

gtgtcgatca gagtacatac ccagactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagataca
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga aaagaggctg
480

caacaaaggc tatcaaggaa tggggtcaac ctaagtccaa gattactcac ctcatctttt
540

gcaccacaag tggtgtggac atgcctggcg ccgactatca gcttacaaag cttttag
597

<210> 82
<211> 616
<212> DNA
<213> Trifolium repens

<220>
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<222> (70)..(70)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (616)..(616)
<223> Any nucleotide

<400> 82
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60

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120

cttcctccct gctaacttta gactcagaga agatggtgaa tgttaatgag atccgccagg
180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgtcgatca gagtacatac ccagactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagataca
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga aaagaggctg
480

caacaaaggc tatcaaggaa tggggtcaac ctaagtccaa gattactcac ctcatctttt
540

gcaccacaag tggtgtggac atgcctggcg ccgactatca gcttacaaag cttttaggcc
600

ttcgtccgca tgtgan
616

<210> 83
<211> 585
<212> DNA
<213> Trifolium repens

<220>
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<222> (1)..(3)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (7)..(7)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (20)..(20)
<223> Any nucleotide

<220>
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<222> (37)..(37)
<223> Any nucleotide

<220>
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<222> (61)..(61)
<223> Any nucleotide

<220>
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<222> (451)..(451)
<223> Any nucleotide

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<222> (507)..(507)
<223> Any nucleotide

<400> 83
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60

ntcaaccatt ccaattcctt aatataacct atcagtactc accatctttt cttcctccct
120

gctaacttta gactcagaga agatggtgaa tgttaatgag atccgccagg cacagagagc
180

tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact gtgttgatca
240

gagtacatac ccggactact acttccgcat cacaaacagt gagcacaaga cagagctcaa
300

agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagataca tgcatttaac
360

agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt cattggatgc
420

aagacaagac atggtggttg tggaagtacc naggctagga aaagaggcag taacaaaggc
480

aattagggaa tggggtcaac ctaagtncaa gattacccac ctcatctttt gcaccaccag
540

tggtgtggac atgcccggtg ccgactatca gctcacaaag ctctt
585

<210> 84
<211> 596
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nculeotide

<220>
<221> misc_feature
<222> (14)..(14)
<223> Any nculeotide

<220>
<221> misc_feature
<222> (37)..(37)
<223> Any nculeotide

<400> 84
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60

atccgccagg cacagagagc tgaaggccct gcaactgtgt ttgcaatcgg cactgcaact
120

cctaaaaact gtgttgatca gagtacttac cccgactact atttccgaat cacaaacagc
180

gaacacaaga ctgaactcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag
240

aagagataca tgcatttgac agaagagatt ttgaaggaga attcaagttt atgtgagtac
300

atggcacctt cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga
360

aaagaggctg caacaaaggc tatcaaggaa tggggtcaac ctaagtccaa gattactcac
420

ctcatctttt gcaccacaag tggtgtggac atgcctggtg ccgactatca gcttacaaag

480

cttttaggcc ttcgtccgca tgtgaagcgt tatatgatgt accaacaagg ttgttttgct
540

ggtggcacgg tgcttcgttt ggctaaagac ttggctgaaa acaacaaagg tgcccg
596

<210> 85
<211> 618
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (6)..(6)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (9)..(9)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (14)..(14)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (37)..(37)
<223> Any nucleotide

<400> 85
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60

atccgccagg cacagagagc tgaaggccct gcaactgtgt ttgcaatcgg cactgcaact
120

cctaaaaact gtgttgatca gagtacttac cccgactact atttccgaat cacaaacagc
180

gaacacaaga ctgaactcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag
240

aagagataca tgcatttgac agaagagatt ttgaaggaga attcaagttt atgtgagtac
300

atggcacctt cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga
360

aaagaggctg caacaaaggc tatcaaggaa tggggtcaac ctaagtccaa gattactcac
420

ctcatctttt gcaccacaag tggtgtggac atgcctggtg ccgactatca gcttacaaag
480

cttttaggcc ttcgtccgca tgtgaagcgt tatatgatgt accaacaagg ttgttttgct
540

ggtggcacgg tgcttcgttt ggctaaagac ttggctgaaa acaacaaagg tgcccgtgta
600

ttggtggttt gttcagag
618

<210> 86
<211> 609
<212> DNA
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<222> (32)..(33)
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gccaggcaca gagagctgaa ggccctgcaa ctgtgtttgc aatcggcact gcaactccta
120

aaaactgtgt tgatcagagt acttaccccg actactattt ccgaatcaca aacagcgaac
180

acaagactga actcaaagaa aaattccagc gcatgtgtga caaatctatg attaagaaga
240

gatacatgca tttgacagaa gagattttga aggagaattc aagtttatgt gagtacatgg
300

caccttcatt ggatgcaaga caagacatgg tggttgtgga agtaccaagg ctaggaaaag
360

aggctgcaac aaaggctatc aaggaatggg gtcaacctaa gtccaagatt actcacctca
420

tcttttgcac cacaagtggt gtggacatgc ctggtgccga ctatcagctt acaaagcttt
480

taggccttcg tccgcatgtg aagcgttata tgatgtacca acaaggttgt tttgctggtg
540

gcacggtgct tcgtttggct aaagacttgg ctgaaaacaa caaaggtgcc cgtgtattgg
600

tggtttgtt
609

<210> 87
<211> 571
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<222> (247)..(247)
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<222> (571)..(571)
<223> Any nucleotide

<400> 87
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agctgaaggc cctgccactg tgttggnant nggcactgca actcctccaa actgtgtcga 120
tcagagtaca tacccggact actacttccg catcacaaac agtgagcaca agacagagct 180
caaagaaaaa ttccagcgca tgtgtgacaa atctatgatt aagaagagat acatgcattt 240
gacagangag attttgaagg agaatccaag tttatgtgag tacatggcac cttcattgga 300
tgcaagacaa gacatggtgg ttgtggaagt accaaggcta ggaaaagagg cagcaacaaa 360
ggcaattaag gaatggggcc aacctaagtc caagattacc cacctcatct tttgcaccac 420
cagtggtgtc gacatgcccg gtgccgacta tcagctcaca aagctcttag gcctgcgtcc 480
atatgtgaag cgttacatga tgtatcaaca aggttgtttt gctggtggca cggtgcttcg 540
tttggctaaa gacttggctg aaaacaacaa n 571

<210> 88
<211> 603
<212> DNA
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<222> (9)..(9)
<223> Any nucleotide

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<221> misc_feature
<222> (13)..(14)
<223> Any nucleotides

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<223> Any nucleotide

<400> 88
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aaggccctgc cactgtgttg gcaatcggca ctgcaactcc tccaaactgt gtcgatcaga 120

gtacataccc ggactactac ttccgcatca caaacagtga gcacaagaca gagctcaaag 180

aaaaattcca gcgcatgtgt gacaaatcta tgattaagaa gagatacatg catttgacag 240

aagagatttt gaaggagaat ccaagtttat gtgagtacat ggcaccttca ttggatgcaa 300

gacaagacat ggtggttgtg gaagtaccaa ggctaggaaa agaggcagca acaaaggcaa 360

ttaaggaatg ggccaacct aagtccaaga ttacccacct catcttttgc accaccagtg 420

gtgtcgacat gcccggtgcc gactatcagc tcacaaagct cttaggcctg cgtccatatg 480

tgaagcgtta catgatgtat caacaaggtt gttttgctgg tggcacggtg cttcgtttgg 540

ctaaagactt ggctgaaaac aacaaangtg cccgtgtgtt ggtgggttgt tcanagataa 600

ctg 603

<210> 89
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<212> DNA
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<222> (12)..(12)
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<222> (43)..(43)

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<220>
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<222> (68)..(68)
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<400> 89
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gccctgcncc tgtgtttgca atcggcactg caactcctaa aaactgtgtt gatcagagta 120

cttaccccga ctactatttc cgaatcacaa acagcgaaca caagactgag ctcaaagaaa 180

aattccagcg catgtgtgac aaatctatga ttaagaagag atacatgcat ttgacagaag 240

agattttgaa ggagaatcca agtttatgtg agtacatggc accttcattg gatgcaagac 300

aagacatggt ggtagtggaa gtaccaaggc taggaaaaga ggcagcaaca aaggcaatta 360

aagaatgggg tcaacctaag tccaagatta cccacctcat cttttgcacc accagtggtg 420

tggacatgcc cggtgccgac tatcagctca caaagctctt aggcctgcgt ccatatgtga 480

agcgttacat gatgtatcaa caaggttgtt ttgctggtgg cacggtactt cgtttggcta 540

aagacttggc tgaaaacaac aaaggtgccc gtgtgttggt ggtttgtt 588

<210> 90
<211> 250
<212> DNA
<213> Trifolium repens

<220>
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<222> (35)..(35)
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<222> (247)..(247)
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<223> Any nucleotide

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cacaagactg agctcaaaga aaaattccag cgcatgtgtg acaaatctat gattaagaag
120

agatacatgc atttgacaga agagattttg aaggagaatc caagnttatg tgagtacatg

180

gcaccttnat tggatgcaag acaagacatg gnggccgccc accnnccntc cnccncaccn
240

caacccnccn
250

<210> 91
<211> 583
<212> DNA
<213> Trifolium repens

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<222> (47)..(47)
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<222> (552)..(552)
<223> Any nucleotide

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tgctaagtca tcaaccattc caattcctta atataaccta tcagtactca ccatcttttc
120

ttcctccctg ctaactttag actcagtaga agatggtgaa tgttaatgag atccgccagg
180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgttgatca gagtacatac ccggactact acttccgcat cacaaacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcacgt gtaagatatt tatcttatac tccatgcatg
360

tctttttctg ctgactgccg tgtttatata ttgttttgtt ttgttcctta aatttgttat
420

gtcactctca catgtacaaa acacttaaga ctaaactgca tatcattttt ttcagggaca
480

aatctatgat taagaagaga tacatgcatt tgacagaaga gattttgaag gagaatccaa
540

gtttatgtga gnacatggca ccttcttggg atgcaagaca agt
583

<210> 92
<211> 95

<212> PRT
<213> Trifolium repens

<220>
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<222> (86)..(86)
<223> Any amino acid

<400> 92

Met Val Asn Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
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Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Thr Arg Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Xaa Met Ala Pro Ser Trp Asp Ala Arg Gln
85 90 95

<210> 93
<211> 582
<212> DNA
<213> Trifolium repens

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120

ttcctccctg ctaactttag actcagagaa gatggtgaat gttaatgaga tccgccaggc
180

acagagagct gaaggccctg ccaccgtgtt ggcaatcggc actgcaactc ctccaaactg
240

tgttgatcag agtacatacc cggactacta cttccgcatc acaaacagtg agcacaagac

300

agagctcaaa gaaaaattcc agcgcacgtg taagatattt atcttatact ccatgcatgt
360

ctttttctgc tgactgccgt gtttatatat tgttttgttt tgttccttaa atttgttatg
420

tcactctcac atgtacaaaa cacttaagac taaactgcat atcatttttt tcagggacaa
480

atctatgatt aagaagagat acatgcattt gacagaagag attttgaagg agaatccaag
540

tttatgtgag nacatggcac cttcttggga tgcaagacaa gt
582

<210> 94
<211> 167
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

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<223> Any nucleotide

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<223> Any nucleotide

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60

aacctatcag tactcaccat cttttcttcc tccctgctaa ctttagactc agtagaagat
120

ggtgaatgtt aatgagatcc gccaggcaca gagagctgaa ggccctg
167

<210> 95
<211> 613
<212> DNA
<213> Trifolium repens

<220>
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<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (16)..(16)

<223> Any nucleotide

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60

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120

acgtgctcct actcagggaa aggcaacgat acttgcatta ggaaaggctt tccccgccca
180

agtcctccct caagagtgct tggtggaagg attcattcgc gacactaagt gtgacgatac
240

ttatattaag gagaaattgg agcgtctttg caaaaacaca actgtaaaaa caagatacac
300

agtaatgtca aaggagatct tagacaacta tccagagcta gccatagatg gaacaccaac
360

aataaggcaa aagcttgaaa tagcaaatcc agcagtagtt gaaatggcaa caagagcaag
420

caaagattgc atcaaagaat ggggaaggtc acctcaagat atcacacaca tagtctatgt
480

ttcctcgagc gaaattcgtc tacccggtgg tgacctttat cttgcaaatg aactcggctt
540

aaacagcgat gttaatcgcg taatgctcta tttcctcggt tgctacggcg gtgtcactgg
600

cttacgtgtc gcc
613

<210> 96
<211> 182
<212> PRT
<213> Trifolium repens

<400> 96

Met Pro Gln Gly Asp Leu Asn Gly Ser Ser Ser Val Asn Gly Ala Arg
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Ala Arg Arg Ala Pro Thr Gln Gly Lys Ala Thr Ile Leu Ala Leu Gly
20 25 30

Lys Ala Phe Pro Ala Gln Val Leu Pro Gln Glu Cys Leu Val Glu Gly
35 40 45

Phe Ile Arg Asp Thr Lys Cys Asp Asp Thr Tyr Ile Lys Glu Lys Leu
50 55 60

Glu Arg Leu Cys Lys Asn Thr Thr Val Lys Thr Arg Tyr Thr Val Met
65 70 75 80

Ser Lys Glu Ile Leu Asp Asn Tyr Pro Glu Leu Ala Ile Asp Gly Thr

85 90 95

Pro Thr Ile Arg Gln Lys Leu Glu Ile Ala Asn Pro Ala Val Val Glu
100 105 110

Met Ala Thr Arg Ala Ser Lys Asp Cys Ile Lys Glu Trp Gly Arg Ser
115 120 125

Pro Gln Asp Ile Thr His Ile Val Tyr Val Ser Ser Ser Glu Ile Arg
130 135 140

Leu Pro Gly Gly Asp Leu Tyr Leu Ala Asn Glu Leu Gly Leu Asn Ser
145 150 155 160

Asp Val Asn Arg Val Met Leu Tyr Phe Leu Gly Cys Tyr Gly Gly Val
165 170 175

Thr Gly Leu Arg Val Ala
180

<210> 97
<211> 613
<212> DNA
<213> Trifolium repens

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120

acgtgctcct actcagggaa aggcaacgat acttgcatta ggaaaggctt tccccgccca
180

agtcctccct caagagtgct tggtggaagg attcattcgc gacactaagt gtgacgatac
240

ttatattaag gagaaattgg agcgtctttg caaaaacaca actgtaaaaa caagatacac
300

agtaatgtca aaggagatct tagacaacta tccagagcta gccatagatg gaacaccaac
360

aataaggcaa aagcttgaaa tagcaaatcc agcagtagtt gaaatggcaa caagagcaag
420

caaagattgc atcaaagaat ggggaaggtc acctcaagat atcacacaca tagtctatgt
480

ttcctcgagc gaaattcgtc tacccggtgg tgacctttat cttgcaaatg aactcggctt
540

aaacagcgat gttaatcgcg taatgctcta tttcctcggt tgctacggcg gtgtcactgg
600

cttacgtgtc gcc
613

<210> 98
<211> 570
<212> DNA
<213> Trifolium repens

<220>
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<222> (13)..(13)
<223> Any nucleotide

<400> 98
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aaaaatgcct caaggtgatt tgaatggaag ttcctcggtg aatggagcac gtgctagacg
120

tgctcctact cagggaaagg caacgatact tgcattagga aaggctttcc ccgcccaggt
180

cctccctcaa gagtgcttgg tggaaggatt cattcgcgac actaagtgtg acgatactta
240

tattaaggag aaattggagc gtctttgcaa aaacacaact gtgaaaacaa gatacacagt
300

aatgtcaaag gagatcttag acaactatcc agagctagcc atagatggaa caccaacaat
360

aaggcaaaag cttgaaatag caaatccagc agtagttgaa atggcaacaa gagcaagcaa
420

agattgcatc aaagaatggg gaaggtcacc tcaagatatc acacacatag tctatgtttc
480

ctcgagcgaa attcgtctac ccggtggtga cctttatctt gcaaatgaac tcggcttaaa
540

cagcgatgtt aatcgcgtaa tgctctattt
570

<210> 99
<211> 575
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (33)..(33)
<223> Any nucleotide

<400> 99
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gcctcaaggt gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc
120

tactcaggga aaggcaacga tacttgcatt aggaaaggct ttccccgccc aggtcctccc
180

tcaagagtgc ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa
240

ggagaaattg gagcgtcttt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc
300

aaaggagatc ttagacaact atccagagct agccatagat ggaacaccaa caataaggca
360

aaagcttgaa atagcaaatc cagcagtagt tgaaatggca acaagagcaa gcaaagattg
420

catcaaagaa tggggaaggt cacctcaaga tatcacacac atagtctatg tttcctcgag
480

cgaaattcgt ctacccggtg gtgaccttta tcttgcaaat gaactcggct taaacagcga
540

tgttaatcgc gtaatgctct atttcctcgg ttgct
575

<210> 100
<211> 573
<212> DNA
<213> Trifolium repens

<400> 100
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tgatttgaat ggaagttcct cggtgaatgg agcacgtgct agacgtgctc ctactcaggg
120

aaaggcaacg atacttgcat taggaaaggc tttccccgcc caagtcctcc ctcaagagtg
180

cttggtggaa ggattcattc gcgacactaa gtgtgacgat acttatatta aggagaaatt
240

ggagcgtctt tgcaaaaaca caactgtaaa aacaagatac acagtaatgt caaaggagat
300

cttagacaac tatccagagc tagccataga tggaacacca acaataaggc aaaagcttga
360

aatagcaaat ccagcagtag ttgaaatggc aacaagagca agcaaagatt gcatcaaaga
420

atggggaagg tcacctcaag atatcacaca catagtctat gtttcctcga gcgaaattcg
480

tctacccggt ggtgaccttt atcttgcaaa tgaactcggc ttaaacagcg atgttaatcg
540

cgtaatgctc tatttcctcg gttgctacgg cgg
573

<210> 101
<211> 607
<212> DNA
<213> Trifolium repens

<400> 101
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60

aacaacaaag gtgcccgtgt gttggtggtt tgttcagaga taactgcagt tactttccgt
120

ggacccagtg acactcacct tgatagcctt gtggggcaag cattgtttgg agatggtgca
180

gcagctgtga ttgttggttc agaccctttg ccagaagttg agaagccttt gtttgaattg
240

gtatggaccg cacaaacaat cgctccagat agtgaaggag ccattgatgg tcaccttcgc
300

gaagcagggc tgacattcca tctcctcaag gatgttccta gccttgtctc aaataacatt
360

gagaaagcgc ttgttgatgc ctttcaacct ttgaatattt ctgactacaa ttccatcttt
420

tggattgcac acccaggcgg accagcaatt cttgaccaag ttgaagctaa gttaggctta
480

aagccagaga aaatgcaagc cactcgacat gtacttagcg aatatggtaa catgtcaagt
540

gcgtgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga cggacttgcc
600

acaacag
607

<210> 102
<211> 202
<212> PRT
<213> Trifolium repens

<400> 102

Val Tyr Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys
1 5 10 15

Asp Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser
20 25 30

Glu Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp
35 40 45

Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Val Ile
50 55 60

Val Gly Ser Asp Pro Leu Pro Glu Val Glu Lys Pro Leu Phe Glu Leu
65 70 75 80

Val Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp
85 90 95

Gly His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val
100 105 110

Pro Ser Leu Val Ser Asn Asn Ile Glu Lys Ala Leu Val Asp Ala Phe
115 120 125

Gln Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His
130 135 140

Pro Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ala Lys Leu Gly Leu
145 150 155 160

Lys Pro Glu Lys Met Gln Ala Thr Arg His Val Leu Ser Glu Tyr Gly
165 170 175

Asn Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Arg
180 185 190

Lys Ser Lys Glu Asp Gly Leu Ala Thr Thr
195 200

<210> 103
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<222> (46)..(46)
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<400> 103
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aacaacaaag gtgcccgtgt gttggtggtt tgttcagaga taactgcagt tactttccgt
120

ggacccagtg acactcatct tgatagcctt gtggggcaag cattgtttgg agatggtgca
180

gcagctgtga ttgttggttc agaccctttg ccagaagttg agaagccttt gtttgaattg
240

gtatggaccg cacaaacaat cgctccagat agtgaaggag ccattgatgg tcaccttcgc
300

gaagcagggc tgacattcca tctcctcaag gatgttccta gccttgtctc aaataacatt
360

gagaaagctc ttgttgatgc ctttcaacct ttgaatatct ccgattacaa ttccatcttt
420

tggattgcac acccaggcgg accagcaatt cttgaccaag ttgaagctaa gttaggctta
480

aagccagaga aaatgcaatc cactcgacat gtacttagcg aatatggtaa catgtcgagt
540

gcgtgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga cggacttgcc
600

acaacag
607

<210> 104
<211> 591
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

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<222> (589)..(589)
<223> Any nucleotide

<400> 104
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60

caaaggtgcc cgtgtgttgg tggtttgttc agagataact gcagttactt tccgtggacc
120

cagtgacact caccttgata gccttgtggg gcaagcattg tttggagatg gtgcagcagc
180

tgtgattgtt ggttcagacc ctttgccaga agttgagaag cctttgtttg aattggtatg
240

gaccgcacaa acaatcgctc cagatagtga aggagccatt gatggtcacc ttcgcgaagc
300

agggctgaca ttccatctcc tcaaggatgt tcctagcctt gtctcaaata acattgagaa
360

agcgcttgtt gatgcctttc aacctttgaa tatttctgac tacaattcca tcttttggat

420

tgcacaccca ggcggaccag caattcttga ccaagttgaa gctaagttag gcttaaagcc
480

agagaaaatg caagccactc gacatgtact tagcgaatat ggtaacatgt caagtgcgtg
540

tgtgttattt atcttggatg anatgaggag gaagtcaaaa gaacacngnc t
591

<210> 105
<211> 590
<212> DNA
<213> Trifolium repens

<220>
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<400> 105
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60

ggtgcccgtg tgttggtggt ttgttcagag ataactgcag ttactttccg tggacccagt
120

gacactcacc ttgatagcct tgtggggcaa gcattgtttg gagatggtgc agcagctgtg
180

attgttggtt cagacccttt gccagaagtt gagaagcctt tgtttgaatt ggtatggacc
240

gcacaaacaa tcgctccaga tagtgaagga gccattgatg gtcaccttcg cgaagcaggg
300

ctgacattcc atctcctcaa ggatgttcct agccttgtct caaataacat tgagaaagcg
360

cttgttgatg cctttcaacc tttgaatatt tctgactaca attccatctt ttggattgca
420

cacccaggcg gaccagcaat tcttgaccaa gttgaagcta agttaggctt aaagccagag
480

aaaatgcaag ccactcgaca tgtacttagc gaatatggta acatgtcaag tgcgtgtgtg
540

ttatttatct tggatgagat gaggaggaag tcaaaagaag acggacttgc
590

<210> 106
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<213> Trifolium repens

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<400> 106
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ttggtacatc ttttgttacc tccaacaaaa aaatggtgac cgtagaagag attcgtaacg
120

cccaacgttc aaatggccct gccactatct tagcttttgg cacagccact ccttctaact
180

gtgtcactca agctgattat cctgattact actttcgtat caccaacagc gaacatatga
240

ctgatcttaa ggaaaaattc aagcggatgt gtgatagatc aatgataaag aaacgttaca
300

tgcacctaac agaagacttt ctgaaggaga atccaaatat gtgtgaatac atggcaccat
360

cactagatgt aagacgagac atagtggttg ttgaagnacc aaagctaggt aaagaancac
420

caaaaaaagc catatgngaa tggggacaac caaaatcnaa aatcacacat gcttggtttc
480

tgaccacttc cggtgntgac atgcccgggg
510

<210> 107
<211> 137
<212> PRT
<213> Trifolium repens

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<223> Any amino acid

<220>
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<222> (121)..(121)
<223> Any amino acid

<400> 107

Met Val Thr Val Glu Glu Ile Arg Asn Ala Gln Arg Ser Asn Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Phe Gly Thr Ala Thr Pro Ser Asn Cys Val Thr
20 25 30

Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Met Thr Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp Arg Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Asp Phe Leu Lys Glu Asn
65 70 75 80

Pro Asn Met Cys Glu Tyr Met Ala Pro Ser Leu Asp Val Arg Arg Asp
85 90 95

Ile Val Val Val Glu Xaa Pro Lys Leu Gly Lys Glu Pro Lys Lys Ala
100 105 110

Ile Xaa Glu Trp Gly Gln Pro Lys Xaa Lys Ile Thr His Ala Trp Phe
115 120 125

Leu Thr Thr Ser Gly Asp Met Pro Gly
130 135

<210> 108
<211> 240
<212> DNA
<213> Trifolium repens

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<222> (217)..(218)
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60

aagatgcaat cgttgaagcc atcaaacaag gttatagaca ctttgatact gctgctgctt
120

atggctcana acaagctctt ggtgaaggtt tgaaagaagc anttgaactt ggtcttgtca
180

ctanagaaga gctntttgtt acttctaaac tttgggnnac tgaaaatcat nctaaccttg
240

<210> 109
<211> 79
<212> PRT
<213> Trifolium repens

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<223> Any amino acid

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<223> Any amino acid

<220>
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<223> Any amino acid

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<223> Any amino acid

<220>
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<222> (77)..(77)
<223> Any amino acid

<400> 109

Gln Met Xaa Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr Cys Lys
1 5 10 15

Lys Asp Thr Lys Asp Ala Ile Val Glu Ala Ile Lys Gln Gly Tyr Arg
20 25 30

His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Xaa Gln Ala Leu Gly Glu
35 40 45

Gly Leu Lys Glu Ala Xaa Glu Leu Gly Leu Val Thr Xaa Glu Glu Xaa
50 55 60

Phe Val Thr Ser Lys Leu Trp Xaa Thr Glu Asn His Xaa Asn Leu
65 70 75

<210> 110
<211> 604
<212> DNA
<213> Trifolium repens

<220>
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<222> (13)..(13)
<223> Any nucleotide

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60

tgttattgaa ttcaggacac aaaatgccag tcataggaat gggaacatca gtagacaatc
120

gtccatcaaa tgatgttctt gcttcaatct ttgttgatgc aattgaagtt ggttatcgcc
180

atttcgattc tgcttctgtg tatggaacag aggaagccat aggaattgct ttagcaaaag
240

ctttagaaaa agggcttatt aagagtagag atgaagtttt catcacttca aagccatgga
300

atactgatgc agattatgaa cttattgttc cagctctcaa gaccacattg aaaaagctgg
360

ggacggagta tgtggatctt tatctgatcc attggccagt gagacttaga catgatcttg
420

aaaaccctgt tgttttcacc aaagaagatt tacttccctt tgatatagaa gggacatgga
480

aagctatgga agaatgttat aagttaggct tagcaaagtc tattggtata tgcaattatg
540

gtaccaaaaa actcaccaaa ctcttggaaa cagccaccat tacccctgca gtcaatcagg
600

tgga
604

<210> 111
<211> 189
<212> PRT
<213> Trifolium repens

<400> 111

Met Ala Gly Lys Lys Ile Pro Glu Val Leu Leu Asn Ser Gly His Lys
1 5 10 15

Met Pro Val Ile Gly Met Gly Thr Ser Val Asp Asn Arg Pro Ser Asn
20 25 30

Asp Val Leu Ala Ser Ile Phe Val Asp Ala Ile Glu Val Gly Tyr Arg

35 40 45

His Phe Asp Ser Ala Ser Val Tyr Gly Thr Glu Glu Ala Ile Gly Ile
50 55 60

Ala Leu Ala Lys Ala Leu Glu Lys Gly Leu Ile Lys Ser Arg Asp Glu
65 70 75 80

Val Phe Ile Thr Ser Lys Pro Trp Asn Thr Asp Ala Asp Tyr Glu Leu
85 90 95

Ile Val Pro Ala Leu Lys Thr Thr Leu Lys Lys Leu Gly Thr Glu Tyr
100 105 110

Val Asp Leu Tyr Leu Ile His Trp Pro Val Arg Leu Arg His Asp Leu
115 120 125

Glu Asn Pro Val Val Phe Thr Lys Glu Asp Leu Leu Pro Phe Asp Ile
130 135 140

Glu Gly Thr Trp Lys Ala Met Glu Glu Cys Tyr Lys Leu Gly Leu Ala
145 150 155 160

Lys Ser Ile Gly Ile Cys Asn Tyr Gly Thr Lys Lys Leu Thr Lys Leu
165 170 175

Leu Glu Thr Ala Thr Ile Thr Pro Ala Val Asn Gln Val
180 185

<210> 112
<211> 334
<212> DNA
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<220>
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<222> (17)..(17)
<223> Any nucleotide

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<222> (21)..(21)
<223> Any nucleotide

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<222> (277)..(277)
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<222> (328)..(328)
<223> Any nucleotide

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<222> (330)..(330)
<223> Any nucleotide

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<222> (334)..(334)
<223> Any nucleotide

<400> 112
gtgtagcagn attaganaaa natataaaaa aaaacatggc aggaaagaaa atcccagaag
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tgttattgaa ttcaggacac aaaatgccag tcataggaat gggaacatca gtagacaatc
120

gtccatcaaa tgatgttctt gcttcaatct ttgttgatgc aattgaagtt ggttatcgcc
180

atttcgattc tgcttctgtg tatggaacag aggaagccat aggaattgct ttagcaaaag
240

ctttanaaaa agggcttatt aagagtanag atgaagnttt natcacttgc aagncatgga
300

atactgatgc acattatgaa cttattgntn caan
334

<210> 113
<211> 602

<212> DNA
<213> Trifolium repens

<220>
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<222> (8)..(8)
<223> Any nucleotide

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<222> (14)..(14)
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<222> (20)..(20)
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<222> (22)..(22)
<223> Any nucleotide

<400> 113
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ttattgaatt caggacacaa aatgccagtc ataggaatgg gaacatcagt agacaatcgt
120

ccatcaaatg atgttcttgc ttcaatcttt gttgatgcaa ttgaagttgg ttatcgccat
180

ttcgattctg cttctgtgta tggaacagag gaagccatag gaattgcttt agcaaaagct
240

ttagaaaaag ggcttattaa gagtagagat gaagttttca tcacttcaaa gccatggaat
300

actgatgcag attatgaact tattgttcca gctctcaaga ccacattgaa aaagctgggg
360

acggagtatg tggatcttta tctgatccat tggccagtga gacttagaca tgatcttgaa
420

aaccctgttg ttttcaccaa agaagattta cttccctttg atatagaagg gacatggaaa
480

gctatggaag aatgttataa gttaggctta gcaaagtcta ttggtatatg caattatggt
540

accaaaaaac tcaccaaact cttggaaaca gccaccatta cccctgcagt caatcaggtg
600

ga
602

<210> 114
<211> 584
<212> DNA
<213> Trifolium repens

<220>
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<222> (4)..(5)
<223> Any nucleotides

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<222> (27)..(27)
<223> Any nucleotide

<400> 114
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60

attcaggaca caaaatgcca gtcataggaa tgggaacatc agtagacaat cgtccatcaa
120

atgatgttct tgcttcaatc tttgttgatg caattgaagt tggttatcgc catttcgatt
180

ctgcttctgt gtatggaaca gaggaagcca taggaattgc tttagcaaaa gctttagaaa
240

aagggcttat taagagtaga gatgaagttt tcatcacttc aaagccatgg aatactgatg
300

cagattatga acttattgtt ccagctctca agaccacatt gaaaaagctg gggacggagt
360

atgtggatct ttatctgatc cattggccag tgagacttag acatgatctt gaaaaccctg
420

ttgttttcac caaagaagat ttacttccct ttgatataga agggacatgg aaagctatgg
480

aagaatgtta taagttaggc ttagcaaagt ctattggtat atgcaattat ggtaccaaaa
540

aactcaccaa actcttggaa acagccacca ttacccctgc agtc
584

<210> 115
<211> 547
<212> DNA
<213> Trifolium repens

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<223> Any nucleotides

<220>
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<222> (27)..(27)
<223> Any nucleotide

<400> 115
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60

attcaggaca caaaatgcca gtcataggaa tgggaacatc agtagacaat cgtccatcaa
120

atgatgttct tgcttcaatc tttgttgatg caattgaagt tggttatcgc catttcgatt
180

ctgcttctgt gtatggaaca gaggaagcca taggaattgc tttagcaaaa gctttagaaa
240

aagggcttat taagagtaga gatgaagttt tcatcacttc aaagccatgg aatactgatg
300

cagattatga acttattgtt ccagctctca agaccacatt gaaaaagctg ggacggagt
360

atgtggatct ttatctgatc cattggccag tgagacttag acatgatctt gaaaaccctg
420

ttgttttcac caaagaagat ttacttccct ttgatataga agggacatgg aaagctatgg
480

aagaatgtta taagttaggc ttagcaaagt ctattggtat atgcaattat ggtaccaaaa
540

aactcac
547

<210> 116
<211> 334
<212> DNA
<213> Trifolium repens

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60

taggaatggg aacatcagta gacaatcgtc catcaaatga tgttcttgct tcaatctttg
120

ttgatgcaat tgaagttggt tatcgtcatt tcgattctgc ttctgtttat ggaacagagg
180

aagctatagg aattgcttta gcaaaagctt tagaaaaagg gcttattaag agtagagatg
240

aagttttcat cacttcaaag ccatggaata ctgatgcaga ttatgatctt attgntccag
300

ctctcaagac cacattgaaa aagctgggga caga
334

<210> 117

<211> 694
<212> DNA
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<222> (101)..(101)
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<222> (106)..(106)
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<400> 117
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gncttaaagt gtgtaacata ttcttaactt aaannntttt nacccnacaa aaaaaaacaa 120

agacaataac atgggtagtg ttgaaattcc aacaaaggtt cttactaaca cttctagtca 180

agtgaaaatg cctgtggttg gaatgggatc agctcctgat ttcacatgta agaaagatac 240

aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata ctgctgctgc 300

ttatggctca gaacaagctc ttggtgaagg tttgaaagaa gcaattgaac ttggccttgt 360

cactagagaa gagcttttg ttacttctaa actttgggtc actgaaaatc atcctcacct 420

tgttgttcct gctcttcaaa aatctctcaa gactcttcaa ttggagtact tggacttgta 480

tttgatccat tggccactta gttctcagcc tggaaagttt tcatttccaa ttgatgtggc 540

agatctcttg ccatttgatg tgaagggtgt ttgggaatcc atggaagaag gcttgaaact 600

tggactcact aaagctattg gtgttagtaa cttctctgtc aagaaacttc aaaatcttgt 660

ctcagttgcc accgttcttc ctgcggtcaa tcag 694

<210> 118
<211> 188
<212> PRT
<213> Trifolium repens

<400> 118

Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Thr Ser Ser
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Gln Val Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
20 25 30

Cys Lys Lys Asp Thr Lys Asp Ala Ile Ile Glu Ala Ile Lys Gln Gly
35 40 45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
50 55 60

Gly Glu Gly Leu Lys Glu Ala Ile Glu Leu Gly Leu Val Thr Arg Glu

65 70 75 80

Glu Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
85 90 95

Leu Val Val Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Glu
100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Gly Leu Lys Leu Gly Leu Thr
145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Asn Leu
165 170 175

Val Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln
180 185

<210> 119
<211> 576
<212> DNA
<213> Trifolium repens

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gnctnaaagt gtgtaacata ttcttaactt aaacnatttt cacccaacaa aaaaaaacaa
120

agacaataac atgggtagtg ttgaaattcc aacaaaggtt cttactaaca cttctagtca
180

agtgaaaatg cctgtggttg gaatgggatc agctcctgat ttcacatgta agaaagatac
240

aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata ctgctgctgc
300

ttatggctca gaacaagctc ttggtgaagg tttgaaagaa gcaattgaac ttggtcttgt
360

cactagagaa gagcttttttg ttgcttctaa actttgggtc actgaaaatc atcctcatct
420

tgttgttcct gctcttcaaa aatctctcaa gactcttcaa ttggagtact tggacttgta
480

tttgattcac tggccactta gttctcagcc cggaaagttt tcatttccaa ttgaggtggc
540

agatctcttg ccatttgatg tgaagggtgt ttgggg
576

<210> 120
<211> 524
<212> DNA
<213> Trifolium repens

<220>
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<222> (13)..(14)
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<223> Any nucleotide

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attcttaact taaacnattt tcacccaaca aaaaaaaaca aagacaataa catgggtagt 120

gttgaaattc caacaaaggt tcttactaac acttctagtc aagtgaaaat gcctgtggtt 180

ggaatgggat cagctcctga tttcacatgt aagaaagata caaaagatgc aatcattgaa

240

gccatcaaac aaggttatag acactttgat actgctgctg cttatggctc agaacaagct
300

cttggtgaag gtttgaaaga agcaattgaa cttggtcttg tcactagaga agagcttttt
360

gttgcttcta aactttgggt cactgaaaat catcctcatc ttgttgttcc tgctcttcaa
420

aaatctctca agactcttca attggagtac ttggacttgt atttgattca ctggccactt
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120

acacttctag tcaagtgaaa atgcctgtgg ttggaatggg atcagctcct gatttcacat
180

gtaagaaaga tacaaaagat gcaatcattg aagccatcaa acaaggttat agacactttg
240

atattgctgc tgcttatggc tcagaacaag ctcttggtga aggtttgaaa gaagcaattg
300

aacttggtct tgtcactaga gaagaccttt ttgttacttc taaactttgg gtcactgaaa
360

atcatcctca ccttgttatt cctgctcttc aaaaatctct caagactctt caattggagt
420

acttggactt gtatttgatc cactggccac ttagttctca gcccggaaag ttttcatttc
480

caattgaggt ggcagatctc ttgccatttg atgtgagggg tgtttggcaa tccatggaag
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aaggcttgaa acttggactc actaaagcta ttggtgt
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120

acttctagtc aagtgaaaat gcctgtggtt ggaatgggat cagctcctga tttcacatgt
180

aagaaagata caaaagatgc aatcattgaa gccatcaaac aaggttatag acactttgat
240

attgctgctg cttatggctc agaacaagct cttggtgaag gtttgaaaga agcaattgaa
300

cttggtcttg tcactagaga agaccttttt gttacttcta aactttgggt cactgaaaat
360

catcctcacc ttgttattcc tgctcttcaa aaatctctca agactcttca attggagtac
420

ttggacttgt atttgatcca ctggccactt agttctcagc ccggaaagtt ttcatttcca
480

attgaggtgg cagatctctt gccatttgat gtgaggggtg tttggcaatc catggaagaa
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120

gttctagtca agtgaaaatg cctgtggttg gaatgggatc agctcctgac ttcacatgta
180

agaaagacac aaaagatgca atcattgaag ccatcaaaca aggntataga cactttgaaa
240

ctgctgctgn ttatgcntca caacaagctc ttgnnnnann cttcnatgcc ccn
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aaaaaaacaa agacaacaac atgggnaggg ttgaaattcc aacaaaggtt cttactaaca
120

cttctagtca agtgaaaatg cctgtggttg gaatgggatc agctcctgat tttacatgta
180

aaaaagacac aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata
240

ctgntgctgc ttatggctca naacaagctc ttggtgaagg tttgaaagaa gcaattgaac
300

ttggccttgt cactagaaaa gagctttttg ttacttctaa actttgggtc actgaaaatc
360

atcctcacct tgttgttcct gctcttcaaa aatctctcaa gactcttcaa ttggagtact
420

tggacttgta tttgatccat tggccactta attctcancc tggaaagttt tcatttccca
480

ttgangtggc aaatctcttg ccatttnatg tgaanggtgt ttgggaatcc atggaaaaan
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gcttnaaact tggactcact aaagctattg gtgncannaa cttctctntc aanaaacttc
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aaaatcttnt ctcaattgcc accgttcttn ctgcgg
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120

tagtcaagtg aaaatgcctg tggttggaat gggatcagca cctgatttca catgtaagaa
180

agacacaaaa gatgcaatca ttgaagccat caaacaaggt tatagacact ttgatactgc
240

tgctgcttat ggctcagaac aagctcttgg tggaggtttg aaagaagcaa ttgaacttgg
300

ccttgtcact agagaagagc tttttgttac ttctaaactt tgggtcactg aaaatcatcc
360

tcaccttgtt gttcctgctc ttcaaaaatc tctcaagact cttcaattgg agtacttgga
420

cttgtatttg atccattggc cacttagttc tcagcctgga aagttttcat ttccaattga
480

tgtggcagat ctcttgccat ttgatgtgaa gggtgtttgg caatccatgg aagaaggctt
540

gaaacttgga ctcactaaag ctattggtgt
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120

tcaagtgaaa atgcctgtgg ttggaatggg atcagctcct gatttcacat gtaagaaaga
180

tacaaaagat gcaatcattg aagccatcaa acaaggttat agacactttg atactgctgc
240

tgcttatggc tcagaacaag ctcttggtga aggtttgaaa gaagcaattg aacttggcct
300

tgtcactaga gaagagcttt ttgttacttc taaactttgg gtcactgaaa atcatcctca
360

tcttgttgtt cctgctcttc aaaaatctct caagactctt caattggagt acttggactt
420

gtatttgatc cattggccac ttagttctca gcctggaaag ttttcatttc caattgatgt
480

ggcagatctc ttgccatttg atgtgaaggg tgtttgggaa tccatggaag aaggcttgaa
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acttggactc actaaagcta ttggtgttag taacttctct gtcaagaaac ttcaaaatct
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tgtctcagtt gccaccgttc t
621

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120

caagtgaaaa tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac
180

acaaaagatg caatcattga agccatcaaa caaggttata gacactttga tactgctgct
240

gcttatggct cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt
300

gtcactagag aagagctttt tgttacttct aaactttggg tcactgaaaa tcatcctcac
360

cttgttgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa
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cttggactca ctaaagctat tggtgttagt aan
573

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120

caagtgaaaa tgcctgtggt tggaatggga tcagctcctg atttcacatg taagaaagat
180

acaaaagatg caatcattga agccatcaaa caaggttata gacactttga tactgctgnt
240

gcttatggct cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt
300

gtcactagag aagagctttt tgttacttct aaactttggg tcactgaaaa tcatcctcac
360

cttgttattc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa
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cttggactca ctaaagctat tggtgttagt aacttctctg tcc
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120

caagtgaaaa tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac
180

acaaaagatg caatcattga agccatcaaa cagggttata gacactttga tactgctgct
240

gcttatggct cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggtctt
300

gtcactagag aagacctttt tgttacttct aaactttggg tcactgaaaa tcatcctcat
360

cttgttgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa
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120

caagtgaaaa tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac
180

acaaaagatg caatcattga agccatcaaa caaggttata gacactttga tactgctgct
240

gcttatggct cagaacaagc tcttggtgga ggtttgaaag aagcaattga acttggcctt
300

gtcactagag aagagctttt tgttacttct aaactttggg tcactgaaaa tcatcctcac
360

cttgttgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttggcaat ccatggaaga aggcttgaaa
540

cttggactca ctaaagctat tggtgttagt aacttctctg tcaagaaact tcaaaat
597

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120

tgcctgtggt tggaatggga tcagctcctg atttcacatg taagaaagat acaaaagatg
180

caatcattga agccatcaaa caaggttata gacactttga tactgctgct gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300

aagagctttt tgttacttct aaactttggg tcactgaaaa tcatcctcac cttgttgttc
360

ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg gcagatctct
480

tgccatttga tgtgaagggt gtttgggaat ccatggaana aggcttgaaa cttggactcn
540

ctaaagctat tggtgttann nacttctntg tnan
574

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120

tgcctgtggt tggaatggga tcagctcctg atttcacatg taagaaagat acaaaagatg
180

caatcattga agccatcaaa caaggttata gacactttga tactgctgct gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300

aagagctttt tgttacttct aaactttggg tcactgaaaa tcatcctcac cttgttgttc
360

ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag cctggaaagt tttcatttcc aattgatgtg gcagatctct
480

tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa cttggactca
540

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578

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120

tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaaagac acaaaagatg
180

caatcattga agccatcaaa caaggttata gacactttga tactgctgct gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300

aagagctttt tgttacttct aaactttggg tcactgaaaa tcatcctcac cttgttgttc
360

ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag cccgaaaagt tttcatttcc aattgatgtg gcagatctct
480

tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa cttggactca
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120

atgggatcag ctcctgattt cacatgtaag aaagatacaa aagatgcaat cattgaagcc
180

atcaaacaag gttatagaca ctttgatact gctgctgctt atggctcaga acaagctctt
240

ggtgaaggtt tgaaagaagc aattgaactt ggccttgtca ctagagaaga gctttttgtt
300

acttctaaac tttgggtcac tgaaaatcat cctcaccttg ttgttcctgc tcttcaaaaa
360

tctctcaaga ctcttcaatt ggagtacttg gacttgtatt tgatccattg gccacttagt
420

tctcagcctg gaaagttttc atttccaatt gatgtggcag atctcttgcc atttgatgtg
480

aagggtgttt gggaatccat ggaagaaggc ttgaaacttg gactcactaa agctattggt
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gttagtaact tctctgtcaa gaaacttcaa aatcttgtct cagttgccac cgttcttcct
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cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt 180

ggaagcaatg gaaggagcaa agggtcatct caaatttttc gaaatggatc ttcttaacag 240

cgactctatt gcggccgccg tgaaaggttg tgccggagtt atacatcttg catgtcctaa 300

catcattggt gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaac 360

ggttaatgtg ttgaaggtgg caaaggaagc aggggtggag cgtgtggtgg cgacatcgtc 420

gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg 480

ttggacagac cttgattatt gcaaggaaaa gaagttatac taccccattg caaagacact 540

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35 40 45

Glu Gly Ala Lys Gly His Leu Lys Phe Phe Glu Met Asp Leu Leu Asn
50 55 60

Ser Asp Ser Ile Ala Ala Ala Val Lys Gly Cys Ala Gly Val Ile His
65 70 75 80

Leu Ala Cys Pro Asn Ile Ile Gly Glu Val Lys Asp Pro Glu Lys Gln
85 90 95

Ile Leu Glu Pro Ala Ile Gln Gly Thr Val Asn Val Leu Lys Val Ala
100 105 110

Lys Glu Ala Gly Val Glu Arg Val Val Ala Thr Ser Ser Ile Ser Ala
115 120 125

Ile Ile Pro Ser Pro Asn Trp Pro Ala Asp Lys Ile Lys Gly Glu Asp
130 135 140

Cys Trp Thr Asp Leu Asp Tyr Cys Lys Glu Lys Lys Leu Tyr Tyr Pro
145 150 155 160

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120

cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
180

ggaagcaatg gaaggagcaa agggtcatct caaatttttc gaaatggatc ttcttaacag
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cgactctatt gcggncgccg tgaaaggttg ngccggagtt atacatnttg nctgtcctac
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120

cggctacatc gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
180

ggaagcaatg gaaggggcaa agggtcatct taaatttttc gaaatggatc ttcttaacag
240

tgactctatt gcggccgccg tgaaaggttg tgccggagtt atacatnttg catgtgctaa
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120

cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
180

ggaagcaatg gaaggagcaa agggtcatct caaatttttt gaaatggatc ttcttaacag
240

cgactctatt gcggccgccg tgaaaggttg tgccggagtt atacatcttg catgtcctaa
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catcattggt gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaac
360

ggttaatgtg ttgaaggtgg caaaggaagc aggggtggag cgtgtggtgg cgacatcgtc
420

gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg
480

ntggacagac cttgattatt gcaangaaaa gaagttatac taccccattg caaagacatt
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cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
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ggaagcaatg gaaggagcaa agggtcatct caaatttttc gaaatggatc ttctcaacag
240

cgactctatt gcggccgccg tgaaaggttg tgccggagtt atacatcttg catgtcctag
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catcattggt gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaac
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420

gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg
480

ttggacagac cttgattatt gcaaggaaaa gaagttatac taccccattg caaagacact
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gctacattgt ccacgccacc atccaagatc tcgaggatga gaacgagaca aaacatttgg 180

aagcaatgga aggagcaaag ggtcatctca aatttttcga aatggatctt cttaacagcg 240

actctattgc ggccgccgtg aaaggttgtg ccggagttat acatcttgca tgtcctaaca 300

tcattggtga agtcaaagac cccgagaagc aaattttgga accggcaatt caaggaacgg 360

ttaatgtgtt gaaggtggca aaggaagcag gggtggagcg tgtggtggcg acatcgtcga 420

tctctgccat cataccgagt cctaattggc cagctgataa gattaaggga gaagattgtt 480

ggacagacct tgattattgc aaggaaaaga agttatacta ccccattgca aagacactag 540

cagaaaaagc tggttgggaa tttgctagag agaccggttt tgt 583

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120

gctacattgt ccacgccacc atccaagatc tcgaggatga gaacgagaca aaacatttgg
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aagcaatgga aggagcaaag ggtcatctca aatttttcga aatggatctt ctcaacagcg
240

actctattgc ggccgccgtg aaaggttgtg ccggagttat acatcttgca tgtcctagca
300

tcattggtga agtcaaagac cccgagaagc aaattttgga accggcaatt caaggaacgg
360

ttaatgtgtt gaaggtggca aaggaagcag gggtggagcg tgtggtggcg acatcgtcga
420

tctccgccat cataccgagt cctaattggc cagctgataa gattaaggga gaagattgtt
480

ggacagacct tgattattgc aaggaaaaga agttatacta ccccattgca aagacactag
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acattgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa catttggaag
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caatggaagg agcaaagggt catctcaaat tttttgaaat ggatcttctt aacagcgact
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ctattgcggc cgccgtgaaa ggttgtgccg gagttataca tcttgcatgt cctaacatca
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ttggtgaagt caaagacccc gagaagcaaa ttttggaacc ggcaattcaa ggaacggtta
360

atgtgttgaa ggtggcaaag gaagcagggg tggagcgtgt ggtggcgaca tcgtcgatct
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ccgccatcat accgagtcct aattggccag ctgataagat taagggagaa gattgttgga
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acatcgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa catttggaag
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caatggaagg ggcaaagggt tatcttaaat ttttcgaaat ggatcttctt aacagtgact
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ctattgcggc cgccgtgaaa ggttgtgccg gagttataca tcttgcatgt cctaacatca
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420

ccgccatcat accgagtcct aattggccag ctgataagat taagggagaa gattgttgga
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120

cattgtccac gccaccatcc aagatctcga ggatgagaac gagacaaaac atttggaagc
180

aatggaagga gcaaagggtc atctcaaatt ttttgaaatg gatcttctta acagcgactc
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60

ccacgcggnt acattgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa
120

catttggaag caatggaagg agcaaagggt catntnaaat ttttcgaaat ggatcttntt
180

aacagngact ctattgcggc cgccgtgaaa ggttgtgccg gagttataca tn
232

<210> 147
<211> 623
<212> DNA
<213> Trifolium repens

<220>
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<222> (11)..(11)
<223> Any nucleotide

<220>
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<222> (14)..(14)
<223> Any nucleotide

<400> 147
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60

gttttgtgtt acagggggca ctggcttcat agcagcctac ctagtgaaag ccttattaga
120

aaagggtcac acagtaagga ctactgtaag aaacccagat gatttggaga aggttggtta
180

tctaactgaa ctaagtgaag acaaagagag attgaagatt ttaaaagcag atctattggt
240

ggaagggagt tttgatgagg cagtgagtgg tgttgatggt gtgtttcata cagcttcccc
300

tgttcttgtt ccacatgatg acaacattca ggttactttg attgatccat gtataaaagg
360

aacacaaaat gtgcttaact catgcatcaa agcaaaggtg aaacgtgtgg tgttaacatc
420

ttcatgctct tccataagat accgtgacga tgtgcaacaa atttctcctc ttaatgaatc
480

tcattggagt gattctgaat actgcaaacg ctataacctg tggtatgcat atgcaaagac
540

tttaggagaa aaagaagcat ggaggattgc aaaggaaagt ggaattgatc tagttgtagt
600

taacccctct tttgttggtg gtc
623

<210> 148
<211> 190
<212> PRT
<213> Trifolium repens

<400> 148

Met Pro Glu Phe Cys Val Thr Gly Gly Thr Gly Phe Ile Ala Ala Tyr
1 5 10 15

Leu Val Lys Ala Leu Leu Glu Lys Gly His Thr Val Arg Thr Thr Val
20 25 30

Arg Asn Pro Asp Asp Leu Glu Lys Val Gly Tyr Leu Thr Glu Leu Ser
35 40 45

Glu Asp Lys Glu Arg Leu Lys Ile Leu Lys Ala Asp Leu Leu Val Glu
50 55 60

Gly Ser Phe Asp Glu Ala Val Ser Gly Val Asp Gly Val Phe His Thr
65 70 75 80

Ala Ser Pro Val Leu Val Pro His Asp Asp Asn Ile Gln Val Thr Leu
85 90 95

Ile Asp Pro Cys Ile Lys Gly Thr Gln Asn Val Leu Asn Ser Cys Ile
100 105 110

Lys Ala Lys Val Lys Arg Val Val Leu Thr Ser Ser Cys Ser Ser Ile
115 120 125

Arg Tyr Arg Asp Asp Val Gln Gln Ile Ser Pro Leu Asn Glu Ser His
130 135 140

Trp Ser Asp Ser Glu Tyr Cys Lys Arg Tyr Asn Leu Trp Tyr Ala Tyr
145 150 155 160

Ala Lys Thr Leu Gly Glu Lys Glu Ala Trp Arg Ile Ala Lys Glu Ser
165 170 175

Gly Ile Asp Leu Val Val Val Asn Pro Ser Phe Val Gly Gly
180 185 190

<210> 149
<211> 570
<212> DNA
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<220>
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<222> (14)..(14)
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<400> 149
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gttttgtgtt acagggggca ctgggttcat agcagcctac ctagtgaaag ccttattaga
120

aaagggtcac acagtaagga ctactgtaag aaacccagat gatttggaga aggttggtta
180

tctaactgaa ctaagtgaag acaaagagag attgaagatt ttaaaagcag atctattggt
240

ggaagggagt tttgatgagg cagtgagtgg tgttgatggt gtgtttcata cagcttcccc
300

tgttcttgtt ccacatgatg acaatattca ggttactttg attgatccat gtataaaagg
360

aacacaaaat gtgcttagct catgcatcaa agcaaaggtg aaacgtgtgg tgttaacatc
420

ttcatgctct tccataagat accgtgacga tgtgcaacaa atttcaccac ttaatgaatc
480

tcattggagt gattctgaat actgcaaacg ctataacctg tggtatgcat atgcaaagac
540

attaggagaa aaagaagcat ggaggattgc
570

<210> 150
<211> 572
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(2)
<223> Any nucleotide

<220>
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<222> (8)..(9)
<223> Any nucleotides

<400> 150
gnacctcnna aaaatagaag aaaagagatg cctgagtttt gtgttacagg gggcactggg
60

ttcatagcag cctacctagt gaaagcccta ttagaaaagg gtcacacagt aaggactact

120

gtaagaaacc cagatgattt ggagaaggtt ggttatctaa ctgaactaag tgaagacaaa
180

gagagattga agattttaaa agcagatcta ttggtggaag ggagttttga tgaggcagtg
240

agtggtgttg atggtgtgtt tcatacagct tcccctgttc ttgttccaca tgatgacaat
300

attcaggtta ctttgattga tccatgtata aaaggaacac agaatgtgct taactcatgc
360

atcaaagcaa aggtgaaacg tgtggtgtta acatcctcat gctcttccat aagataccgt
420

gacgatgtgc aacaaatttc tcctcttaat gaatctcatt ggagtgattc tgattactgc
480

aaacgctata acctgtggta tgcatatgca aagactttag gagaaaaaga agcatggagg
540

attgcaaagg aaagtgggat taatctagtt gt
572

<210> 151
<211> 572
<212> DNA
<213> Trifolium repens

<400> 151
ggaaagagat gcctgagttt tgtgttacag ggggcactgg cttcatagca gcttacctag
60

tgaaagcctt attagaaaag ggtcacacag taaggactac tgtaagaaac ccagatgatt
120

tggagaaggt tggttatcta actgaactta gtgaagacaa agagagattg aagattttaa
180

aagcagatct attggtggaa gggagttttg atgaggcagt gagtggtgtt gatggtgtgt
240

ttcatacagc ttcccctgtt cttgttccac atgatgacaa cattcaggtt actttgattg
300

atccatgtat aaaaggaaca caaaatgtgc ttaactcatg catcaaagca aaggtgaaac
360

gtgtggtgtt aacatcttca tgctcttcca taagataccg tgacgatgtg caacaaattt
420

ctcctcttaa tgaatctcat tggagtgatt ctgaatactg caaacgctat aacctgtggt
480

atgcatatgc aaagacttta ggagaaaaag aagcatggag gattgcaaag gaaagtggaa
540

ttgatctagt tgtagttaac cctcttttg tt
572

<210> 152
<211> 574

<212> DNA
<213> Trifolium repens

<220>
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<222> (40)..(40)
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<400> 152
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60

gccttattag aaaagggtca cacagtaagg actactgtaa gaaacccaga tgctttggag
120

aaggttggtt atctaactga acttagtgaa gacaaagaga gattgaagat tttaaaagca
180

gatctattgg tggaagggag ttttgatgag gcagtgagtg gtgttgatgg tgtgtttcat
240

acagcttccc ctgttcttgt tccacatgat gacaacattc aggttacttt gattgatcca
300

tgtataaaag gaacacaaaa tgtgcttaac tcatgcatca tagcaaaggt gaaacgtgtg
360

gtgttaacat cttcatgctc ttccataaga taccgtgacg atgtgcaaca aatttctcct
420

cttaatgaat ctcattggag tgattctgaa tactgcaaac gctataacct gtggtatgca
480

tatgcaaaga ctttaggaga aaaagaagca tggaggattg caaaggaaag tggaattgat
540

ctagttgtag ttaacccctc ttttgttggt ggtc
574

<210> 153
<211> 641
<212> DNA
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<220>
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<220>
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<222> (641)..(641)
<223> Any nucleotide

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60

ccctactcca aaaacactac aaaattcacg ccacaatctt ccccaattcc aacgcatctc
120

atctcttcac actccacccg gaagctcaat cccggatcac aattttccct gtcgatatcc
180

tcgactccac cgccgtcttc tccgctatca ataactgctc aggtgtcttt catgccgctt
240

ctccatgtac cctcgaagat ccaactgatc cgcaaaaaga gcttctagaa cctgctgtac
300

aaggaaccct aaatgttcta gaagcatcca gcgcgcaggt accaaaccct aattggccgg
360

agaaaaaggc gatcgatgag gcgtcgtgga cggatgttga gtactgtaaa ttgagaggga
420

agtggtatct ggtgtcgaaa acggaggcgg agaaggcggc ttgggatttt cgagagaaaa
480

atggtggtgt tgatgtgggg gcggntcatc cggggacttg tttgggagag ttgatacaga

540

aggagttgaa tgcgagttca gcggntttac agaggttgat gatggggagt gaggatactc
600

aagagtgnta ttggnngggg ggctgnnnat gntaaagatg n
641

<210> 154
<211> 206
<212> PRT
<213> Trifolium repens

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<223> Any amino acid

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<223> Any amino acid

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<223> Any amino acid

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<222> (204)..(204)
<223> Any amino acid

<400> 154

Glu Xaa Leu Val Cys Val Thr Arg Xaa Asn Gly Phe Ile Gly Thr Trp
1 5 10 15

Leu Val Lys Thr Leu Leu Gln Lys His Tyr Lys Ile His Ala Thr Ile
20 25 30

Phe Pro Asn Ser Asn Ala Ser His Leu Phe Thr Leu His Pro Glu Ala
35 40 45

Gln Ser Arg Ile Thr Ile Phe Pro Val Asp Ile Leu Asp Ser Thr Ala
50 55 60

Val Phe Ser Ala Ile Asn Asn Cys Ser Gly Val Phe His Ala Ala Ser
65 70 75 80

Pro Cys Thr Leu Glu Asp Pro Thr Asp Pro Gln Lys Glu Leu Leu Glu
85 90 95

Pro Ala Val Gln Gly Thr Leu Asn Val Leu Glu Ala Ser Ser Ala Gln
100 105 110

Val Pro Asn Pro Asn Trp Pro Glu Lys Lys Ala Ile Asp Glu Ala Ser
115 120 125

Trp Thr Asp Val Glu Tyr Cys Lys Leu Arg Gly Lys Trp Tyr Leu Val
130 135 140

Ser Lys Thr Glu Ala Glu Lys Ala Ala Trp Asp Phe Arg Glu Lys Asn
145 150 155 160

Gly Gly Val Asp Val Gly Ala Xaa His Pro Gly Thr Cys Leu Gly Glu
165 170 175

Leu Ile Gln Lys Glu Leu Asn Ala Ser Ser Ala Leu Gln Arg Leu Met
180 185 190

Met Gly Ser Glu Asp Thr Gln Glu Xaa Tyr Trp Xaa Gly Gly
195 200 205

<210> 155
<211> 822
<212> DNA
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<222> (614)..(614)
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120

tcctccgcgg ctacactgtt cacgccaccg tccaaaatct caatgatgag aacgaaacga
180

agcatctaga agctctcgaa ggagcacaaa ctaatctccg tctcttccag atcgatctcc
240

ttaactacga cacaatcctc gctgctgtcc gcggttgcgt cggaattttc cacctcgctt
300

caccttgcac tgtagacaaa gttcatgatc ctcagaagga gcttttggat cctgcaatta
360

aagggacttt gaatgtgctt actgcagcta aggaagtagg ggtgaagcgt gtggttgtta
420

cctcgtctgt ctcggcgatt actcctagtc ctgattggcc ttctgatgtt gttaaaagag
480

aggattgttg gactgatgtt gaatattgca agaaaaaaga gttggggtat ccgttgtcca
540

aaacattggc tgaaaaagct gcgtgggatt tttncaaaga aaatggtttg gatgttgttg
600

nggtgaatcc cggnactgng atgggtcctg tttttccacc acggcataat gcaagcatgc
660

tcatgccttg ggaaactttt ttgaaggctg gnnctgaaac atttgaagac tattttatgg
720

gattggccnn ctttaaagat gtngcattgg cncatnnttt ggggtatgag aacaaanann
780

ctttgggana catnggnggg ttgaaactat cnntccttac gg
822

<210> 156
<211> 256
<212> PRT
<213> Trifolium repens

<220>
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<400> 156

Met Ser Lys Leu Val Cys Val Thr Gly Gly Ser Gly Cys Ile Gly Ser
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Trp Leu Val His Leu Leu Leu Leu Arg Gly Tyr Thr Val His Ala Thr
20 25 30

Val Gln Asn Leu Asn Asp Glu Asn Glu Thr Lys His Leu Glu Ala Leu
35 40 45

Glu Gly Ala Gln Thr Asn Leu Arg Leu Phe Gln Ile Asp Leu Leu Asn
50 55 60

Tyr Asp Thr Ile Leu Ala Ala Val Arg Gly Cys Val Gly Ile Phe His
65 70 75 80

Leu Ala Ser Pro Cys Thr Val Asp Lys Val His Asp Pro Gln Lys Glu
85 90 95

Leu Leu Asp Pro Ala Ile Lys Gly Thr Leu Asn Val Leu Thr Ala Ala
100 105 110

Lys Glu Val Gly Val Lys Arg Val Val Val Thr Ser Ser Val Ser Ala
115 120 125

Ile Thr Pro Ser Pro Asp Trp Pro Ser Asp Val Val Lys Arg Glu Asp
130 135 140

Cys Trp Thr Asp Val Glu Tyr Cys Lys Lys Lys Glu Leu Gly Tyr Pro
145 150 155 160

Leu Ser Lys Thr Leu Ala Glu Lys Ala Ala Trp Asp Phe Xaa Lys Glu
165 170 175

Asn Gly Leu Asp Val Val Xaa Val Asn Pro Xaa Thr Xaa Met Gly Pro
180 185 190

Val Phe Pro Pro Arg His Asn Ala Ser Met Leu Met Pro Trp Glu Thr
195 200 205

Phe Leu Lys Ala Xaa Xaa Glu Thr Phe Glu Asp Tyr Phe Met Gly Leu
210 215 220

Ala Xaa Phe Lys Asp Xaa Ala Leu Xaa His Xaa Leu Gly Tyr Glu Asn
225 230 235 240

Lys Xaa Xaa Leu Gly Xaa Xaa Xaa Gly Leu Lys Leu Xaa Xaa Leu Thr
245 250 255

<210> 157
<211> 535
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

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<223> Any nucleotide

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agctagtttg cgtcaccggc ggcagcggat gcatcggttc atggctagtc catctccttc
120

tcctccgcgg ctacactgtt cacgccaccg tccaaaatct caatgatgag aacgaaacga
180

agcatctaga agctctcgaa ggagcacaaa ctaatctccg tctcttccag atcgatctcc
240

ttaactacga cacaatcctc gctgctgtcc gcggttgcgt cggaattttc cacctcgctt
300

caccttgcac tgtagacaaa gttcatgatc ctcagaagga gcttttggat cctgcaatta
360

aagggacttt gaatgtgctt actgcagcta aggaagtagg ggtgaagcgt gtggttgtta
420

cctcgtctgt ctcggcgatt actcctagtc ctgattggcc ttctgatgtt gttaaaagag
480

aggattgttg gactgatgtt gaatattgca agaaaaaaga gttgtggtat ccgtt
535

<210> 158
<211> 801
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

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<222> (5)..(6)
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<222> (553)..(553)
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<222> (776)..(776)
<223> Any nucleotide

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<222> (791)..(792)
<223> Any nucleotides

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gnggcggatg catcggttca tggctagtcc atctccttct cctccgcggc tacactgttc
120

acgccaccgt ccaaaatctc aatgatgaga acgaaacgaa gcatctagaa gctctcgaag
180

gagcacaaac taatctccgt ctcttccaga tcgatctcct taactacgac acaatcctcg
240

ctgctgtccg cggttgcgtc ggaattttcc acctcgcttc accttgcact gtagacaaag
300

ttcatgatcc tcagaaggag cttttggatc ctgcaattac agggactttg aatgtgctta
360

ctgcagctaa ggaagtaggg gtgaagcgtg tggttgttac ctcgtctgtc tcggcgatta
420

ctcctagtcc tgattggcct tctgatgttg ttaaaagaga ggattgttgg actgatgttg
480

aatattgcaa gaaaaaagag ttggggtatc cgttgtccaa aacattggct gaaaaagctg
540

cgtgggattt ttncaaagaa aatggtttgg atgttgttgn ggtgaatccc ggnactgnga
600

tgggtcctgt ttttccacca cggcataatg caagcatgct catgccttgg gaaacttttt
660

tgaaggctgg nnctgaaaca tttgaagact attttatggg attggccnnc tttaaagatg
720

tngcattggc ncatnntttg gggtatgaga acaaanannc tttggganac atnggngggt
780

tgaaactatc nntccttacg g
801

<210> 159
<211> 582
<212> DNA
<213> Trifolium repens

<400> 159
gtcacttatg aaatggaaca caaaggtgga gacaaagtat gtgtgacagg ggcatcaggc
60

tttttagcat cttggcttat taagaaactt cttttgtctg gctatcaagt cattggaaca
120

gttagagatt tagggaagaa gaagaaagtt gaacatttat ggaaattgga aggagcaaca
180

gaaagactag aactaatcca agctgattta atggaagaaa atagtttcga caaagcgatc
240

atgggatgca aaggtgtctt ccacattgcc tctccagtac tcaatcatat atcagataat
300

cctaaggcgg aaatcttgga accggcagtc caaggtacgc taaatgtgtt gcgttcttgt
360

aagaggaacc ccgatcttgt tcgagtggtg ctagcctcat catcttcggc tgttagagta
420

agagctgatt ttgatccaag cataccaatt gatgaatcat cttggagctc cttggaattg
480

tgcgagaaac tcaaggcatg gtacccaatg tcaaagacaa tggcagaaaa agcagcttgg
540

gaatatagca aagagaatgg aatagactta gtgactattt tc
582

<210> 160
<211> 190
<212> PRT
<213> Trifolium repens

<400> 160

Met Glu His Lys Gly Gly Asp Lys Val Cys Val Thr Gly Ala Ser Gly
1 5 10 15

Phe Leu Ala Ser Trp Leu Ile Lys Lys Leu Leu Leu Ser Gly Tyr Gln
20 25 30

Val Ile Gly Thr Val Arg Asp Leu Gly Lys Lys Lys Lys Val Glu His
35 40 45

Leu Trp Lys Leu Glu Gly Ala Thr Glu Arg Leu Glu Leu Ile Gln Ala
50 55 60

Asp Leu Met Glu Glu Asn Ser Phe Asp Lys Ala Ile Met Gly Cys Lys
65 70 75 80

Gly Val Phe His Ile Ala Ser Pro Val Leu Asn His Ile Ser Asp Asn
85 90 95

Pro Lys Ala Glu Ile Leu Glu Pro Ala Val Gln Gly Thr Leu Asn Val
100 105 110

Leu Arg Ser Cys Lys Arg Asn Pro Asp Leu Val Arg Val Val Leu Ala
115 120 125

Ser Ser Ser Ser Ala Val Arg Val Arg Ala Asp Phe Asp Pro Ser Ile
130 135 140

Pro Ile Asp Glu Ser Ser Trp Ser Ser Leu Glu Leu Cys Glu Lys Leu
145 150 155 160

Lys Ala Trp Tyr Pro Met Ser Lys Thr Met Ala Glu Lys Ala Ala Trp
165 170 175

Glu Tyr Ser Lys Glu Asn Gly Ile Asp Leu Val Thr Ile Phe
180 185 190

<210> 161
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120

gtttgtgtca ccggtggtgc tggttatatt ggttctcttt tagtcaaaaa gcttttggaa
180

aagggttaca ccgttcatgc tactcttaga aacttgaagg acgaatccaa agtagatttt
240

ttgagaggct ttccacatgc agatactaga cttatgttat ttgaagctga tatatacaaa
300

tcagatgaat tttggcccgc aattcaaggt tgtgagtttg tttttcacct tgctactcct
360

tttcaacatc aaactgattc tcagtttaag agcatagagg aagctgcaat agcaggggta
420

aaaagcatag ctgaaaattg cataaaatca ggaacagtga gaaaattgat atacactgga
480

actgtaattg cttcttcttc tctgaaagat gatggaagtg gctacaaaga cttcattgat
540

gaaacttgtt ggacacctct ccatcttcct ct
572

<210> 162
<211> 156

<212> PRT
<213> Trifolium repens

<400> 162

Met Glu Arg Ser Cys Lys Val Cys Val Thr Gly Gly Ala Gly Tyr Ile
1 5 10 15

Gly Ser Leu Leu Val Lys Lys Leu Leu Glu Lys Gly Tyr Thr Val His
20 25 30

Ala Thr Leu Arg Asn Leu Lys Asp Glu Ser Lys Val Asp Phe Leu Arg
35 40 45

Gly Phe Pro His Ala Asp Thr Arg Leu Met Leu Phe Glu Ala Asp Ile
50 55 60

Tyr Lys Ser Asp Glu Phe Trp Pro Ala Ile Gln Gly Cys Glu Phe Val
65 70 75 80

Phe His Leu Ala Thr Pro Phe Gln His Gln Thr Asp Ser Gln Phe Lys
85 90 95

Ser Ile Glu Glu Ala Ala Ile Ala Gly Val Lys Ser Ile Ala Glu Asn
100 105 110

Cys Ile Lys Ser Gly Thr Val Arg Lys Leu Ile Tyr Thr Gly Thr Val
115 120 125

Ile Ala Ser Ser Ser Leu Lys Asp Asp Gly Ser Gly Tyr Lys Asp Phe
130 135 140

Ile Asp Glu Thr Cys Trp Thr Pro Leu His Leu Pro
145 150 155

<210> 163
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<400> 163
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ttaataattg gaagggagaa taaatagttg aaaaacacac agttggagtg tttttgttgt 120

taaagaagct ngaaaatgga ggaagcnaca aagatggtga aaaagagtgg acaaattgtt 180

cctactgcca aatactgtgt tacaggagca acaggctata ttggttcatg gcttgttgaa 240

gctcttcttc aaagaggttg cactgttcat gctactgtta gagatcctga aaaatcgtta 300

cacctcctgt cgttgtggaa aggtagtgac caattgagaa ttttccgtgc ggatttgcaa 360

gaagaaggaa gtttcgatga tgccgtaaaa ggatgtattg gtgtgttcca tgttgcagct 420

tcaatgcaat tcaatattag tgacaaagaa aacactgagg actttgttga agcaaatata 480

attgaccctg caatcaaagg aaccataaat cttctcaaat catgcttgaa atcaaattca 540

gtgaaaaggg ttgttttcac atcttccata agtactatta ctgctaaaga caacgacgga 600

aaatggaaac ctattgttga tgaatcttgc caaacaaaaa ctgagattct gtggaataca 660

caaccaagtg gatgggttta tgcactttca aagcttcatg cagaagaagc ggct 714

<210> 164
<211> 187
<212> PRT
<213> Trifolium repens

<400> 164

Met Val Lys Lys Ser Gly Gln Ile Val Pro Thr Ala Lys Tyr Cys Val
1 5 10 15

Thr Gly Ala Thr Gly Tyr Ile Gly Ser Trp Leu Val Glu Ala Leu Leu
20 25 30

Gln Arg Gly Cys Thr Val His Ala Thr Val Arg Asp Pro Glu Lys Ser
35 40 45

Leu His Leu Leu Ser Leu Trp Lys Gly Ser Asp Gln Leu Arg Ile Phe
50 55 60

Arg Ala Asp Leu Gln Glu Glu Gly Ser Phe Asp Asp Ala Val Lys Gly
65 70 75 80

Cys Ile Gly Val Phe His Val Ala Ala Ser Met Gln Phe Asn Ile Ser
85 90 95

Asp Lys Glu Asn Thr Glu Asp Phe Val Glu Ala Asn Ile Ile Asp Pro
100 105 110

Ala Ile Lys Gly Thr Ile Asn Leu Leu Lys Ser Cys Leu Lys Ser Asn
115 120 125

Ser Val Lys Arg Val Val Phe Thr Ser Ser Ile Ser Thr Ile Thr Ala
130 135 140

Lys Asp Asn Asp Gly Lys Trp Lys Pro Ile Val Asp Glu Ser Cys Gln
145 150 155 160

Thr Lys Thr Glu Ile Leu Trp Asn Thr Gln Pro Ser Gly Trp Val Tyr
165 170 175

Ala Leu Ser Lys Leu His Ala Glu Glu Ala Ala
180 185

<210> 165
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ttaataattg gaagggagaa taaatagttg aaaaacacac agttggagtg tttttgttgt
120

taaagaagct ataaaatgga ggaaacaaca aagatggtga aaaatagtgg acaaattgtt
180

cctatagcca aatactgtgt cacaggagcc acaggctata ttggttcatg gcttgttgaa
240

gctcttcttc aaagaggttg cactgttcat gctactgtta gagatcctg
289

<210> 166
<211> 591
<212> DNA
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<220>
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<222> (23)..(24)
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<400> 166
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actgccaaat actgtgttac aggagcaaca ggctatattg gttcatggct tgttgaagct
120

cttcttcaaa gaggttgcac tgttcatgct actgttagag atcctgaaaa atcgttacac
180

ctcctgtcgt tgtggaaagg tagtgaccaa ttgagaattt tccgtgcgga tttgcaagaa
240

gaaggaagtt tcgatgatgc cgtaaaagga tgtattggtg tgttccatgt tgcagcttca
300

atgcaattca atattagtga caaagaaaac actgaggact ttgttgaagc aaatataatt
360

gaccctgcaa tcaaaggaac cataaatctt ctcaaatcat gcttgaaatc aaattcagtg
420

aaaagggttg ttttcacatc ttccataagt actattactg ctaaagacaa cgacggaaaa
480

tggaaaccta ttgttgatga atcttgccaa acaaaaactg agattctgtg gaatacacaa
540

ccaagtggat gggtttatgc actttcaaag cttcatgcag aagaagcggc t
591

<210> 167
<211> 572
<212> DNA
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<400> 167
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caaatactgt gttacaggag caacaggcta tattggttca tggcttgttg aagctcttct
120

tcaaagaggt tgcactgttc atgctactgt tagagatcct gaaaaatcgt tacacctcct
180

gtcgttgtgg aaaggtagtg accaattgag aattttccgt gcggatttgc aagaagaagg
240

aagtttcgat gatgccgtaa aaggatgtat tggtgtgttc catgttgcag cttcaatgca
300

attcaatatt agtgacaaag aaaacactga ggactttgtt gaagcaaata taattgaccc
360

tgcaatcaaa ggaaccataa atcttctcaa atcatgcttg aaatcaaatt cagtgaaaag
420

ggttgttttc acatcttcca taagtactat tactgctaaa gacaacgacg gaaaatggaa
480

acctattgtt gatgaatctt gccaaacaaa aactgagatt ctgtggaata cacaaccaag
540

tggatgggtt tatgcacttt caaagcttca tg
572

<210> 168
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60

agtgaagtga aaacatacat gggttccgaa tcagaaatag tttgtgttac cggagcttca
120

ggtttcatcg gatcgtggct tgttatgaga cttatagagc gtggctacac ggttcgagcc

180

accgttcgcg acccagataa catgaagaag gtgaagcatt tggtggaact gccgggtgca
240

aaaagcaaat tgtctctttg gaaggctgat cttgataaag aggggagttt tgatgaagca
300

attaaagggt gcacaggagt tttcatgtt gctacaccaa tggattttga atccaaggac
360

cctgagaatg aagtgataaa gcctacaata aatggattaa tagacatact gaaagcatgc
420

gaaaaggcaa aaacagttag aaaattggtt ttcacatcat cggctggaac tgtggacgtt
480

actgaacatc caaagtctat tattgatgaa acatgctgga gtgacgttga cttttgccgt
540

agagtcaaga tgaccggttg gatgtatttt gtttcaaaga ccctagcaga gcaagaagct
600

tggaagtatt cgaaagagca caacatagac tttgtctcca tcattccacc tcttgttgtt
660

ggcccctttc ttatggcctc aatgccacct agtctaatca ctgctctttc tcttatcaca
720

ggaaatgagg cccattactc aatcataaag caagggcaat acgtccattt agatgacctt
780

tgtcttgctc atatatttct gtatgagaat ccaaaagctc aagggagata catttgctgt
840

tcacatgaag caaccattca tcaagttgca aaacttatta aagaaaaata cccagagttc
900

aatgtcccaa caaaattcaa tgatatccca gatgaattgg aaattattaa attttctaaa
960

aagaagatca cagact
976

<210> 169
<211> 299
<212> PRT
<213> Trifolium repens

<400> 169

Met Gly Ser Glu Ser Glu Ile Val Cys Val Thr Gly Ala Ser Gly Phe
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Ile Gly Ser Trp Leu Val Met Arg Leu Ile Glu Arg Gly Tyr Thr Val
20 25 30

Arg Ala Thr Val Arg Asp Pro Asp Asn Met Lys Lys Val Lys His Leu
35 40 45

Val Glu Leu Pro Gly Ala Lys Ser Lys Leu Ser Leu Trp Lys Ala Asp
50 55 60

Leu Asp Lys Glu Gly Ser Phe Asp Glu Ala Ile Lys Gly Cys Thr Gly
65 70 75 80

Val Phe His Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu
85 90 95

Asn Glu Val Ile Lys Pro Thr Ile Asn Gly Leu Ile Asp Ile Leu Lys
100 105 110

Ala Cys Glu Lys Ala Lys Thr Val Arg Lys Leu Val Phe Thr Ser Ser
115 120 125

Ala Gly Thr Val Asp Val Thr Glu His Pro Lys Ser Ile Ile Asp Glu
130 135 140

Thr Cys Trp Ser Asp Val Asp Phe Cys Arg Arg Val Lys Met Thr Gly
145 150 155 160

Trp Met Tyr Phe Val Ser Lys Thr Leu Ala Glu Gln Glu Ala Trp Lys
165 170 175

Tyr Ser Lys Glu His Asn Ile Asp Phe Val Ser Ile Ile Pro Pro Leu
180 185 190

Val Val Gly Pro Phe Leu Met Ala Ser Met Pro Pro Ser Leu Ile Thr
195 200 205

Ala Leu Ser Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Ile Lys
210 215 220

Gln Gly Gln Tyr Val His Leu Asp Asp Leu Cys Leu Ala His Ile Phe
225 230 235 240

Leu Tyr Glu Asn Pro Lys Ala Gln Gly Arg Tyr Ile Cys Cys Ser His
245 250 255

Glu Ala Thr Ile His Gln Val Ala Lys Leu Ile Lys Glu Lys Tyr Pro
260 265 270

Glu Phe Asn Val Pro Thr Lys Phe Asn Asp Ile Pro Asp Glu Leu Glu
275 280 285

Ile Ile Lys Phe Ser Lys Lys Lys Ile Thr Asp
290 295

<210> 170
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<212> DNA
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agtgaagtga aaacatacat gggttccgaa tcagaaatag tttgtgttac cggagcttca
120

tgtttcatcg gatcgtggct tgttatgaga cttatagagc gtggctacac ggttcgagcc
180

accgttcgcg acccagataa catgaagaag gtgaagcatt tggtggaact gccgggtgca
240

aaaagcaaat tgtctctttg gaaggctgat cttgataaag aggggagttt tgatgaagca
300

attaaagggt gcacaggagt ttttcatgtt gctacaccaa tggattttga atccaaggac
360

cctgagaatg aagtgataaa gcctacaata aatggattaa tagacatact gaaagcatgc
420

gaaaaggcaa aaacagttaa aaaattggtt ttcacatcat cggctggaac tgtggacgtt
480

actgaacatc caaagtctat tattgatgaa acatgctgga gtgacgttga cttttgccgt
540

agagtcaaga tgaccggttg gatgtatttt gtttcaaaga ccctag

586

<210> 171
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<212> DNA
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<222> (209)..(209)
<223> Any nucleotide

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ctggagtgaa aatatacatg ggttctgaat cggaaatagt ttgtgttacc ggagcttcag
120

gtttcatcgg gtcgtggctt gttatgagac ttatggagca tggctacact gttcgagcca
180

ccgttcgtga cccagataac atgaagaang tgaagcattt gctggaactg ccaggtgcaa
240

aaagcaaatt gtctctttgg aaggctgatc ttgataaaga ggggagtttt gatgaagcaa
300

ttaaagggtg cacaggagtt tttcatgttg ctacaccaat ggattttgag tccaaggacc
360

ctgagaatga agtgataaag cctacaataa acggattaat agacatactg aaagcatgcg
420

aaaaggcaaa aacagttaga aaattggttt tcacatcatc ggctggaact gtggacgtta
480

ctgaacatcc aaagtctatt attgatgaaa catgctggag tgacgttgac ttttgccgta
540

gagtcaaaat gaccggttgg atgtatttt
569

<210> 172
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<400> 172
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gaagtgaana catacatggg ttccgaatca gaaatagttt gngttaccgg agcttcatgt 120

ttnatcggat cgtggcttgt tatgagactt atanagcgtg nctacacggc tcgagccacc 180

gttcgcgacc cagataacat gaagaaggtg aagcatttgg tggaactgcc gggtgcaaaa 240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt 300

aaagggtgca caggagtttt tnatgttgct acaccaatgg attttgaatc caaggacccct 360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcnaa 420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctgnaactgt ggacgttact 480

gaacatccaa agn 493

<210> 173
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<212> DNA
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gaagtgaaaa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcatgt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccacc
180

gttcgcgacc cagataacat gaagaaggtg aagcatttgg tggaactgcc gggtgcaaaa
240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggacccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtana
540

gtcaanatga ccggctggat gtattttgtt tcaaanaccc

580

<210> 174
<211> 581
<212> DNA
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gaagtgaaaa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcaggt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccacc
180

gttcgcgacc cagataacat gaagaaggtg aagcatttgg tggaactgcc gggtgcaaaa
240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttagaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga ccggttggat gtattttgtt tcaaagaccc t
581

<210> 175
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120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccacc
180

gttcgcgacc cagataacat gaagaaggtg aagcatttgg tggaactgcc gggtgcaaaa
240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggacccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttagaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga ccggttggat gtattttgtt tcaaagaccc tagcagagca ag
592

<210> 176
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gaagtgaaaa catacatggg ttctgaatca gaaatagttt gtgttaccgg agcatcaggt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccact
180

gttcgcgacc cagataacat gaagaaggtg aagcatttgg tggaactgcc gggtgcaaaa
240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt

300

aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggacccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga ccggttggat gtattttgtt tcaaagaccc tagcagagca agaagctt
598

<210> 177
<211> 576
<212> DNA
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<222> (18)..(18)
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<220>
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<222> (21)..(21)
<223> Any nucleotide

<400> 177
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aagtgaaaat atacatgggt tccgaatcgg aaatagtttg tgttaccgga gcttcaggtt
120

tcatcgggtc gtggcttgtt atgagactta tggagcgcgg ctacacggtt cgagccactg
180

ttcgcgaccc agataacatg aagaaggtga agcatttgat ggaactgccg ggtgcaaaaa
240

gcaaattgtc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300

aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360

agaacgaagt gataaagcct acaataaatg gactaataga catactgaga gcatgtgaaa 420

aggcaaaaac aattagaaga ttggttttca catcatcagc tggaactgtg gacgtaactg 480

aacactcaaa atcaattgtt gatgaaacat gttggagtga cgttgacttt tgccgtagag 540

tcaaaatgac cggttggatg tattttgttt caaaga 576

<210> 178
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<222> (21)..(21)
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<400> 178
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aagtgaaaac atacatgggt tctgaatcag aaatagtttg tgttaccgga gcatcaggtt 120

tcatcggatc gtggcttgtt atgagactta tagagcgtgg ctacacggtt cgagccactg 180

ttcgcgaccc agataacatg aagaaggtga agcatttggt ggaactgccg ggtgcaaaaa 240

gcaaattgtc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta 300

aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg 360

agaatgaagt gataaagcct acaataaatg gattaataga catactgaaa gcatgcgaaa 420

aggcaaaaac agttaaaaaa ttggttttca catcatcggc tggaactgtg gacgttactg 480

aacatccaaa gtctattatt gatgaaacat gctggagtga cgttgacttt tgccgtagag 540

tcaagatgac cggttggatg tattttgttt caaagaccct agcagag 587

<210> 179
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<220>
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<223> Any nucleotides

<220>
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<222> (21)..(21)
<223> Any nucleotide

<400> 179
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60

aagtgaaaac atacatgggt tctgaatcag aaatagtttg tgttaccgga gcatcaggtt
120

tcatcggatc gtggcttgtt atgagactta tagagcgtgg ctacacggtt cgagccactg
180

ttcgcgaccc agataacatg aagaaggtga agcatttggt ggaactgccg ggtgcaaaaa
240

gcaaattgtc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300

aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360

agaatgaagt gataaagcct acaataaatg gattaataga catactgaaa gcatgcgaaa
420

aggcaaaaac agttaaaaaa ttggttttca catcatcggc tggaactgtg gacgttactg
480

aacatccaaa gtctattatt gatgaaacat gctggagtga cgttgacttt tgccgtagag
540

tcaagatgac cggttggatg tattttgttt caaagaccct agcagagcaa gaagcttgga
600

agtattctaa agagcacaac atagattttg
630

<210> 180
<211> 579
<212> DNA
<213> Trifolium repens

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<220>
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<222> (11)..(11)
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<220>

<221> misc_feature
<222> (17)..(17)
<223> Any nucleotide

<220>
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<400> 180
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agtgaaaata tacatgggtt ccgaatcgga aatagtttgt gttaccggag cttcaggttt
120

catcgggtcg tggcttgtta tgagacttat ggagcgcggc tacacggttc gagccactgt
180

tcgcgaccca gataacatga agaaggtgaa gcatttgatg gaactgccgg gtgcaaaaag
240

caaattgtct ctttggaagg ctgatcttga taaagagggg agttttgatg aagcaattaa
300

agggtgcaca ggagtttttc atgttgctac accaatggat tttgaatcca aggaccctga
360

gaacgaagtg ataaagccta caataaatgg actaatagac atactgagag catgtgaaaa
420

ggcaaaaaca attagaagat tggttttcac atcatcagct ggaactgtgg acgtaactga
480

acactcaaaa tcaattgttg atgaaacatg ttggagtgac gttgactttt gccgtagagt
540

caaaatgacc ggttggatgt attttgtttc aaagaccct
579

<210> 181
<211> 604
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<222> (17)..(17)
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<222> (20)..(20)
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<222> (52)..(53)
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agtgaaaaca tacatgggtt ccgaatcaga aatagtttgt gttaccggag cttcaggttt
120

catcggatcg tggcttgtta tgagacttat agagcgtggc tacacggttc gagccaccgt
180

tcgcgaccca gataacatga agaaggtgaa gcatttggtg gaactgccgg gtgcaaaaag
240

caaattgtct ctttggaagg ctgatcttga taaagagggg agttttgatg aagcaattaa
300

agggtgcaca ggagtttttc atgttgctac accaatggat tttgaatcca aggaccctga
360

gaatgaagtg ataaagccta caataaatgg attaatagac atactgaaag catgcgaaaa
420

ggcaaaaaca gttagaaaat tggttttcac atcatcggct ggaactgtgg acgttactga
480

acatccaaag tctattattg atgaaacatg ctggagtgac gttgactttt gccgtagagt
540

caagatgacc ggttggatgt attttgtttc aaagacccta gcagagcaag aagcttggaa
600

gtat
604

<210> 182
<211> 586
<212> DNA
<213> Trifolium repens

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<222> (10)..(10)
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<400> 182
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gaaaatatac atgggttctg aatcggaaat agtttgtgtt accggagctt caggtttcat
120

cgggtcgtgg cttgttatga gacttatgga gcgtggctac actgttcgag ccaccgttcg
180

tgacccagat aacatgaaga aggtgaagca tttgctggaa ctgccgggtg caaaaagcaa
240

attgtctctt tggaaggctg atcttgataa agaggggagt tttgatgaag caattaaagg
300

gtgcacagga gtttttcatg ttgctacacc aatggatttt gaatccaagg accctgagaa
360

tgaagtgata aagcctacaa taaacggatt aatagacata ctgaaagcat gcgaaaaggc
420

aaaaacagtt agaaaattgg ttttcacatc atcggctgga actgtggacg ttactgaaca
480

tccaaagtct attattgatg aaacatgctg gagtgacgtt gacttttgcc gtagagtcaa
540

aatgaccggt tggatgtatt ttgtttcaaa gaccctagca gagcag
586

<210> 183
<211> 586
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<223> Any nucleotide

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accggagctt caggtttcat cgggtcgtgg cttgttatga gacttatgga gcgtggctac
120

actgttcgag ccaccgttcg tgacccagat aacatgaaga aggtgaagca tttgctggaa
180

ctgccgggtg caaaaagcaa attgtctctt tggaaggctg atcttgataa agaggggagt
240

tttgatgaag caattaaagg gtgcacagga gtttttcatg ttgctacacc aatggatttt
300

gagtccaagg accctgagaa tgaagtgata aagcctacaa taaacggatt aatagacata
360

ctgaaagcat gcgaaaaggc aaaaacagtt agaaaattgg ttttcacatc atcggctgga 420

actgtggacg ttactgaaca tccaaagtct attattgatg aaacatgctg gagtgacgtt 480

gacttttgcc gtagagtcaa aatgaccggt tggatgtatt ttgtttcaaa gaccctagca 540

gagcaagaag cttggaagta ttcgaaagag cacaacatag actttg 586

<210> 184
<211> 570
<212> DNA
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<220>
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<222> (10)..(11)
<223> Any nucleotides

<220>
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<222> (23)..(23)
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<400> 184
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gaactgtgga cgttactgaa catccaaagt ctattattga tgaaacatgc tggagtgacg 120

ttgacttttg ccgtagagtc aaaatgaccg gttggatgta ttttgtttca aagaccctag 180

cagagcaaga agcttggaag tattcgaaag agcacaacat agactttgtc tccatcattc 240

cacctcttgt tgttggcccc tttcttatgg cctcaatgcc acctagtcta atcactgctc 300

tttctcttat cacaggaaat gaggcccatt actcaatcat aaagcaaggg caatacgtcc 360

atttagatga cctttgtctt gctcatatat ttctgtatga gaatccaaaa gctcaaggga 420

gatacatttg ctgttcacat gaagcaacca ttcatcaagt tgcaaaactt attaaagaaa 480

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ttaaattttc taaaaagaag atcacagact 570

<210> 185
<211> 833
<212> DNA
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<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (34)..(34)
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<400> 185
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120

gttttgttgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180

ctgttagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240

gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gctcctatag
300

caggatgtga gcttgttttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360

agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420

gagcaaaaga agtcaaaaga gttatcttaa catcttcggc agccgcggtg actataaatg
480

aactcaaagg gacaggtcat gttatggatg aaaccaactg gtcagatgtt gaatttctga
540

acactgcaaa gccacccact tggggttatc ctgcttcaaa aatgctagct gaaaaggctg
600

catggaaatt tgctgaagaa aatgacattg atctaatcac tgtgatacct agtttaacaa
660

ctggtccttc tctcacacca gatatcccat ctagtgttgg cttggcaatg tctctaataa
720

caggcaatga tttcctcata aatgctctga aaggaatgca atttctgtcg ggttcgttat
780

ccatcactca tgttgaggat atttgccgag ctcatatatt tctggcagag aag
833

<210> 186
<211> 256
<212> PRT
<213> Trifolium repens

<400> 186

Met Ala Ser Ile Lys Gln Ile Gly Asn Lys Lys Ala Cys Val Ile Gly
1 5 10 15

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Gly Thr Gly Phe Val Ala Ser Met Leu Ile Lys Gln Leu Leu Glu Lys
            20                  25                  30

Gly Tyr Ala Val Asn Thr Thr Val Arg Asp Pro Asp Ser Pro Lys Lys
        35                  40                  45

Ile Ser His Leu Val Ala Leu Gln Ser Leu Gly Glu Leu Asn Leu Phe
    50                  55                  60

Arg Ala Asp Leu Thr Val Glu Glu Asp Phe Asp Ala Pro Ile Ala Gly
65                  70                  75                  80

Cys Glu Leu Val Phe Gln Leu Ala Thr Pro Val Asn Phe Ala Ser Gln
                85                  90                  95

Asp Pro Glu Asn Asp Met Ile Lys Pro Ala Ile Lys Gly Val Leu Asn
            100                 105                 110

Val Leu Lys Ala Ser Ala Arg Ala Lys Glu Val Lys Arg Val Ile Leu
        115                 120                 125

Thr Ser Ser Ala Ala Ala Val Thr Ile Asn Glu Leu Lys Gly Thr Gly
    130                 135                 140

His Val Met Asp Glu Thr Asn Trp Ser Asp Val Glu Phe Leu Asn Thr
145                 150                 155                 160

Ala Lys Pro Pro Thr Trp Gly Tyr Pro Ala Ser Lys Met Leu Ala Glu
                165                 170                 175

Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Asp Ile Asp Leu Ile Thr
            180                 185                 190

Val Ile Pro Ser Leu Thr Thr Gly Pro Ser Leu Thr Pro Asp Ile Pro
        195                 200                 205

Ser Ser Val Gly Leu Ala Met Ser Leu Ile Thr Gly Asn Asp Phe Leu
    210                 215                 220

Ile Asn Ala Leu Lys Gly Met Gln Phe Leu Ser Gly Ser Leu Ser Ile
225                 230                 235                 240

Thr His Val Glu Asp Ile Cys Arg Ala His Ile Phe Leu Ala Glu Lys
                245                 250                 255
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<211> 576
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120

gttttgttgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180

ctgttagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240

gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gctcctatag
300

caggatgtga gcttgttttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360

agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420

gagcaaaaga agtcaaaaga gttatcttaa catcttcggc agccgcggtg actataaatg
480

aactcaaagg gacaggtcat gttatggatg aaaccaactg gtcagatgtt gaatttctga
540

acactgcaaa gccacccact tggggttatc ctgctt
576

<210> 188
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<212> DNA
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120

gttttgttgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180

ctgttagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240

gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gctcctatag
300

caggatgtga gcttgttttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360

agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420

gagcaaaaga agtcaaaaga gttatcttaa catcttcggc agccgcggtg actataaatg
480

aactcaaagg gacaggtcat gttatggatg aaaccaactg gtcagatgtt gaatttctga
540

acactgcaaa gccacccact tggggttatc ctgcttcaan
580

<210> 189
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<220>
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<222> (29)..(30)
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atggctagta tcaaacaaat tggaaacaag aaagcatgtg tgattggtgg cactggtttt
120

gttgcatcta tgttgatcaa acagttactt gaaaagggtt atgctgttaa tactactgtt
180

agagacccag atagtcctaa gaaaatatct cacctagtgg cactgcaaag tttgggggaa
240

ctgaatctat ttagagcaga cttaacagtt gaagaagatt ttgatgctcc tatagcagga
300

tgtgagcttg tttttcaact tgctacacct gtgaactttg cttctcaaga tcctgagaat
360

gacatgataa agccagcaat caaaggtgtg ttgaatgtgt tgaaagcaag tgcaagagca
420

aaagaagtca aaagagttat cttaacatct tcggcagccg cggtgactat aaatgaactc
480

aaagggacag gtcatgttat ggatgaaacc aactggtcag atgttgaatt tctgaacact
540

gcaaagccac ccacttgggg ttatcctgct tcaaaaat
578

<210> 190
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<212> DNA
<213> Trifolium repens

<400> 190
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atggctagta tcaaacaaat tggaaacaag aaagcatgtg tgattggtgg cactggtttt
120

gttgcatcta tgttgatcaa gcagttactt gaaaagggtt atgctgttaa tactaccgtt
180

agagacccag atagccctaa gaaaatatct cacctagtgg cactgcaaag tttgggggaa
240

ctgaatctat ttagagcaga cttaacagtt gaagaagatt ttgatgctcc tatagcagga
300

tgtgaacttg tttttcaact tgctacacct gtgaactttg cttctcaaga tcctgagaat
360

gacatgataa agccagcaat caaaggtgtg ttgaatgtgt tgaaagcaat tgcaagagca
420

aaagaagtta aaagagttat cttaacatct tcggcagccg cggtgactat aaatgaactc
480

aaagggacag gtcatgttat ggatgaaacc aactggtctg atgttgaatt tctcaacact
540

gcaaaaccac ccacttgggg ttatcctgcc tcaaaaatgc tagctgaaaa ggctgcatgg
600

aaatttgctg aagaaaatg
619

<210> 191
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<213> Trifolium repens

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<222> (59)..(59)
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<400> 191
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tatcaaacaa attggaaaca agaaagcatg tgtgattggt ggcactggtt ttgttgcatc
120

tatgttgatc aagcagttac ttgaaaaggg ttatgctgtt aatactaccg ttagagaccc
180

agatagccct aagaaaatat ctcacctagt ggcactgcaa agtttggggg aactgaatct
240

atttagagca gacttaacag ttgaagaaga ttttgatgct cctatagcag gatgtgaact
300

tgtttttcaa cttgctacac ctgtgaactt tgcttctcaa gatcctgaga atgacatgat
360

aaagccagca atcaaaggtg tgttgaatgt gttgaaagca attgcaagag caaaagaagt
420

taaaagagtt atcttaacat cttcggcagc cgcggtgact ataaatgaac tcaaagggac
480

aggtcatgtt atggatgaaa ccaactggtc tgatgttgaa tttctcaaca ctgcaaaacc
540

acccacttgg ggttatcctg cctcaaaaat gctagctgaa aaggctgcat ggaaatttgc
600

tgaagaaaat gacnttgat
619

<210> 192
<211> 586
<212> DNA
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<220>
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<220>
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<222> (4)..(4)
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<220>
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<222> (23)..(23)
<223> Any nucleotide

<400> 192
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gcaggatgtg agcttgtttt tcaacttgct acacctgtga cctttgcttc tcaagatcct
120

gagaatgaca tgataaagcc agcaatcaaa ggtgtgttga atgtgttgaa agcaagtgca
180

agagcaaaag aagtcaaaag agttatctta acatcttcgg cagccgcggt gactataaat
240

gaactcaaag ggacaggtca tgttatggat gaaaccaact ggtcaggtgt tgaatttctg
300

aacactgcaa agccacccac ttggggttat cctgcttcaa aaatgctagc tgaaaaggct
360

gcatggaaat ttgctgaaga aaatgacatt gatctaatca ctgtgatacc tagtttaaca
420

actggtcctt ctctcacacc agatatccca tctagtgttg gcttggcaat gtctctaata
480

acaggcaatg atttcctcat aaatgctctg aaaggaatgc aatttctgtc gggttcgtta
540

tccatcactc atgttgagga tatttgccga gctcatatat ttctgg
586

<210> 193
<211> 567
<212> DNA
<213> Trifolium repens

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<222> (55)..(55)
<223> Any nucleotide

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gctacacctg tgacctttgc ttctcaagat cctgagaatg acatgataaa gccagcaatc 120

aaaggtgtgt tgaatgtgtt gaaagcaagt gcaagagcaa aagaagtcaa aagagttatc 180

ttaacatctt cggcagccgc ggtgactata aatgaactca aagggacagg tcatgttatg 240

gatgaaacca actggtcaga tgttgaattt ctgaacactg caaagccacc cacttggggt 300

tatcctgctt caaaaatgct agctgaaaag gctgcatgga aatttgctga agaaaatgac 360

attgatctaa tcactgtgat acctagttta acaactggtc cttctctcac accagatatc 420

ccatctagtg ttggcttggc aatgtctcta ataacaggca atgatttcct cataaatgct 480

ctgaaaggaa tgcaatttct gtcgggttcg ttatccatca ctcatgttga ggatatttgc 540

cgagctcata tatttctggc agagaag 567

<210> 194
<211> 597
<212> DNA
<213> Trifolium repens

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aaagagatgg atgtcttggt tccacgtttt gatagcatat ttgaaaaaat gattggtgaa 120

cgtaagaaga aggaagtgga ggggaaagaa aatgaaagta aggattttct gcagtttttg 180

ttgaatttga aggatgaggg tgattctaag actccattca caattaccca tgttaaggct 240

ctactcatgg acatggttgt gggtggatca gacacatcct ccaacacaat tgagtttgca 300

ttggcagaaa tgatgaacaa cccagaagta atgaggaagg ttcaagagga attagaagat 360

gtagttggga aagataactt agtagaagag tctcacattc ataagctacc ctacttgcat 420

gcagtgatga aagaaacact tcgtttacac ccagcacttc cacttttagt ccctcactgt
480

ccaagtgaaa ccaccaatgt tggaggctac acaattccaa agggatctcg tgtgtttgtg
540

aacgtttggg ctattcatag agacccttcc atttgggaga aaccactaga atttgat
597

<210> 195
<211> 199
<212> PRT
<213> Trifolium repens

<400> 195

Gly Thr Asn Leu Ser Asp Phe Phe Pro Gly Leu Ala Arg Phe Asp Leu
1 5 10 15

Gln Gly Val Val Lys Glu Met Asp Val Leu Val Pro Arg Phe Asp Ser
20 25 30

Ile Phe Glu Lys Met Ile Gly Glu Arg Lys Lys Lys Glu Val Glu Gly
35 40 45

Lys Glu Asn Glu Ser Lys Asp Phe Leu Gln Phe Leu Leu Asn Leu Lys
50 55 60

Asp Glu Gly Asp Ser Lys Thr Pro Phe Thr Ile Thr His Val Lys Ala
65 70 75 80

Leu Leu Met Asp Met Val Val Gly Gly Ser Asp Thr Ser Ser Asn Thr
85 90 95

Ile Glu Phe Ala Leu Ala Glu Met Met Asn Asn Pro Glu Val Met Arg
100 105 110

Lys Val Gln Glu Glu Leu Glu Asp Val Val Gly Lys Asp Asn Leu Val
115 120 125

Glu Glu Ser His Ile His Lys Leu Pro Tyr Leu His Ala Val Met Lys
130 135 140

Glu Thr Leu Arg Leu His Pro Ala Leu Pro Leu Leu Val Pro His Cys
145 150 155 160

Pro Ser Glu Thr Thr Asn Val Gly Gly Tyr Thr Ile Pro Lys Gly Ser
165 170 175

Arg Val Phe Val Asn Val Trp Ala Ile His Arg Asp Pro Ser Ile Trp
180 185 190

Glu Lys Pro Leu Glu Phe Asp

195

<210> 196
<211> 700
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<213> Trifolium repens

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<222> (2)..(2)
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<222> (10)..(10)
<223> Any nucleotide

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<222> (22)..(22)
<223> Any nucleotide

<220>
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<222> (698)..(698)
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<400> 196
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atcactcaat accaaacctt cctttacaaa gaactttcta tatccttttt cattttcttg
120

ataacccatt tcatcataag ttttctcttc aaaaaaaatc tcaaaaaact tccaccaggc
180

ccaaaaggtt ttccagttgt tggtgcactc ccactaatgg gatccatgcc tcatgttacc
240

ctattcaaaa tgtcacaaaa atatggtccc ataatgtacc taaaaatggg atcaaataac
300

atggttgtag catcaactcc ttcttcagcc aaagcatttc tcaaaacact tgacctaaat
360

ttctccaata gaccgccgaa cgctggcgca actcacctag cttatgattc acaagacttg
420

gttttcgccg actatggatc taggtggaaa ttacttagga aactaagtaa cttgcacatg
480

ctcggcggaa aagccctcga aaattggtcg aaagttcgtg agattgaaat gggtcacatg
540

attcgtacaa tgtacgattg tagcaagaaa gacgaatccg ttgttgtggc cgaaatgttg
600

acatatgcta tggccaatat gataggtcaa gttatattga gtcgtcgcgt gttcgagaca
660

aaaggtagtg actcaaatga atttaaggat atggttgntg
700

<210> 197
<211> 216
<212> PRT
<213> Trifolium repens

<220>
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<222> (216)..(216)
<223> Any amino acid

<400> 197

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Ile Ser Phe Phe Ile Phe Leu Ile Thr His Phe Ile Ile Ser Phe Leu
20 25 30

Phe Lys Lys Asn Leu Lys Lys Leu Pro Pro Gly Pro Lys Gly Phe Pro
35 40 45

Val Val Gly Ala Leu Pro Leu Met Gly Ser Met Pro His Val Thr Leu
50 55 60

Phe Lys Met Ser Gln Lys Tyr Gly Pro Ile Met Tyr Leu Lys Met Gly
65 70 75 80

Ser Asn Asn Met Val Val Ala Ser Thr Pro Ser Ser Ala Lys Ala Phe
85 90 95

Leu Lys Thr Leu Asp Leu Asn Phe Ser Asn Arg Pro Pro Asn Ala Gly
100 105 110

Ala Thr His Leu Ala Tyr Asp Ser Gln Asp Leu Val Phe Ala Asp Tyr
115 120 125

Gly Ser Arg Trp Lys Leu Leu Arg Lys Leu Ser Asn Leu His Met Leu
130 135 140

Gly Gly Lys Ala Leu Glu Asn Trp Ser Lys Val Arg Glu Ile Glu Met
145 150 155 160

Gly His Met Ile Arg Thr Met Tyr Asp Cys Ser Lys Lys Asp Glu Ser
165 170 175

Val Val Val Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly
180 185 190

Gln Val Ile Leu Ser Arg Arg Val Phe Glu Thr Lys Gly Ser Asp Ser

195 200 205

Asn Glu Phe Lys Asp Met Val Xaa
210 215

<210> 198
<211> 584
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

<220>
<221> misc_feature
<222> (10)..(10)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (27)..(27)
<223> Any nucleotide

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atcactcaat accaaacctt ccttttcaaa gaactttcta tctccttttt cattttcttg
120

ataacccgtt tcatcataag ttttctcttc aaaaaaaatc tcaaaaaact tccaccaggc
180

ccaaagggtt ttccagttgt tggtgcactc ccactaatgg gatccatgcc tcatgttacc
240

ctattcaaaa tgtcacaaaa atatggtccc ataatgtacc taaaaatggg atcaaatagc
300

atggttgtag catcaactcc ttcttcagcc aaagcatttc tcaaaacact tgacctaaat
360

ttctccaata gaccgccgaa cgctggcgcg actcacctag cttatgattc acaagacttg
420

gttttcgccg actatggatc taggtggaaa ttacttagga aactaagtaa cttgcacatg
480

ctcggcggaa aagccctcga agattggtcg aaagttcgtg agattgaaat gggtcacatg
540

attcgtacaa tgtatgattg tagcaagaaa gacgaatccg ttgt
584

<210> 199
<211> 694
<212> DNA
<213> Trifolium repens

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<223> Any nucleotide

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<223> Any nucleotide

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caacaccaaa ccttccttta caaagaactt tctatatcct ttttcatttt cttgataacc
120

catttcatca ttagttttct cttcaaaaaa aatctcaaaa aacttccacc aggcccaaaa
180

ggttttccag ttgttggtgc actcccacta atgggatcca tgcctcatgt taccctattc
240

aaaatgtcac aaaaatatgg tcctataatg tacctaaaaa tgggatcaaa taacatggtt
300

gtagcatcaa ctccttcttc agccaaagca tttctcaaaa cacttgacct aaatttctcc
360

aataggccgg cgaacgctgg cgcaactcac ctagcttatg atccacaaga cttggttttc
420

gccgactatg gatctaggtg gaaattactt aggaaactaa gtaacttgca catgctcggc
480

ggaaaagccc ttgaaaattg gtcgaaagtt cgtgagattg aaatgggtca catgattcgt
540

acaatgtacg attgtagcaa gaaagacgaa tccgttgttg tggccgaaat gttgacatat
600

gctatggcca atatgatagg tcaagttata ttgagtcgtc gcgtgttcga gacaaaaggt
660

agtgactcaa atgaatttaa ggatatggtt gntg
694

<210> 200
<211> 580
<212> DNA

<213> Trifolium repens

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<222> (2)..(2)
<223> Any nucleotide

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<222> (55)..(56)
<223> Any nucleotides

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ataccaaacc ttccttttca aagaactttc tatctccttt ttcattttct tgataacccg
120

tttcatcata agtcttctct tcaaaaaaaa tctcaaaaaa cttccaccag gcccaaaggg
180

ttttccagtt gttggtgcac tcccactaat gggatccatg cctcatgtta ccctattcaa
240

aatgtcacaa aaatatggtc ccataatgta cctaaaaatg ggatcaaata acatggttgt
300

agcatcaact ccttcttcag ccaaagcatt tctcaaaaca cttgacctaa atttctccaa
360

tagaccgccg aacgctggcg cgactcacct agcttatgat tcacaagact tggttttcgc
420

cgactatgga tctaggtgga aattgcttag gaaactaagt aacttgcaca tgctcggcgg
480

aaaagccctc gaagattggt cgaaagttcg cgagattgag atgggtcaca tgattcgtac
540

aatgtacgat tgtagcaaga aagacgaata tgttgttgtg
580

<210> 201
<211> 574

<212> DNA
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<222> (56)..(56)
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<222> (569)..(569)
<223> Any nucleotide

<220>
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<222> (572)..(572)
<223> Any nucleotide

<400> 201
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caaaccttcc tttacaaaga actttctata tcctttttca ttttcttgat aacccatttc
120

atcattagtt ttctcttcaa aaaaaatctc aaaaaacttc caccaggccc aaaaggtttt
180

ccagttgttg gtgcactccc actaatggga tccatgcctc atgttaccct attcaaaatg
240

tcacaaaaat atggtcctat aatgtaccta aaaatgggat caaataacat ggttgtagca
300

tcaactcctt cttcagccaa agcatttctc aaaacacttg acctaaattt ctccaatagg
360

ccggcgaacg ctggcgcaac tcacctagct tatgattcac aagacttggt tttcgccgac
420

tatggatcta ggtggaaatt acttaggaaa ctaagtaact tgcacatgct cggcggaaaa
480

gcccttgaaa attggtcgaa agttcgtgag attgaaatgg gtcacatgat tcgtacaatg
540

tacgattgta gcaagaaaga cgaatccgnt gntg
574

<210> 202
<211> 1261
<212> DNA
<213> Trifolium repens

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<222> (7)..(7)
<223> Any nucleotide

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<222> (31)..(31)
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<222> (43)..(43)
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<220>
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<222> (92)..(93)
<223> Any nucleotides

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<222> (96)..(96)
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<220>
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<222> (957)..(957)
<223> Any nucleotide

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accacaaaca ccaaaaccga gtccgtttcc tnntcnaaca tggcaccaag ccaaactcta
120

agttatctct cacaacaaaa cactcttgag tcaagtttcg ttagggaaga agatgagcgt
180

ccaaaagttg cctacaataa cttcagcaac gagattccaa tcatttctct tgctggaatt
240

gatgaggttg atggtcgtag aacagagata tgtaacaaga ttgttgaagc ttgtgagaat

300

tggggtattt ttcaggttgt tgatcatggt gttgatacaa aacttgtttc tgagatgacc
360

cgttttgcta gagagttttt tgctttgcca ccggaagaga agctccggtt tgacatgtcc
420

ggtggtaaaa agggtggttt cattgtctct agtcatctcc aaggagaagc agtgaaggat
480

tggagagagc tagtgacata tttttcatac ccaattaaac aaagagatta ttcaaggtgg
540

ccagacaagc cagaaggatg gaaagaggta acagaaaaat acagtgaaaa cctaatgaat
600

ttagcttgca aactattgga agttttatca gaagcaatgg gtttagaaaa agaagctcta
660

acaaaagcat gtgttgatat ggatcaaaaa gttgttataa attattaccc aaaatgccct
720

gaacctgacc tcacacttgg ccttaaacgt cacactgacc ctggcacaat tactcttttg
780

cttcaagatc aagttggtgg ccttcaagct accaaagata atggtaagac gtggattaca
840

gttcaaccag ttgaaggtgc ttttgttgtt aatcttggag accatggtca ctatctaagt
900

aatggacggt tcaaaaatgc tgaccaccaa gcagtggtga attcgaacta cagccgntta
960

tcaatagcaa catttcaaaa tccagctccc gatgcaactg tatacccttt gaagattaga
1020

gagggtgaaa aatctgtgtt ggaagaacca atcacttttg ctgaaatgta tagaaggaag
1080

atgaccaaag accttgaaat tgctaggatg aagaagttgg ctaaggaaca acaacttagg
1140

gacttggagg agaacaagac taaatatgag gccaaacctt tgaatgagat ctttgcttaa
1200

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1260

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1261

<210> 203
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<212> PRT
<213> Trifolium repens

<220>
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<222> (286)..(286)
<223> Any amino acid

<400> 203

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            20                  25                  30

Asn Asn Phe Ser Asn Glu Ile Pro Ile Ile Ser Leu Ala Gly Ile Asp
        35                  40                  45

Glu Val Asp Gly Arg Arg Thr Glu Ile Cys Asn Lys Ile Val Glu Ala
    50                  55                  60

Cys Glu Asn Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Thr
65                  70                  75                  80

Lys Leu Val Ser Glu Met Thr Arg Phe Ala Arg Glu Phe Phe Ala Leu
                85                  90                  95

Pro Pro Glu Glu Lys Leu Arg Phe Asp Met Ser Gly Gly Lys Lys Gly
            100                 105                 110

Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Ala Val Lys Asp Trp
        115                 120                 125

Arg Glu Leu Val Thr Tyr Phe Ser Tyr Pro Ile Lys Gln Arg Asp Tyr
    130                 135                 140

Ser Arg Trp Pro Asp Lys Pro Glu Gly Trp Lys Glu Val Thr Glu Lys
145                 150                 155                 160

Tyr Ser Glu Asn Leu Met Asn Leu Ala Cys Lys Leu Leu Glu Val Leu
                165                 170                 175

Ser Glu Ala Met Gly Leu Glu Lys Glu Ala Leu Thr Lys Ala Cys Val
            180                 185                 190

Asp Met Asp Gln Lys Val Val Ile Asn Tyr Tyr Pro Lys Cys Pro Glu
        195                 200                 205

Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
    210                 215                 220

Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala Thr Lys Asp
225                 230                 235                 240

Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly Ala Phe Val
                245                 250                 255

Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
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260 265 270

Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Tyr Ser Xaa Leu Ser
275 280 285

Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val Tyr Pro Leu
290 295 300

Lys Ile Arg Glu Gly Glu Lys Ser Val Leu Glu Glu Pro Ile Thr Phe
305 310 315 320

Ala Glu Met Tyr Arg Arg Lys Met Thr Lys Asp Leu Glu Ile Ala Arg
325 330 335

Met Lys Lys Leu Ala Lys Glu Gln Gln Leu Arg Asp Leu Glu Glu Asn
340 345 350

Lys Thr Lys Tyr Glu Ala Lys Pro Leu Asn Glu Ile Phe Ala
355 360 365

<210> 204
<211> 586
<212> DNA
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120

tctcacaaca aaacactctc gagtcaagtt tcgttaggga agaagatgag cgtccaaaag
180

ttgcctacaa taacttcagc aacgagattc caatcatttc tcttgctgga attgatgagg
240

ttgatggtcg tagaacagag atatgtaaca agattgttga agcttgtgag aattggggta
300

tttttcaggt tgttgatcat ggtgttgata caaaacttgt ttctgagatg acccgttttg
360

ctagagagtt ttttgctttg ccaccggaag agaagctccg gtttgacatg tccggtggta
420

aaaagggtgg tttcattgtc tctagtcatc ttcaaggaga agcagtgaag gattggagag
480

agctagtgac atatttttca tacccaatta aacaaagaga ttattcaagg tggccagaca
540

agccagaagg atggaaagag gtaacagaaa aatacagtga aaacct
586

<210> 205
<211> 597
<212> DNA
<213> Trifolium repens

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<222> (2)..(2)
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<222> (5)..(5)
<223> Any nucleotide

<220>
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<222> (7)..(7)
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<222> (31)..(31)
<223> Any nucleotide

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120

acaaaagact cttgagtcaa gtttcgttag ggaagaagat gagcgtccaa aagttgccta
180

caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg aggttgatgg
240

tcgcagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg gtatttttca
300

ggttgttgat catggtgttg atacaaagct tgtttctgag atgactcgtt ttgctagaga
360

gtttttgct ttgccgccgg aagagaagct ccggtttgac atgtccggtg gtaaaaaggg
420

tggtttcatt gtctctagtc atctccaagg agaagcagtg aaagattgga gagagctagt
480

gacatatttt tcatacccaa ttaaacaaag agattattca aggtggccag acaagccaga
540

agaatggaaa gaagtaacag aaaaatacag tgaaaaccta atgaatttag cttgcag
597

<210> 206

<211> 605
<212> DNA
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120

gttatctctc acaacaaaac actctcgagt caagtttcgt tagggaagaa gatgagcgtc
180

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
240

atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
300

ggggtatttt tcaggttgtt gatcatggtg ttgatacaaa acttgtttct gagatgaccc
360

gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
420

gtggtaaaaa gggtggtttc attgtctcta gtcatcttca aggagaagca gtgaaggatt
480

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc

540

cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac ctaatgaatt
600

tagct
605

<210> 207
<211> 492
<212> DNA
<213> Trifolium repens

<220>
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<222> (10)..(10)
<223> Any nucleotide

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120

ttatctctca caacaaaaca ctctcgagtc aagtttcgtt agggaagaag atgagcgtcc
180

aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg ctggaattga
240

tgaggttgat ggtcgtagaa cagagatatg taacaagatt gttgaagctt gtgagaattg
300

gggtattttt caggttgttg atcatggtgt tgatacaaaa cttgtttctg agatgacccg
360

ttttgctaga gagtttttttg ctttgccacc ggaagagaag ctccggtttg acatgtccgg
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agggaagaag atgagcgtcc aaaagttgcc tacaataact tcagcaacga gattccaatc
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atttctcttg ctggaattga tgaggttgat ggtcgtagaa cagagatatg taacaagatt
240

gttgaagctt gtgagaattg ggtatttttt caggttgttg atcatggtgt tgatacaaaa
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cttgtttctg agatgacccg ttttgctaga gagtttttttg ctttgccacc ggaagagaag
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ctccggtttg acatgtccgg tggtaaaaag ggtggtttca ttgtctctag tcatctccaa
420

ggagaagcag tgaaggattg gagagagcta gtgacatatt tttcataccc aattaaacaa
480

agagattatt caaggtggcc agacaagcca gaaggatgga aagaggtaac agaaaaatac
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agtgaaaacc taatgaattt agcttgcaaa ctattggaag ttttatcaga agcaatgggt
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ttagaaaaag aagctctaac aaaagcatgt gttgatatgg atcaaaaagt tgttataaat
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aagatgagcg tccaaaagtt gcctacaata acttcagcaa cgagattcca atcatttctc 180

ttgctggaat tgatgaggtt gatggtcgta gaacagagat atgtaacaag attgttgaag 240

cttgtgagaa ttggggtatt tttcaggttg ttgatcatgg tgttgataca aaacttgttt 300

ctgagatgac ccgttttgct agagagtttt ttgctttgcc accggaagag aagctccggt 360

ttgacatgtc cggtggtaaa aagggtggtt tcattgtctc tagtcatctc caaggagaag 420

cagtgaagga ttggagagag ctagtgacat atttttcata cccaattaaa caaagagatt 480

attcaaggtg gccagacaag ccagaaggat ggaaagaggt aacagaaaaa tacagtgaaa 540

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120

agaagatgag cgtccaaaag ttgcctacaa taacttcagc aacgagattc caatcatttc
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tcttgctgga attgatgagg ttgatggtcg tagaacagag atatgtaaca agattgttga
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agcttgtgag aattggggta tttttcaggt tgttgatcat ggtgttgata caaaacttgt
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ttctgagatg acccgttttg ctagagagtt ttttgctttg ccaccggaag agaagctccg
360

gtttgacatg tccggtggta aaaagggtgg tttcattgtc tctagtcatc tccaaggaga
420

agcagtgaag gattggagag agctagtgac atatttttca tacccaatta aacaaagaga
480

ttattcaagg tggccagaca agccagaagg atggaaagag gtaacagaaa aatacagtga
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aaacctaatg aatttagctt gcaaactatt ggaagnttta tcagaagcaa tgggtttaga
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aaaagaagct ctaacaaang catgtgttga tatggatcaa aaagttgtta taaattatta
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120

gaagatgagc gtccaaaagt tgcctacaat aacttcagca acgagattcc aatcatttct
180

cttgctggaa ttgatgaggt tgatggtcgt agaacagaga tatgtaacaa gattgttgaa
240

gcttgtgaga attggggtat ttttcaggtt gttgatcatg gtgttgatac aaaacttgtt
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tctgagatga cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg
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tttgacatgt ccggtggtaa aaagggtggt ttcattgtct ctagtcatct ccaaggagaa
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gcagtgaagg attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat
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tattcaaggt ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtgaa
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aacctaatga atttagcttg caaactattg gaagttttat cagaagcaat gggtttagaa
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aaagaagctc taacaaaagc atgtgttgat atggatcaaa aagttgttat aaattattac
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120

agatgaccgt ccaaaagttg cctacaatac cttcagcacc gagattccaa tcntttctct
180

tgctggaatt gatgaggttg atggccgaaa aacanaaatn tttaccaaga ttggnggggc
240

ttgtnaaaat tggggtnttt ttcaggttgg tgatcatggg gtnnaacaaa acttgtttcc
300

canaaanccc nttttgntaa anagtttttt gctttncccc cggaanaaaa cctccggttt
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nacttnnccg ggggnaaaaa aggggggggt ttnattngnc nttaagnccc nccccaaggg
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anaancccan nnaaggnttt ggaananncn nnn
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120

agaagatgag cgtccaaaag ttgcctacaa taacttcagc aacgagattc caatcatttc
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tcttgctgga attgatgagg ttgatggncn cacancacac atctgnncca nattgctgga
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gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
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ggaattgatg aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt
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gagaattggg gtatttttca ggttgttgat catggtgttg atacaaaact tgtttctgag
300

atgacccgtt ttgctagaga gtttttgct ttgccaccgg aagagaagct ccggtttgac
360

atgtccggtg gtaaaaaggg tggtttcatt gtctctagtc atcttcaagg agaagcagtg
420

aaggattgga gagagctagt gacatatttt tcatacccaa ttaaacaaag agattattca
480

aggtggccag acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta
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aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg
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aggttgatgg tcgcagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg
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gtatttttca ggttgttgat catggtgttg atacaaagct tgtttctgag atgactcgtt
300

ttgctagaga gtttttgct ttgccgccgg aagagaagct ccggtttgac atgtccggtg

360

gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg aaagattgga
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gggagctagt gacatatttt tcatacccaa ttaaacaaag agattattca aggtggccag
480

acaagccaga aggatggaaa gaagtaacag aaaaatacag tgaaaaccta atgaatttag
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120

gcgtccaaaa gttgcctaca ataacttcag caacgagatt ccaatcattt ctcttgctgg
180

aattgatgag gttgatggtc gtagaacaga gatatgtaac aagattgttg aagcttgtga
240

gaattggggt atttttcagg ttgttgatca tggtgttgat acaaaacttg tttctgagat
300

gacccgtttt gctagagagt tttttgcttt gccaccggaa gagaagctcc ggtttgacat
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gatgagcgtc caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt
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gctggaattg atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct
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tgtgagaatt ggggtatttt tcaggttgtt gatcatggtg ttgatacaaa acttgtttct
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gagatgaccc gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt
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gacatgtccg gtggtaaaaa gggtggtttc attgtctcta gtcatctcca aggagaagca
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gtgaaggatt ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat
480

tcaaggtggc cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac
540

ctaatgaatt tagcttgcaa actattggaa gttttatcag aagcaatggg tttagaaaaa
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aagatgagcg tccaaaagtt gcctacaata acttcagcaa cgagattcca atcatttctc
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ttgctggaat tgatgaggtt gatggtcgaa gaacagagat atgtaacaag attgttgaag
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cttgtgagaa ttggggtatt tttcaggttg ttgatcatgg tgttgataca aaacttgttt
300

ctgagatgac ccgttttgct agagagtttt ttgctttgcc accggaagag aagctccggt
360

ttgacatgtc cggtggtaaa aagggtggtt tcattgtctc tagtcatctc caaggagaag
420

cagtgaagga ttggagagag ctagtgacat atttttcata cccaattaaa caaagagatt
480

attcaaggtg gccagacaag ccagaaggat ggaaagaggt aacagaaaaa tacagtgaaa

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120

tgagcgtcca aaagttgcct acaataactt cagcaacgag attccaatca tttctcttgc
180

tggaattgat gaggttgatg gtcgtagaac agagatatgt aacaagattg ttgaagcttg
240

tgagaattgg ggtatttttc aggttgttga tcatggtgtt gatacaaaac ttgtttctga
300

gatgacccgt tttgctagag agtttttgc tttgccaccg gaagagaagc tccggtttga
360

catgtccggt ggtaaaaagg gtggtttcat tgtctctagt catctccaag gagaagcagt
420

gaaggattgg agagagctag tgacatattt ttcataccca attaaacaaa gagattattc
480

aaggtggcca gacaagccag aaggatggaa agaggtaaca gaaaaataca gtgaaaacct
540

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600

agctctaaca
610

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120

gatgagcgtc caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt
180

gctggaattg atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct
240

tgtgagaatt ggggtatttt tcaggttgtt gatcatggtg ttgatacaaa acttgtttct
300

gagatgaccc gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt
360

gacatgtccg gtggtaaaaa gggtggtttc attgtctcta gtcatcttca aggagaagca
420

gtgaaggatt ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat
480

tcaaggtggc cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac
540

ctaatgaatt tagcttgcaa gctattggaa gttttatcag aagcaatggg ttn
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aaactctaag ttatctctca caacaaaaca ctctcgagtc aagtttcgtt agggaagaag
120

atgagcgtcc aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg
180

ctggaattga tgaggttgat ggnnnnggna ccnggnnatg tggnnagagg acgnnn
236

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agttatctct cacaacaaaa cactctcgag tcaagtttcg ttagggaaga agatgagcgt
120

ccaaaagttg cctacaataa cttcagcaac nagattccaa tcatttctct tgctggaatt
180

gatgaggttg atggtcgnag aacanagata tgtaacaaga ttgttgaagc ttgtgagaat
240

tggggtattt ttcangttgt tgatcatggn gtn
273

<210> 223
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actctaagtt atctctcaca acaaaaaacc gtcgagtcaa gtttcgttag ggaagaagat
120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgcagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatttttca ggttgttgat catggtgttg atacaaagct tgtttctgag
300

atgactcgtt ttgctagaga gttttttgct ttgccgccgg aagagaagct ccggtttgac
360

atgtccggtg gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg
420

aaagattgga gagagctagt gacatatttt tcatacccaa ttaaacaaag agattattca
480

aggtggccag acaagccaga aggatggaaa gaagtaacag aaaaatacag tgaaaaccta
540

atgaatttag cttgcaagct attggaagtt tt
572

<210> 224
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actctaagtt atctctnnca acaaaacact cttgagtcna gtttcgttag ggaagaagat
120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatttttca ggttgttgat catggtgttg atacaaaact tgtttctgag
300

atgacccgtt ttgctagaga gttttttgct ttgccaccgg aagagaagct ccggtttgac
360

atgtccggtg gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg

420

aaggattgga gagagctagt gacatatttt tcatacccaa ttaaacaaag agattattca
480

aggtggccag acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta
540

atgaatttag cttgcaaact attggaagtt ttatc
575

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taagttatct ctcacaacaa aacactctcg agtcaagttt cgttagggaa gaagatgagc
120

gtccaaaagt tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa
180

ttgatgaggt tgatggtcgt agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attggggtat ttttcaggtt gttgatcatg gtgttgatac aaaacttgtt tctgagatga
300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt
360

ccggtggtaa aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtgaa aacctaatga
540

atttagcttg caaactattg gaagttttat cagaagcaat gggtttagaa aaagag
596

<210> 226
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agttatctct ccaacaaaac actcttgagt caagtttcgt tagggaagaa gatgagcgtc
120

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180

atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240

ggggtatttt tcaggttgtt gatcatggtg ttgatacaaa acttgtttct gagatgaccc
300

gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
360

gtggtaaaaa gggtggtttc attgtctcta gtcatctcca aggagaagca gtgaaggatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc
480

cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac ctaatgaatt
540

tagcttgcaa actattggaa gttttatcag aagcaatggg tttagaaaaa gaagctctaa
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caaaagcatg tg
612

<210> 227
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ttatctctnc aacaaaacac tcttgagtca agtttcgtta gggaagaaga tgagcgtcca 120

aaagttgcct acaataactt cagcaacgag attccaatca tttctcttgc tggaattgat 180

gaggttgatg gtcgtagaac agagatatgt aacaagattg ttgaagcttg tgagaattgg 240

ggtatttttc aggttgttga tcatggtgtt gatacaaaac ttgtttctga gatgacccgt 300

tttgctagag agttttttgc tttgccaccg gaagagaagc tccggtttga catgtccggt 360

ggtaaaaagg gtggtttcat tgtctctagt catctccaag gagaagcagt gaaggattgg 420

agagagctag tgacatattt ttcataccca attaaacaaa gagattattc aaggtggcca 480

gacaagccag aaggatggaa agaggtaaca gaaaaataca gtgaaaacct aatgc 535

<210> 228
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120

aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg ctggaattga
180

tgaggttgat ggtcgtagaa cagagatatg taacaagatt gttgaagctt gtgagaattg
240

gggtattttt caggttgttg atcatggtgt tgatacaaaa cttgtttctg agatgacccg
300

ttttgctaga gagtttttg ctttgccacc ggaagagaag ctccggtttg acatgtccgg
360

tggtaaaaag ggtggtttca ttgtctctag tcatctccaa ggagaagcag tgaaggattg
420

gagagagcta gtgacatatt tttcataccc aattaaacaa agagattatt caaggtggcc
480

agacaagcca gaaggatgga aagaggtaac agaaaaatac agtgaaaacc taatgaattt
540

agcttgcaaa ctattggan
559

<210> 229
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120

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180

atgaggttga tggtcgcaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240

ggggtatttt tcaggttgtt gatcatggtg ttgatacaaa gcttgtttct gagatgactc
300

gttttgctag agagtttttt gctttgccgc cggaagagaa gctccggttt gacatgtccg
360

gtggtaaaaa gggtggtttc attgtctcta gtcatctcca aggagaagca gtgaaagatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc
480

cagacaagcc agaaggatgg aaagaagtaa cagaaaaata cagtgaaaac ctaatgaatt
540

tagcttgcaa gctattggaa gtttt
565

<210> 230
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taagttatct ctcncaacaa aacactctcg agtcaagttt cgttagggaa gaagatgagc
120

gtccaaaagt tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa

180

ttgatgaggt tgatggtcga agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attggggtat ttttcaggtt gttgatcatg gtgttgatac aaaacttgtt tctgagatga
300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt
360

ccggtggtaa aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtgaa aacctaatga
540

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591

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taccaaaagt tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa 180

ttgatgaggt tgatggtcgt agaacagaga tatgtaacaa gattgttgaa gcttgtgaga 240

attggggtat ttttcaggtt gttgatcatg gtgttgatac aaaacttgtt tctgagatga 300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt 360

ccggtggtaa aaagggtggt ttcattgtct ctagtcatct tcaaggagaa gcagtgaagg 420

attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt 480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtgaa aacctaatga 540

atttagcttg caagctattg gaagttttat cagaagcaat gggtttagaa aaagaagctc 600

taacaaaag 609

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tccaacaaaa cactctcgag tcaagtttcg ttagggaaga agatgagcgt ccaaaagttg 120

cctacaataa cttcagcaac gagattccaa tcatttctct tgctggaatt gatgaggttg 180

atggtcgtag aacagagata tgtaacaaga ttgttgaagc ttgtgagaat tggggtattt 240

ttcaggttgt tgatcatggt gttgatacaa aacttgtttc tgagatgacc cgttttgcta 300

gagagttttt tgctttgcca ccggaagaga agctccggtt tgacatgtcc ggtggtaaaa 360

agggtggttt cattgtctct agtcatctcc aaggagaagc agtgaaggat tggagagagc 420

tagtgacata tttttcatac ccaattaaac aaagagatta ttcaaggtgg ccagacaagc 480

cagaaggatg gaaagaggta acagaaaaat acagtgaaaa cctaatgaat ttagcttgca 540

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<210> 233
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120

agttgcctac aataacttca gcaacgagat tccaatcatt tctcttgctg gaattgatga
180

ggttgatggt cgtagaacag agatatgtaa caagattgtt gaagcttgtg agaattgggg
240

tatttttcag gttgttgatc atggtgttga tacaaaactt gtttctgaga tgacccgttt

300

tgctagagag ttttttgctt tgccaccgga agagaagctc cggtttgaca tgtncggtgg
360

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418

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120

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180

atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240

ggggtatttt tcaggttgtt gatcatggtg ttgatacaaa acttgtttct gagatgaccc
300

gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
360

gtggtaaaaa gggtggtttc attgtctcta gtcatctcca aggagaagca gtgaaggatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc
480

cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaaaac ctaatgaatt
540

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570

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120

aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg
180

aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg
240

gtatttttca ggttgttgat catggtgttg atacaaaact tgtttctgag atgacccgtt
300

ttgctagaga gttttttgct ttgccaccgg aagagaagct ccggtttgac atgtccggtg
360

gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg aaggattgga
420

gagagctagt gacatatttt tcatacccaa ttaaataaag agattattca aggtggccag
480

acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta atgaatttag
540

cttgcaaact attggaagtt ttatcagaag caatgggttt agaaaaagaa gctctaacaa
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aagcatgt
608

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120

tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180

tgatggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attggggtat
240

ttttcaggtt gttgatcatg gtgttgatac aaagcttgtt tctgagatga ctcgttttgc
300

tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa
360

aaagggtggt ttcattgtct ctagtcgtct ccaaggagaa gcagtgaaag attggagaga
420

gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt ggccagacaa
480

gccagaagga tggaaagaag taacanaaaa atacagtgaa aacctaatga atttancttg
540

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600

nt
602

<210> 237
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tcccacaaaa cactcttgag tcagtttcgt tagggaagaa gatgagcgtc caaaagttgc
120

ctacaataac ttcagcaacg agattccaat cattnctctt gctggaattg atgaggttga
180

tggtcgcaga acagagatat gtaacaagat tgttgaagct tgtgagaatt ggggtatttt
240

tcaggttgtt gatcatggtg ttgatacaaa ncttgtttct gagatgaccc gttttgctag
300

agagtttttt gctntgccac cggaagagaa gctccggttt gacatgtccg gtggtaaaaa
360

gggtggtttc attgtctcta gtcatctnca agganaagca ntgaaggatt ggagagagct
420

agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc cagacaagcc
480

agaaggatgg aaagaggtna cagaaaaata cagcgaaaac ctaatgaatt tanctn
536

<210> 238
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ctctcacaac aaaagactct tgagtcnagt ttcgttaggg aagaagatga gcgtccaaaa
120

gttgcctaca ataacttcag caacgagatt ccaatcattt ctcttgctgg aattgatgag
180

gttgatggtc gcagaacaga gatatgtaac aagattgttg aagcttgtga gaattggggt
240

atttttcagg ttgttgatca tggtgttgat acaaagcttg tttctgagat gactcgtttt
300

gctagagagt tttttgcttt gccgccggaa gagaagctcc ggtttgacat gtccggtggt
360

aaaaagggtg gtttcattgt ctctagtcat ctccaaggag aagcagtgaa agattggagg
420

gagctagtga catatttttc atacccaatt aaacaaagag attattcaag gtggccagac
480

aagccagaag gatggaaaga agtaacagaa aaatacagtg aaaacctaat gaatttagct
540

tgcaagctat tggaagtttt atcagaagca at
572

<210> 239

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tctcncaaca aaacactctc gagtcaagtt tcgttaggga agaagatgag cgtccaaaag
120

ttgcctacaa taacttcagc aacgagattc caatcatttc tcttgctgga attgatgagg
180

ttgatggtcg aagaacagag atatgtaaca agattgttga agcttgtgag aattggggta
240

tttttcaggt tgttgatcat ggtgttgata caaaacttgt ttctgagatg acccgttttg

300

ctagagagtt ttttgctttg ccaccggaag agaagctccg gtttgacatg tccggtggta
360

aaaagggtgg tttcattgtc tctagtcatc tccaaggaga agcagtgaag gattggagag
420

agctagtgac atatttttca tacccaatta aacaaagaga ttattcaagg tggccagaca
480

agccagaagg atggaaagag gtaacagaaa aatacagtga aaacctaatg aatttagctt
540

gcaaactatt ggaagtttta tcagaagcaa tgg
573

<210> 240
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ctcacaacaa aagactcttg agtcaagttt cgttagggaa gaagatgagc gtccaaaagt
120

tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180

tgatggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attggggtat
240

ttttcaggtt gttgatcatg gtgttgatac aaagcttgtt tctgagatga ctcgttttgc
300

tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa
360

aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaaag attggaggga
420

gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt ggccagacaa
480

gccagaagga tggaaagaag taacagaaaa atacagtgaa aacctaatga atttagcttg
540

caagctattg gaagttttat cagaagcaat ggg
573

<210> 241
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ctcacaacaa aagactcttg agtcaagttt cgttagggaa gaagatgagc gtccaaaagt 120

tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt 180

tgatggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attggggtat 240

ttttcaggtt gttgatcatg gtgttgatac aaagcttgtt tctgagatga ctcgttttgc 300

tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa 360

aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaaag attggagaga 420

gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt ggccagacaa 480

gccagaagga tggaaagaag taacagaaaa atacagtgaa aacctaatga atttagcttg 540

caagctattg gaagttttat cagaagcaat gggattagaa aaag 584

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tccaaaagtt gcctacaata acttcagcaa cgagattcca atnatttctc ttgctggaat
120

tgatgaggtt gatggtcgca gaacagagat atgtaacaag attgttgaag cttgtgagaa
180

ttggggtatt tttcaggttg ctgatcatgg tgttgataca aagcttgttt ctgagatgac
240

tcgttttgct agagagtttt ttgctttgcc gccggaagag aagctccggt ttgacatgtc
300

cggtggtaaa aagggtggtt tcattgtctc tnntcatctc caaggagaag cagngaaaga
360

ttggaganag ctagtgacat atttntcata cccaattaaa caaagagatt atncaaggtg
420

gtcanacnag ccagaaggat ggaaagaagt aacagaaaaa tacagtgaaa acctaatgaa

480

tttacctngc aagctattgg aagttttata ataancnatg gnattaaga
529

<210> 243
<211> 698
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120

ggaagagaag ctccggtttg acatgtccgg tggtaaaaag ggtggtttca ttgtctctag
180

tcatctccaa ggagaagcag tgaaggattg gagagagcta gtgacatatt tttcataccc
240

aattaaacaa agagattatt caaggtggcc agacaagcca gaaggatgga aagaggtaac
300

agaaaaatac agtgaaaacc taatgaattt agcttgcaaa ctattggaag ttttatcaga
360

agcaatgggt ttagaaaaag aagctctaac aaaagcatgt gttgatatgg atcaaaaagt
420

tgttataaat tattacccaa aatgccctga acctgacctc acacttggcc ttaaacgtca
480

cactgaccct ggcacaatta ctcttttgct tcaagatcaa gttggtggtc ttcaagctac
540

caaagataat ggtaagacgt ggattacagt tcaaccagtt gaaggtgctt ttgttgttaa
600

tcttggagac catggtcact atctaagtaa tggacggttc aaaaatgctg accatcaagc
660

agtggtgaat tcgaactaca gccgnttatc aatagcaa
698

<210> 244
<211> 579
<212> DNA
<213> Trifolium repens

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<222> (29)..(29)
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ttaaacgcca cactgaccct ggnacaatta ctcttttgct tcaagatcaa gttggtggcc
120

ttcaagctac caaagataat ggtaagacgt ggattacagt tcaaccagtt gaaggtgctt
180

ttgttgttaa tcttggagac catggtcatt atctaagtaa tggacggttc aaaaatgctg
240

accaccaagc agtggtgaat tcgaactaca gccgtttatc aatagcaaca tttcaaaatc
300

cagctcccga tgcaactgta taccctttga agattagaga gggtgaaaaa tctgtgttgg
360

aagaaccaat cacttttgct gaaatgtata gaaggaagat gaccaaagac cttgaaattg
420

ctaggatgaa gaagttggct aaggaacaac aacttaggga cttggaggag aacaagacta
480

aatatgaggc caaacctttg aatgagatct ttgcttaatt aattagtctt aatttaaata
540

attaataaat tttagactta atttacatat aataatttt
579

<210> 245
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aagtaaaata ccataacaca ataatatgaa taccataatc ttgaatcata caaacaacct
120

tggatcaaac aaaacaacaa ccatggttga tctagaaaca gaaccaagtt caccatttat
180

tcaatcccca gaacacagac caaaatcctc aataatcatt gctgaaggta tccctctaat
240

tgatctcact cctataaact acaaagatga aatcatcacc aacccacttt ccattgaaga
300

cttagtcaaa gaaataggca aagcatgtaa agaatggggt ttctttcaag tgattaatca
360

caaagttcct ttggataaac gtgaaaggat tgaagaatct tcaaagaagt tttttgaact
420

tagtttggag gaaaaactta aggtgagaag agatgaagtt aatttgcttg gttattttga
480

agctgagcat acaaaaaatg ttagggactg gaaggaaatt tatgatttta atgtgcaaca
540

accaactttt ataccacctt cggatgacca aagttttcag tttcaatggg aaaatcgatg
600

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601

<210> 246
<211> 172
<212> PRT
<213> Trifolium repens

<400> 246

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Thr Thr Thr Met Val Asp Leu Glu Thr Glu Pro Ser Ser Pro Phe Ile
20 25 30

Gln Ser Pro Glu His Arg Pro Lys Ser Ser Ile Ile Ile Ala Glu Gly
35 40 45

Ile Pro Leu Ile Asp Leu Thr Pro Ile Asn Tyr Lys Asp Glu Ile Ile
50 55 60

Thr Asn Pro Leu Ser Ile Glu Asp Leu Val Lys Glu Ile Gly Lys Ala
65 70 75 80

Cys Lys Glu Trp Gly Phe Phe Gln Val Ile Asn His Lys Val Pro Leu
85 90 95

Asp Lys Arg Glu Arg Ile Glu Glu Ser Ser Lys Lys Phe Phe Glu Leu
100 105 110

Ser Leu Glu Glu Lys Leu Lys Val Arg Arg Asp Glu Val Asn Leu Leu
115 120 125

Gly Tyr Phe Glu Ala Glu His Thr Lys Asn Val Arg Asp Trp Lys Glu
130 135 140

Ile Tyr Asp Phe Asn Val Gln Gln Pro Thr Phe Ile Pro Pro Ser Asp
145 150 155 160

Asp Gln Ser Phe Gln Phe Gln Trp Glu Asn Arg Trp
165 170

<210> 247
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cagctttctt caaatccaga aaataggcca aaactttcca taatccaagc tgaaggaatt
120

cctgtaatca atctctcccc attaattcac cacacagttc aagactcctc tgccattgaa
180

agcttagtca aagaaatagg aaatgcttgc aaggaatggg gtttcttcca agtaacaaac
240

catggtgtcc ctctaaatct aaggctcaga ctcgaggaag ctaccaaagt tttctttgca
300

cagagtttgg aggagaagag gaagcttacc gtagatgata acagtttgcc tggttatcat
360

gatacagagc acaccaagaa tgtcagagac tggaaagaag tgtttgattt tttatccaaa
420

gaccccactt tgattcctct gaattctgat gaacatgatg atcgagtcac tcaatggact
480

aatccatccc ctcaatatcc tccaaacttc aaagttattt tggaagagta tattaaagag
540

atggaaaagc taggctttaa gttgctagag cttatagctt tgagc
585

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<212> PRT
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<400> 248

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Asn Pro Glu Asn Arg Pro Lys Leu Ser Ile Ile Gln Ala Glu Gly Ile
20 25 30

Pro Val Ile Asn Leu Ser Pro Leu Ile His His Thr Val Gln Asp Ser
35 40 45

Ser Ala Ile Glu Ser Leu Val Lys Glu Ile Gly Asn Ala Cys Lys Glu
50 55 60

Trp Gly Phe Phe Gln Val Thr Asn His Gly Val Pro Leu Asn Leu Arg
65 70 75 80

Leu Arg Leu Glu Glu Ala Thr Lys Val Phe Phe Ala Gln Ser Leu Glu
85 90 95

Glu Lys Arg Lys Leu Thr Val Asp Asp Asn Ser Leu Pro Gly Tyr His
100 105 110

Asp Thr Glu His Thr Lys Asn Val Arg Asp Trp Lys Glu Val Phe Asp
115 120 125

Phe Leu Ser Lys Asp Pro Thr Leu Ile Pro Leu Asn Ser Asp Glu His
130 135 140

Asp Asp Arg Val Thr Gln Trp Thr Asn Pro Ser Pro Gln Tyr Pro Pro
145 150 155 160

Asn Phe Lys Val Ile Leu Glu Glu Tyr Ile Lys Glu Met Glu Lys Leu
165 170 175

Gly Phe Lys Leu Leu Glu Leu Ile Ala Leu Ser
180 185

<210> 249
<211> 604
<212> DNA
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120

attcaaggtg tacaaggaaa aatgaagaaa ttacataaaa gatttgatgc atttttaact
180

agcattattg aagatcacat gatttccaag agtgagaagc ataatgactt attgagtacg
240

ttgttatcac taaaagaaaa agttgatgag gatggtgaca aacttaatga tactgagatc
300

aaagcattac tcttgaacat gttcacagct ggaacagaca catcatcaag cacaacagag
360

tgggctattg ctgaactaat aaaaaatcca aaactaatga ttcgtgttca aaatgagttg
420

gacactgttg tgggccgaga caagcttgta actgaacaag acttggccca tcttccttac
480

ttagaggctg taataaagga gacatttcgt ctccatccat caacccctct ttctctccca
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cgtgttgcaa caaatagttg tgaaatcctc gactatcaca ttcccaaagg tgcaactctc
600

ttgg
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<210> 250
<211> 201
<212> PRT
<213> Trifolium repens

<400> 250

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Val Val Glu Leu Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe
20 25 30

Val Pro Ala Leu Glu Trp Leu Asp Ile Gln Gly Val Gln Gly Lys Met
35 40 45

Lys Lys Leu His Lys Arg Phe Asp Ala Phe Leu Thr Ser Ile Ile Glu
50 55 60

Asp His Met Ile Ser Lys Ser Glu Lys His Asn Asp Leu Leu Ser Thr
65 70 75 80

Leu Leu Ser Leu Lys Glu Lys Val Asp Glu Asp Gly Asp Lys Leu Asn
85 90 95

Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr
100 105 110

Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala Glu Leu Ile Lys
115 120 125

Asn Pro Lys Leu Met Ile Arg Val Gln Asn Glu Leu Asp Thr Val Val
130 135 140

Gly Arg Asp Lys Leu Val Thr Glu Gln Asp Leu Ala His Leu Pro Tyr
145 150 155 160

Leu Glu Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro
165 170 175

Leu Ser Leu Pro Arg Val Ala Thr Asn Ser Cys Glu Ile Leu Asp Tyr
180 185 190

His Ile Pro Lys Gly Ala Thr Leu Leu
195 200

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120

atattcaagg tgtacaagga aaaatgaaga aattacataa aagatttgat gcatttttaa
180

ctagcattat tgaagatcac atgatttcca agagtgagaa gcataatgac ttattgagta

240

cgttgttatc actaaaagaa aaagttgatg aggatggtga caaacttaat gatactgaga
300

tcaaagcatt actcttgaac atgttcacag ctggaacaga cacatcatca agcacaacag
360

agtgggctat tgctgaacta ataaaaaatc caaaactaat gattcgtgtt caaaatgagt
420

tggacactgt tgtgggccga gacaagcttg taactgaaca agacttggcc catcttcctt
480

acttagaggc tgtaataaag gagacatttc gtctccatcc atcaacccct ctttctctcc
540

cacgtgttgc aacaaatagt tgtgaaatcc tcgactatca c
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120

ttcaaggtgt acaaggaaaa atgaagaaat tacataaaag atttgatgca tttttaacta
180

gcattattga agatcacatg atttccaaga gtgagaagca taatgactta ttgagtacgt
240

tgttatcact aaaagaaaaa gttgatgagg atggtgacaa acttaatgat actgagatca
300

aagcattact cttgaacatg ttcacagctg gaacagacac atcatcaagc acaacagagt
360

gggctattgc tgaactaata aaaaatccaa aactaatgat tcgtgttcaa aatgagttgg
420

acactgttgt gggccgagac aagcttgtaa ctgaacaaga cttggcccat cttccttact
480

tagaggctgt aataaaggag acatttcgtc tccatccatc aacccctctt tctctcccac
540

gtgttgcaac aaatagttgt gaaatcctcg actatcacat tcccaaaggt gcaactctct
600

tgg
603

<210> 253
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<212> DNA
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120

tatntactat tttaagatat ggaagtagta gcagcagcaa tcacaaaaaa caatggcaag
180

attgattcat tttgcttgaa tcatgctaat gctaataaca tgaaagtgaa tggtgctgat
240

cctttgaatt ggggtgtggc tgctgaggca atgaagggaa gtcacttgga tgaggtgaag
300

cgtatggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac actgacgatt
360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tggagctatc ggaatctgct
420

agagccggcg ttaaggcgag cagtgactgg gttatggaga gtatgaacaa aggtacagac
480

agttatggtg tcactacagg gttcggcgct acctcgcacc gccgaaccaa acaaggtggt
540

gctttgcaga aagagctcat aaggtntttt gaatgcagga atatttggaa atggaacntg
600

agacaaagcc acacactacc c
621

<210> 254
<211> 159
<212> PRT
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<400> 254

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Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Gly
20 25 30

Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Val
50 55 60

Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Thr Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110

Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Ser His Arg
115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Glu
130 135 140

Cys Arg Asn Ile Trp Lys Trp Asn Arg Gln Ser His Thr Leu Pro
145 150 155

<210> 255
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120

tatntactat tttaagatat ggaagtagta gcancagcaa tcacaaaaaa caatggcaag
180

attgattcat tttgcttgaa tcatgctaat gctaataaca tgaaagtgaa tggtgctgat
240

cctttgaatt ggggtgtggc tgctgaggca atgaagggaa gtcacttgga tgaggtgaag
300

cgtatggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac gctgacgatt
360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tgganctatc ggaatctgct
420

agagccggcg ttaaggcgag cagtgactgg gttatggaga gcatgaacaa aggtacagac
480

agttatggtg tcactacggg gttcggcgct acctcncacc gccgaaccaa acaaggtggt
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120

tatntactat nttaagatat ggaagtagta gcagcagcaa tcacaaaaaa caatggcaag
180

attgattcat tttgcttgaa tcatgctaat gctaataaca tgaaagtgaa tggtgctgat
240

cctttgaatt ggggtgtggc tgctgaggca atgaagggaa gtcacttgga tgaggtgaag
300

cgtatggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac actaaccatt
360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tggagctatc ggaatctgct
420

agagccggcg ttaaggcaag cagtgactgg gttatggaga gtatgaacaa aggtaccgac
480

agctacggtg tcccaacagg gttcggcgct acctcgcacc gccgaaccaa acaaggtggt

540

gctttgcaga aagagctcat aaggtntttt gaatgctgga atatttggaa atggaacntg
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agtcnaagcc acacactacc c
621

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tttaagnnat ggaagtagta gcagcagcaa tcacaaaaaa caacggaaag attgattcat 180

tttgcttgaa tcatgctaat gctaataaca tgaaagtgaa tggtgctgat cctttgaatt 240

ggggtgtggc tgctgaggca atgaaaggaa gtcacttgga tgaggtgaag tgtatggtgg 300

aggagtatcg aaaaccggtt gtccgtcttg gtggcgagac actgacgatt tctcaagtgg 360

ctgccattgc tgcacacgat ggtgcgacgg tggagctatc ggaatctgct agagccggcg 420

ttaaggcgag cagtgactgg gttatggaaa gtatgaacaa aggtactgac agttatggtg 480

tcactacagg gttcggcgct acctcgcacc gccgaaccaa acaaggtggt gctttgcaga 540

aagagctcat aaggtntttt gaatgcagga atatttggaa atggaacttg anacaaatcc 600

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cttatttccc cccacacaac ataacnaata cattntcctc tcctctcatc acaattatta
120

ctttctacac acccccctct caactattat taactaacat aatggaggga attaccaatg
180

gccatgctga agcaactttt tgcgtgacca aaagtgttgg tgatccactc aactggggtg
240

cagccgcgga gtcgttgatg gggagtcatt tggatgaggt gaagcgtatg gtggaggaat
300

accgtaatcc attggttaaa attggcggcg agacgcttac cattgctcag gtggctggaa
360

ttgcttctca tgatagtggt gtgagggtgg agctgtctga gtccgccagg gccggcgtta
420

aggcgagtag tgattgggtg atggacagca tgaacaatgg gactgatagt tatggtgtta
480

ccaccggttt cggcgccacc tctcaccgga gaaccaagca gggtggtgcc ttgcagaagg
540

agctaattag gtttttgaat gctggaatat ttggcaatgg tacagaatct aactgtacac
600

taccacacac agcaaccaga gctgcaatgc ttgtgagaat caacactctt cttcaagagg
660

aatatttctt gaatggcctt tgtaaatttt tgg
693

<210> 259
<211> 177
<212> PRT
<213> Trifolium repens

<400> 259

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Lys Ser Val Gly Asp Pro Leu Asn Trp Gly Ala Ala Ala Glu Ser Leu
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Met Gly Ser His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg
        35                  40                  45

Asn Pro Leu Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Gln Val
    50                  55                  60

Ala Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
65                  70                  75                  80

Ser Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Asp Ser
                85                  90                  95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
            100                 105                 110

Thr Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu
        115                 120                 125

Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Asn
    130                 135                 140

Cys Thr Leu Pro His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile
145                 150                 155                 160

Asn Thr Leu Leu Gln Glu Glu Tyr Phe Leu Asn Gly Leu Cys Lys Phe
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Leu
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120

ttaactangc ataatggagg gaattaccaa tggccagctg ctttcaaaaa aaaaccaatg
180

gccatgctga aacaactttt tgcgtgacca aaagtgttgg tgatccactc aactggggtg
240

cagccgcgga gtcgttgacg ggtagtcatt tggatgaggt gaagcgtatg gtggaggagt
300

accgtaatcc gttggttaaa attggcggcg agacgcttac cattgctcag gtggctggaa
360

ttgcttctca tgatagtggt gtgagggtgg agctgtccga gtccgcaagg gccggcgtta
420

aggcgagtag tgattgggtg atggatagca tgaacaatgg gactgatagt tacggtgtta
480

ccaccggttt tggtgccacc tctcaccgga gaaccaagca gggtggtgcc ttgcagaagg
540

agctaattag gtttttgaat gctggaatat ttggcaatgg tacagaatct an
592

<210> 261
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120

taatggaggg aattaccaat ggccatgctg aagcaacttt ttgcgtgacc aaaagtgttg
180

gtgatccact caactggggt gcagccgcgg agtcgttgat ggggagtcat ttggatgagg
240

tgaagcgtat ggtggaggaa taccgtaatc cattggttaa aattggcggc gagacgctta
300

ccattgctca ggtggctgga attgcttctc atgatagtgg tgtgagggtg gagctgtctg
360

agtccgcgag ggccggcgtt aaggcgagta gtgattgggt gatggacagc atgaacaatg
420

ggactgatag ttatggtgtt accaccggtt tcggtgccac ctctcaccgg agaaccaagc
480

aaggtggtgc cttgcagaag gagctaatta ggtttttgaa tgctggaata tttggcaatg
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gtacagaatc taactgtaca ctaccacaca cagcaaccag agctgcaatg cttgtgagaa
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tcaacactct tcttcaag
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<210> 262
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taatggaggg aattactaat ggccatgctg aagcaacttt ttgcgtnacc aaaagtgttg
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gtgatccact caactggggt gcagccgcgg agtcgntgat ggggagtnat ttggatgagg
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tgaancgtat ggtggaggaa taccgtaatc cattggttaa aattggcggc gagacgctta
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ccattgctca ggtggctgga attgcttctc atgatagngn tgtgagggtg gagctgtctg
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agtncgccag ggccggcgtt aangcgagta gtgattgngt gatggacagn atgaacaatg
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ggactgatag ttatggngtn accaccggtt tcggcgccac ctctcaccgg agaaccaagc
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agggtggtgc cttgcaaaag gagctaatta tgtttttgaa tgctggaata tttggcaatg
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gtacagaatc taactgtaca cttcnacaca cagcaaccan agntgcattg ctttggtgca
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atggagggaa ttactaatgg ccatgctgaa gcaacttttt gcgtgaccaa aagtgttggt
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gatccactca actggggtgc agccgcggag tcgttgatgg ggagtcattt ggatgaggtg
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aagcgtatgg tggaggaata ccgtaatcca ttggttaaaa ttggcggcga gacgcttacc
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tccgccaggg ccggcgttaa ggcgagtagt gattgggtga tggacagcat gaacaatggg
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actgatagtt atggtgttac caccggtttc ggcgccacct ctcaccggag aaccaagcag
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ggtggtgcct tgcagaagga gctaattagg tttttgaatg ctggaatatt tggcaatggt
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tggagggaat taccaatggc catgctgaaa caactttttg cgtgaccaaa agtgttggtg
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atccactcaa ctggggtgca gccgcggagt cgttgacggg gagtcatttg gatgaggtga
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agcgtatggt ggaggagtac cgtaatccgt tggctaaaat tggcggcgag acgcttacca
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ttgctcaggt ggctggaatt gcttctcatg atagtggtgt gagggtggag ctgnncgagt
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360

ccgccagggc cggcgttaag gcgagtagtg gttgggtgat ggacagcatg aacaatggga
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ctgatagtta tggtgttacc actggtttcg gcgccacctc tcaccggaga accaagcagg
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cggggagtca tttggatgag gtgaagcgta tggtggagga gtaccgtaat ccgttggtta
240

aaattggcgg cgagacgctt accattgctc aggtggctgg aattgcttct catgatagtg
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gtgtgagggt ggagctgtcc gagtccgcaa gggccggcgt taaggcgagt agtgattggg
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tgatggatag catgaacaat gggactgata gttacggtgt taccaccggt tttggtgcca
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cctctcaccg gagaaccaag cagggtggtg ccttgcagaa ggagctaatt aggtttttga
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cgatgtttca aggaacaagg ccattcatgg tggtaacttt caaggaacac ctattggagt
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ttcaatggat aacacacgtt tagctcttgc ttcaattggt aaactcatgt ttgctcaatt
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ctctgaactt gttaatgatt tttacaacaa cgggttgcct tcgaatctta ctgctagtag
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gaacccgagc ttggactatg gtttcaaggg atcggaaatt gccatggctt cgtattgttc
360

cgagttacaa tatcttgcta atcctgtcac cacccatgtc caaagtgccg agcaacacaa
420

ccaagatgtt aactctttgg gtttgatttc atctagaaaa acaaatgaag ctattgagat

480

tctcaagctc atgtcttcca ctttcttgat tgcattatgt caagcaatcg acttaaggca
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Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser Arg Asn Lys Ala Ile
35 40 45

His Gly Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn
50 55 60

Thr Arg Leu Ala Leu Ala Ser Ile Gly Lys Leu Met Phe Ala Gln Phe
65 70 75 80

Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu
85 90 95

Thr Ala Ser Arg Asn Pro Ser Leu Asp Tyr Gly Phe Lys Gly Ser Glu
100 105 110

Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu Gln Tyr Leu Ala Asn Pro
115 120 125

Val Thr Thr His Val Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn
130 135 140

Ser Leu Gly Leu Ile Ser Ser Arg Lys Thr Asn Glu Ala Ile Glu Ile
145 150 155 160

Leu Lys Leu Met Ser Ser Thr Phe Leu Ile Ala Leu Cys Gln Ala Ile
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Asp Leu Arg His Leu Glu Glu Asn Leu Arg Asn Thr Val Lys Asn Thr
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gttaatggaa ctgctgttgg ttctggttta gcttctattg ttctttttga ggctaacata
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gaatttactg atcatttgac acataagttg aagcaccacc ctggtcaaat tgaggctgct
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Val Leu Asn Ala Lys Glu Ala Phe Gln Leu Ala Gly Ile Asn Thr Glu
        35                  40                  45

Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr
    50                  55                  60

Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala Asn Ile
65                  70                  75                  80

Leu Ala Val Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val Met
                85                  90                  95

Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys His
            100                 105                 110

His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu Asp
        115                 120                 125

Gly Ser Ala Tyr Val Lys Asp Ala Lys Lys Leu His Glu Met Asp Pro
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Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln
145                 150                 155                 160

Trp Leu Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile
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120

ctattaagat atggaagtag tagcagcagc aatcacaaaa aacaacggca agattgattc
180

attttgcttg aatcatgcta atgctaataa catgaaagtg aatgatgctg atcctttgaa
240

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cgttaaggca agcagtgatt gggttatgga gagtatgaac aaaggtactg acagttatgg
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35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Ile
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Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Met Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110

Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Xaa His Arg
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gaggagtacc gtaatccgnt ggttaaaatt ggcggcgaga cgcttaccat tgctnnggta
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Asn Pro Xaa Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Xaa Val
    50                  55                  60

Xaa Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
65                  70                  75                  80

Phe Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Xaa Val Met Asp Ser
                85                  90                  95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Xaa Phe Gly Ala
            100                 105                 110

Thr Cys His Arg Arg Thr Lys Pro Xaa Trp Cys Leu Ala Glu Gly Ala
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120

ttatcgtgac caaaagtgnt ggtgatccac tcaactgggg tgcagccgcg gagtcgtcga
180

cggggagtca tttggatgag gtgaagcgta tggnggagga gtaccgtaat ccgntggtta
240

aaattggcgg cgagacgctt accattgctn nggtanctgg aattgcttct catgatagtg
300

gagtgagggt ggagctgtcc gagttcgcaa gggccggcgt taaggcgagt agtgattgng
360

tgatggatag catgaacaat gggactgata gttacggtgt taccaccgcn tttggtgcca
420

cctgtcaccg gagaaccaag ccanggtggt gccttgcaga aggagctaaa ttnnggtgtt
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120

atcaagagtc ttcttgaaaa tggatactct gttaatacca ctattagagc tgatccagaa
180

cgtaagaggg atgtaagctt cctaacaaat ctacccggcg catccgaaag gctacatttc
240

ttcaacgccg atctagacga cccagagagt ttcaacgaag caattgaagg ttgtgtcggg
300

atattccaca ccgcttcacc aatcgatttc gccgtgagtg agccagaaga aatagtgaca
360

aaaagaacag tggatggagc attaggaatt ttaaaagcat gtgtgaattc aaagacagtg
420

aagagattta tttacacttc aagnggttct gctgtttcat tcaatggaaa aaacaaagat
480

gnntnggatg agagtgattg gagtgatgtt gatttgctta gaagtgttaa accatttggt
540

tggagttatg gngtgttcaa gactttggct gagaaagcag tgcttgaatt tggtcnacaa
600

aatgggattg atgttgttac tttgattctt ccttttattg ttggaggttt tgtttgtccc
660

aagcttcctg attctgttga gaaagctctt gttttggtac taggcaaaaa ggaacaaatt
720

ggtattataa gtttccacat ggtacatgta gatgatgtgg ctagagcaca tatctatcta
780

cttgagaatc ctgttccagg aggtagatat aattgttcac cattctttgt atctattgaa
840

gaaatgtcac agcttctctc agccaaatat ccagaatatc aaatactatc agtagatgag
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ttgaaggaaa ttaaaggggc aagattgcca gatttgaact cgaagaagct cgtggacgct
960

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Leu Thr Asn Leu Pro Gly Ala Ser Glu Arg Leu His Phe Phe Asn Ala
    50                  55                  60

Asp Leu Asp Asp Pro Glu Ser Phe Asn Glu Ala Ile Glu Gly Cys Val
65                  70                  75                  80

Gly Ile Phe His Thr Ala Ser Pro Ile Asp Phe Ala Val Ser Glu Pro
                85                  90                  95

Glu Glu Ile Val Thr Lys Arg Thr Val Asp Gly Ala Leu Gly Ile Leu
            100                 105                 110

Lys Ala Cys Val Asn Ser Lys Thr Val Lys Arg Phe Ile Tyr Thr Ser
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Xaa Gly Ser Ala Val Ser Phe Asn Gly Lys Asn Lys Asp Xaa Xaa Asp
    130                 135                 140

Glu Ser Asp Trp Ser Asp Val Asp Leu Leu Arg Ser Val Lys Pro Phe
145                 150                 155                 160

Gly Trp Ser Tyr Xaa Val Phe Lys Thr Leu Ala Glu Lys Ala Val Leu
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Glu Phe Gly Xaa Gln Asn Gly Ile Asp Val Val Thr Leu Ile Leu Pro
            180                 185                 190

Phe Ile Val Gly Gly Phe Val Cys Pro Lys Leu Pro Asp Ser Val Glu
        195                 200                 205

Lys Ala Leu Val Leu Val Leu Gly Lys Lys Glu Gln Ile Gly Ile Ile
    210                 215                 220

Ser Phe His Met Val His Val Asp Asp Val Ala Arg Ala His Ile Tyr
225                 230                 235                 240

Leu Leu Glu Asn Pro Val Pro Gly Gly Arg Tyr Asn Cys Ser Pro Phe
                245                 250                 255

Phe Val Ser Ile Glu Glu Met Ser Gln Leu Leu Ser Ala Lys Tyr Pro
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Glu Tyr Gln Ile Leu Ser Val Asp Glu Leu Lys Glu Ile Lys Gly Ala
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120

atcaagagtc ttcttgaaaa tggatactct gttaatacca ctattagagc tgatccagaa
180

cgtaagaggg atgtaagctt cctaacaaat ctacccggcg catccgaaag gctacatttc
240

ttcaacgccg atctagacga cccagagagt ttcaacgaag caattgaagg ttgtgtcggg
300

atattccaca ccgcttcacc aatcgatttc gccgtgagtg agccagaaga aatagtgaca
360

aaaagaacag tggatggagc attaggaatt ttaaaagcat gtgtgaattc aaagacagtg
420

aagagattta tttacacttc aagnggttct gctgtttcat tcaatgnaaa aancaaagat
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120

aagagtcttc ttgaaaatgg atactctgtt aataccacta ttagagctga tccagaacgt
180

aagagggatg taagcttcct aacaaatcta cccggcgcat ccgaaaggct acatttcttc
240

aacgccgatc tagacgaccc agagagtttc aacgaagcaa ttgaaggttg tgtcgggata
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ttccacaccg cttcaccaat cgatttcgcc gtgagtgagc cagaagaaat agtgacaaaa
360

agaacagtgg atggagcatt aggaatttta aaagcatgtg tgaattcaaa gacagtgaag
420

agatttattt acacttcaag tggttctgct gtttcattca atggaaaaaa caaagatgtt
480

ttggatgaga gtgattggag tgatgttgat ttgcttagaa gtgttaaacc atttggttgg
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120

attctgttga gaaagctctt gttttggtac taggcaaaaa ggaacaaatt ggtattataa
180

gtttccacat ggtacatgtg gatgatgtgg ctagagcaca tatctatcta cttgagaatc
240

ctgttccagg aggtagatat aattgttcac cattctttgt atctattgaa gaaatgtcac
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agcttctttc agccaaatat ccagaatatc aaatactatc tgtagatgag ttgaaggaaa
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ttaaaggggc aaggttgcca gatttgaact cgaagaagct cgtggacgct ggttttgagt
420

ttaagtatag tgtcgatgat atgttcgatg atgcgattca atgctgcaag gaaaaaggct
480

atctctaagc atgtgtttga aaattccatg aagttgagaa aacaatactg tgcctaaaat
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120

agaaagctct tgttttggta ctaggcaaaa aggaacaaat tggtattata agtttccaca
180

tggtacatgt ggatgatgtg gctagagcac atatctatct acttgagaat cctgttccag
240

gaggtagata taattgttca ccattctttg tatctattga agaaatgtca cagcttcttt
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cagccaaata tccagaatat caaatactat ctgtagatga gttgaaggaa attaaagggg

360

caaggttgcc agatttgaac tcgaagaagc tcgtggacgc tggttttgag tttaagtata
420

gtgtcgatga tatgttcgat gatgcgattc aatgctgcaa ggaaaaaggc tatctctaag
480

catgtgtttg aaaattccat gaagttgaga aaacaatact gtgcctaaaa tcaatgatgg
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120

aggcaaaaag gaacaaattg gtattataag tttccacatg gtacatgtag atgatgtggc
180

tagagcacat atctatctac ttgagaatcc tgttccagga ggtagatata attgttcacc
240

attctttgta tctattgaag aaatgtcaca gcttctctca gccaaatatc cagaatatca
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aatactatca gtagatgagt tgaaggaaat taaaggtgca agattgccag atttgaactc
360

gaagaagctc gtggacgctg gttttgagtt taagtatagt gtcgatgata tgtttgatga
420

tgcgattcaa tgctgcaagg aaaaaggcta tctctaagca tgtatttgaa aattccatga
480

agttgagaaa acaataatgt gcctaaaatc aatgatggct aatgagatgt acaagtttat
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120

aggcaaaaag gaacaaattg gtattataag tttccacatg gtacatgtag atgatgtggc
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tagagcacat atctatctac ttgagaatcc tgttccagga ggtagatata attgttcacc
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attctttgta tctattgaag aaatgtcaca gcttctctca gccaaatatc cagaatatca
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aatactatca gtagatgagt tgaaggaaat taaaggtgca agattgccag atttgaactc
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gaagaagctc gtggacgctg gttttgagtt taagtatagt gtcgatgata tgtttgatga
420

tgcgattcaa tgctgcaagg aaaaaggcta tctctaagca tgtatttgaa aattccatga
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agttgagaaa acaataatgt gcctaaaatc aatgatggct aatgagatgt acaagtttat
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120

agtcagagac ccaggcaatc agaagaaggt agcacacctc tggaacttag caggggccaa
180

ggaaaggttg gagcttgtca aagctgacct cttggaagaa gggagcttcg atgatgctgt
240

gatggcctgt gagggtgtct tccacactgc atcacctatc atcaccaaat ctgataccaa
300

ggaagaaatg cttgattctg caattaacgg cactctaaac gtgctgagat cgtgcaagaa
360

gaatcctttt ctcaaaaggg ttgttctcac gtcatcatcg tcaaccgtga ggctgaggga
420

tgaagctgaa ttcccaccca acgtgttgct ggatgaaaca tcatggagct ccgtggagtt
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ctgtgaaagt atccaggtat ggtatggtgt cgcgaagatc cttgctgaga aatcagcttg
540

ggagttcgcc aaggagaaca acatcgacct agtggctgtt cttccaacgt tcgtgattgg
600

acctaatctc tcgtctgaat taggacccac tgttttagat gtccttggct tatttaaagg
660

agagacagag aagttcacca tgtttkggaa ggatg
695

<210> 287
<211> 231
<212> PRT
<213> Lolium perenne

<400> 287

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1 5 10 15

Gly Ala Ser Gly Phe Val Ala Ser Trp Leu Val Lys Arg Leu Leu Glu

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Ser Gly Tyr Asn Val Leu Gly Thr Val Arg Asp Pro Gly Asn Gln Lys
        35                  40                  45

Lys Val Ala His Leu Trp Asn Leu Ala Gly Ala Lys Glu Arg Leu Glu
    50                  55                  60

Leu Val Lys Ala Asp Leu Leu Glu Glu Gly Ser Phe Asp Asp Ala Val
65                  70                  75                  80

Met Ala Cys Glu Gly Val Phe His Thr Ala Ser Pro Ile Ile Thr Lys
                85                  90                  95

Ser Asp Thr Lys Glu Glu Met Leu Asp Ser Ala Ile Asn Gly Thr Leu
            100                 105                 110

Asn Val Leu Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Val Val
        115                 120                 125

Leu Thr Ser Ser Ser Ser Thr Val Arg Leu Arg Asp Glu Ala Glu Phe
    130                 135                 140

Pro Pro Asn Val Leu Leu Asp Glu Thr Ser Trp Ser Ser Val Glu Phe
145                 150                 155                 160

Cys Glu Ser Ile Gln Val Trp Tyr Gly Val Ala Lys Ile Leu Ala Glu
                165                 170                 175

Lys Ser Ala Trp Glu Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Ala
            180                 185                 190

Val Leu Pro Thr Phe Val Ile Gly Pro Asn Leu Ser Ser Glu Leu Gly
        195                 200                 205

Pro Thr Val Leu Asp Val Leu Gly Leu Phe Lys Gly Glu Thr Glu Lys
    210                 215                 220

Phe Thr Met Phe Gly Lys Asp
225                 230

<210>  288
<211>  667
<212>  DNA
<213>  Lolium perenne

<220>
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120

caggcaatca gaagaaggta gcacacctct ggaacttagc aggggccaag gaaaggttgg
180

agcttgtcaa agctgacctc ttggaagaag ggagcttcga tgatgctgtg atggcctgtg
240

agggtgtctt ccacactgca tcacctatca tcaccaaatc tgataccaag gaagaaatgc
300

ttgattctgc aattaacggc actctaaacg tgctgagatc gtgcaagaag aatccttttc
360

tcaaaagggt tgttctcacg tcatcatcgt caaccgtgag gctgagggat gaagctgaat
420

tcccacccaa cgtgttgctg gatgaaacat catggagctc cgtggagttc tgtgaaagta
480

tccaggtatg gtatggtgtc gcgaagatcc ttgctgagaa atcagcttgg gagttcgcca
540

aggagaacaa catcgaccta gtggctgttc ttccaacgtt cgtgattgga cctaatctct
600

cgtctgaatt aggacccact gttttagatg tccttggctt atttaaagga gagacagaga
660

agttcac
667

<210> 289
<211> 688
<212> DNA
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<222> (23)..(23)
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gcttcttggc ttgtcaaaag actactcgag tccggttata atgttctagg gacagtcaga
120

gacccaggca atcagaagaa ggtagcacac ctctggaact tagcaggggc caaggaaagg
180

ttggagcttg tcaaagctga cctcttggaa gaagggagct tcgatgatgc tgtgatggcc

240

tgtgagggtg tcttccacac tgcatcacct atcatcacca aatctgatac caaggaagaa
300

atgcttgatt ctgcaattaa cggcactcta aacgtgctga gatcgtgcaa gaagaatcct
360

tttctcaaaa gggttgttct cacgtcatca tcgtcaaccg tgaggctgag ggatgaagct
420

gaattcccac ccaacgtgtt gctggatgaa acatcatgga gctccgtgga gttctgtgaa
480

agtatccagg tatggtatgg tgtcgcgaag atccttgctg agaaatcagc ttgggagttc
540

gccaaggaga acaacatcga cctagtggct gttcttccaa cgttcgtgat tggacctaat
600

ctctcgtctg aattaggacc cactgtttta gatgtccttg gcttatttaa nggagagaca
660

gagaagttca ccatgttttg gaaggatg
688

<210> 290
<211> 425
<212> DNA
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<222> (425)..(425)
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tnaaagacta ctcgagtccg gttataatgt tctagggaca gtcagagacc caggcaatca
120

gaagaaggta gcacacctct ggaacttagc aggggccaag gaaaggttgg agcttgtcaa
180

agctgacctc ttggaagaag ggagcttcga tgatgctgtg atggcctgtg agggtgtctt
240

ccacactgca tcacctatca tcaccaaatc tgataccaag gaagaaatgc ttgattctgc
300

aattaacggc actctaaacg ngctgagatc gngcaagaag aatncttttc tnaaaagggn
360

tgntctcacg tcatcatcgc cacccgngan gctganggat gaanctgant tcccacccaa
420

cgngn
425

<210> 291
<211> 691
<212> DNA
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tgttgcttcc tggcttgtca aaagacttct cgagtccggt tataatgttc tagggacagt
120

cagagaccca ggcaatcaga agaaggtagc acacctctgg agcttagcag gggccaagga
180

aaggctggag cttgtcagag ctgacctctt ggaagaaggg agcttcgatg atgccgtgat
240

ggcctgtgag ggtgtcttcc acactgcatc acctatcatc accaaatctg ataccaagga
300

agaaatgctt gattctgcaa taaacggcac tctaaacgtg ctgagatcgt gcaagaagaa
360

tccttttctc aaaagggttg ttctcacgtc atcatcgtca accgtgaggc tgagggatga
420

agctgaattc ccacccaacg tgttgctgga tgaaacatca tggagctccg tggagttctg
480

tgaaagtatc caggtatggt acggtgtcgc aaagatcctt gccgagaaat cagcctggga
540

gtttgccaag gagaacaaca tcgacctagt ggctgttctt ccaacattcg tgattggacc
600

taatctctcg tctgaattag gacccactgt tttagatgtc cttggcttat ttaaaggaga
660

gacagagaag ttcaccatgt ttgggaagga n
691

<210> 292

<211> 365
<212> DNA
<213> Lolium perenne

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<222> (365)..(365)
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<400> 292
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tttgttgctt cctggcttgt caaaagactt ctcgagtccg gttataatgt tctagggaca
120

gtcagagacc caggcaatca gaagaaggta gcacacctct ggagcttagc aggggccaag
180

gaaaggctgg agcttgtcag agctgacctc ttggaagaag ggagcttcga tgatgccgtg
240

atggcctgtg agggtgtctt ccacactgca tcacctatca tcaccaaatc tgataccaag
300

gaagaaatgc ttgattctgc aataaacggc nctctaaacg tgctgnnatc cgggtnaaaa
360

aaaan
365

<210> 293
<211> 524
<212> DNA
<213> Lolium perenne

<220>
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<222> (169)..(169)
<223> Any nucleotide

<400> 293
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caccgcgcgc acttcctaaa gcttctcaag gacctcttcc cgcagtactc cttcaccgcc 120

aagtgcgaag acgacggcaa gcccatggcg aagccgtaca agttctccna ccagaggctc 180

agggacctgg gattaaaatt cactccgctg gcggaaagtt tgtacgagac cgtgacgtgc 240

ctgcaaaaaa atggccacct gcctctgccc gctcccatgg cgccaaagcg tgcataccta 300

taatactaca aagacacggc cgggatcgac aagccaagaa acagaggatt ctcccgaggt 360

tcaccatgga attgtgtatt tcacaaagtt tgaattctta ttttttttat tatgaagaaa 420

tacggaaaac caatactgta taccagaggc aagtgtaaca atgtaaatag tcgtgtaaat 480

cttgttcaag aatgaatgat aaagtatttt ttgcaaaaaa aaaa 524

<210> 294
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<213> Lolium perenne

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<223> Any amino acid

<400> 294

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Gly Ala Val Leu His Arg Ala His Phe Leu Lys Leu Leu Lys Asp Leu
20 25 30

Phe Pro Gln Tyr Ser Phe Thr Ala Lys Cys Glu Asp Asp Gly Lys Pro
35 40 45

Met Ala Lys Pro Tyr Lys Phe Ser Xaa Gln Arg Leu Arg Asp Leu Gly
50 55 60

Leu Lys Phe Thr Pro Leu Ala Glu Ser Leu Tyr Glu Thr Val Thr Cys
65 70 75 80

Leu Gln Lys Asn Gly His Leu Pro Leu Pro Ala Pro Met Ala Pro Lys
85 90 95

Arg Ala Tyr Leu
100

<210> 295
<211> 524
<212> DNA
<213> Lolium perenne

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<222> (482)..(482)
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<222> (519)..(519)
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caccgcgcgc acttcctaaa gcttctcaag gacctcttcc cgcagtactc cttcaccgcc
120

aagtgcgaag acgacggcaa gcccatggcg aagccgtaca agttctccaa ccagaggctc
180

agggacctgg gattaaaatt cactccgctg gcggaaagtt tgtacgagac cgtgacgtgc
240

ctgcaaaaaa atggccacct gcctctgccc gctcccgtgg cgccaaagcg tgcataccta
300

taatantacc aagacacggc cgggatcgac aagccaagaa acagaggatt ctcccgaggt
360

tcaccatgga attgtgtatt tcagaaagtt tgaattctta ttttttttat tatgaaggaa
420

tacggataac caatactgta taccagaggc aagtgtaaca atgtaaatag tcgtgtaaat
480

cntgttcaag attgaatgat aaagtatttt ttgcaaaana aaaa
524

<210> 296
<211> 374
<212> DNA
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<223> Any nucleotide

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<222> (25)..(26)
<223> Any nucleotides

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gcggaaagtt tgtacgagac cgtgacgtgc ctgcaaaaaa atggccacct gcctctgccc
120

gctcccatgg cgccaaagcg tgcataccta taatactaca aagacacggc cgggatcgac
180

aagccaagaa acagaggatt ctcccgaggt tcaccatgga attgtgtatt tcacaaagtt
240

tgaattctta tttttttat tatgaagaaa tacggaaaac caatactgta taccagaggc
300

aagtgtaaca atgtaaatag tcgtgtaaat cttgttcaag aatgaatgat aaagtatttt
360

ttgcaaaaaa aaaa
374

<210> 297
<211> 363
<212> DNA
<213> Lolium perenne

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<222> (7)..(8)
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<222> (363)..(363)
<223> Any nucleotide

<400> 297
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gtacgagacc gtgacgtgcc tgcaaaaaaa tggccacctg cctctgcccg ctcccatggc
120

gccaaagcgt gcatacctat aatactacaa agacacggcc gggatcgaca agccaagaaa
180

cagaggattc tcccgaggtt caccatggaa ttgtgtattt cacaaagttt gaattcttat
240

tttttttatt atgaagaaat acggaaaacc aatactgtat accagaggca agtgtaacaa
300

tgtaaatagt cgtgtaaatc ttgttcaaga atgaatgata aagtattttt tgcaaaaaaa

360

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363

<210> 298
<211> 1381
<212> DNA
<213> Lolium perenne

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<222> (5)..(5)
<223> Any nucleotide

<220>
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<222> (1280)..(1280)
<223> Any nucleotide

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<223> Any nucleotide

<400> 298
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tcagctaacc attcctcaac tagaataagc atggctccgg cgatgtccaa ccctctcctc
120

agtgatcggg tggcacgctc caagaaagtc ccatctagcc acgttagagc ggtgggagac
180

cgcccagacc tcgccaatgt cgaccacgag tccggcgcgg gcattccgct catcgacctg
240

aagcagctcg aaggtccagg gcgccgcagg gtcgtcgagg ccatcggctc cgcgtgcgag
300

aacgatgggt ttttcatggt gacgaatcat ggcatcccag aggcggtcgt ggaggggatg
360

ctgagcgtgg cgagggagtt cttccacctg ccggagtcgg agcggctcaa gtgctactcc
420

gacgacccca agaaggcggt ccggctgtcg acgagcttca acgtgcgcac ggagaaggtg
480

agcaactggc gcgacttcct ccggctgcat tgctaccctc ttgagagctt cgtcgaccag
540

tggccgtcga acccgcccgc cttcaggcaa gtcgtcggca cctactcgac ggaagcgaga
600

gcgctggcgc tgaggctcct ggaggcgata tcggagagcc tagggctgga gagaggccac
660

atggtgaagg ccatggggcg gcacgcgcag cacatggcgg tgaactacta cccgccgtgc
720

ccgcagccgg agctcaccta cggtctgcca gggcacacgg accccaacgc cctcaccatc
780

ctcctcatgg atccccacgt ctccggcctc caggtcctca gggacggcgc caagtggatc
840

gccgtccacc cacgccccaa cgccctggtc atcaacctag gcgaccagct acaggcgctg
900

agcaacggcg cgtacaagag cgtgtggcac cgggcagtgg tgaacgcgga gcaggagcgt
960

ctgtcggtgg catctttcct gtgcccgtgc aacagcgcgg ttatctgccc cgcgccgagg
1020

ctcgtcggcg acggggagga ccccgtctac cggagctaca cctacgacga gtactacaag
1080

aggttttgga gcaggaacct ggatcaggag cactgcctcg agctcttcag gagtcagcac
1140

tgatgcttga accttgagtt actagctagc tctccttaac agtgcaaatc catggcccaa
1200

gagggccccg attgcatggt tacttatgtt gtttgaactg gtattgctta agtgcctaat
1260

aacattgcta cattctactn ctatcttgtc cgtttaaaat tataagatgg cctaaccttt
1320

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1380

a
1381

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<211> 346
<212> PRT
<213> Lolium perenne

<400> 299

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Pro Ser Ser His Val Arg Ala Val Gly Asp Arg Pro Asp Leu Ala Asn
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Val Asp His Glu Ser Gly Ala Gly Ile Pro Leu Ile Asp Leu Lys Gln
35 40 45

Leu Glu Gly Pro Gly Arg Arg Arg Val Val Glu Ala Ile Gly Ser Ala
50 55 60

Cys Glu Asn Asp Gly Phe Phe Met Val Thr Asn His Gly Ile Pro Glu
65 70 75 80

Ala Val Val Glu Gly Met Leu Ser Val Ala Arg Glu Phe Phe His Leu
85 90 95

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Pro Glu Ser Glu Arg Leu Lys Cys Tyr Ser Asp Asp Pro Lys Lys Ala
            100                 105                 110

Val Arg Leu Ser Thr Ser Phe Asn Val Arg Thr Glu Lys Val Ser Asn
        115                 120                 125

Trp Arg Asp Phe Leu Arg Leu His Cys Tyr Pro Leu Glu Ser Phe Val
    130                 135                 140

Asp Gln Trp Pro Ser Asn Pro Pro Ala Phe Arg Gln Val Val Gly Thr
145                 150                 155                 160

Tyr Ser Thr Glu Ala Arg Ala Leu Ala Leu Arg Leu Leu Glu Ala Ile
                165                 170                 175

Ser Glu Ser Leu Gly Leu Glu Arg Gly His Met Val Lys Ala Met Gly
            180                 185                 190

Arg His Ala Gln His Met Ala Val Asn Tyr Tyr Pro Pro Cys Pro Gln
        195                 200                 205

Pro Glu Leu Thr Tyr Gly Leu Pro Gly His Thr Asp Pro Asn Ala Leu
    210                 215                 220

Thr Ile Leu Leu Met Asp Pro His Val Ser Gly Leu Gln Val Leu Arg
225                 230                 235                 240

Asp Gly Ala Lys Trp Ile Ala Val His Pro Arg Pro Asn Ala Leu Val
                245                 250                 255

Ile Asn Leu Gly Asp Gln Leu Gln Ala Leu Ser Asn Gly Ala Tyr Lys
            260                 265                 270

Ser Val Trp His Arg Ala Val Val Asn Ala Glu Gln Glu Arg Leu Ser
        275                 280                 285

Val Ala Ser Phe Leu Cys Pro Cys Asn Ser Ala Val Ile Cys Pro Ala
    290                 295                 300

Pro Arg Leu Val Gly Asp Gly Glu Asp Pro Val Tyr Arg Ser Tyr Thr
305                 310                 315                 320

Tyr Asp Glu Tyr Tyr Lys Arg Phe Trp Ser Arg Asn Leu Asp Gln Glu
                325                 330                 335

His Cys Leu Glu Leu Phe Arg Ser Gln His
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<211> 755
<212> DNA
<213> Lolium perenne

<220>
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<223> Any nucleotide

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120

agtgatcggg tggcacgctc caagaaagtc ccatctagcc acgttagagc ggtgggagac
180

cgcccagacc tcgccaatgt cgaccacgag tccggcgcgg gcattccgct catcgacctg
240

aagcagctcg aaggtccagg gcgccgcagg gtcgtcgagg ccatcggctc cgcgtgcgag
300

aacgatgggt ttttcatggt gacgaatcat ggcatcccag aggcggtcgt ggaggggatg
360

ctgagcgtgg cgagggagtt cttccacctg ccggagtcgg agcggctcaa gtgctactcc
420

gacgacccca agaaggcggt ccggctgtcg acgagcttca acgtgcgcac ggagaaggtg
480

agcaactggc gcgacttcct ccggctgcat tgctaccctc ttgagagctt cgtcgaccag
540

tggccgtcga acccgcccgc cttcaggcaa gtcgtcggca cctactcgac ggaagcgaga
600

gcgctggcgc tgaggctcct ggaggcgata tcggagagcc tagggctgga gagaggccac
660

atggtgaagg ccatggggcg gcacgcgcag cacatggcgg tgaactacta cccgccgtgc
720

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755

<210> 301
<211> 780
<212> DNA
<213> Lolium perenne

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<222> (21)..(21)
<223> Any nucleotide

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<222> (778)..(778)

<223> Any nucleotide

<400> 301
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tgatcgggtg gcacgctcca agaaagtccc atctagccac gttagagcgg tgggagaccg 180

cccagacctc gccaatgtcg accacgagtc cggcgcgggc attccgctca tcgacctgaa 240

gcagctcgaa ggtccagggc gccgcagggt cgtcgaggcc atcggctccg cgtgcgagaa 300

cgatgggttt ttcatggtga cgaatcatgg catcccagag gcggtcgtgg aggggatgct 360

gagcgtggcg agggagttct tccacctgcc ggagtcggag cggctcaagt gctactccga 420

cgaccccaag aaggcggtcc ggctgtcgac gagcttcaac gtgcgcacgg agaaggtgag 480

caactggcgc gacttcctcc ggctgcattg ctaccctctt gagagcttcg tcgaccagtg 540

gccgtcgaac ccgccccgcct tcaggcaagt cgtcggcacc tactcgacgg aagcgagagc 600

gctggcgctg aggctcctgg aggcgatatc ggagagccta gggctggaga gaggccacat 660

ggtgaaggcc atggggcggc acgcgcagca catggcggtg aactactacc cgccgtgccc 720

gcagccggag ctcacctacg gtctgccagg gcacacggac cccaatgccc tcaccatnct 780

<210> 302
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<213> Lolium perenne

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<223> Any nucleotide

<220>
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<222> (692)..(692)
<223> Any nucleotide

<220>
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<222> (750)..(750)
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<400> 302
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tacccgcggt gccccgagcc ggacctcacc tacggcctgc ccaagcacac ggaccccaac 180

gccctcacca tcctcctcat ggatccccac gtctccggcc tccaggtcct cagggacggc 240

gccaagtgga tcgccgtcca cccacgcccc aacgccctgg tcatcaacct aggcgaccag 300

ctacaggcgc tgagcaacgg cgcgtacaag agcgtgtggc accgggcagt ggtgaacgcg 360

gagcaggagc gtctgtcggt ggcatctttc ctgtgcccgt gcaacagcgc ggttatctgc 420

cccgcgccga ggctcgtcgg cgacggggag gaccccgtct accggagcta cacctacgac 480

gagtactaca agaggttttg gagcaggaac ctggatcagg agcactgcct cgagctcttc 540

aggagtcagc actgatgctt gaaccttgag ttactagcta gctctcctta acagtgcaaa 600

tccatggccc aagagggccc cgattgcatg gttacttatg ttgtttgaac tggtattgct 660

taagtgccta ataacattgc tacattctac tnctatcttg tccgtttaaa attataagat 720

ggcctaacct ttttcttaat tgtatgcatn ctgaacatat ttaagtgtgt gtgttcagac 780

agtttagtct gca 793

<210> 303
<211> 1395
<212> DNA
<213> Lolium perenne

<400> 303
gaattcgatt aagcagtggt aacaacgcag agtacgcggg gactctcaga acacactgtg 60

taaccacggt agcgagtggc aagactagca gaaagtacgg acatcagcta accattcctc 120

aactagaata agcatggctc cggcgatgtc caaccctctc ctcagtgatc gggtggcacg 180

ctccaagaaa gtcccatcta gccacgttag agcggtggga gaccgcccag acctcgccaa 240

tgtcgaccac gagtccggcg cgggcattcc gctcatcgac ctgaagcagc tcgaaggtcc 300

agggcgccgc agggtcgtcg aggccatcgg ctccgcgtgc gagaacgatg ggtttttcat
360

ggtgacgaat catggcatcc cagaggcggt cgtggagggg atgctgagcg tggcgaggga
420

gttcttccac ctgccggagt cggagcggct caagtgctac tccgacgacc ccaagaaggc
480

ggtccggctg tcgacgagct tcaacgtgcg cacggagaag gtgagcaact ggcgcgactt
540

cctccggctg cattgctacc ctcttgagag cttcgtcgac cagtggccgt cgaacccgcc
600

cgccttcagg caagtcgtcg gcacctactc gacggaagcg agagcgctgg cgctgaggct
660

cctggaggcg atatcggaga gcctagggct ggagagaggc cacatggtga aggccatggg
720

gcggcacgcg cagcacatgg cggtgaacta ctacccgccg tgcccgcagc cggagctcac
780

ctacggtctg ccagggcaca aggaccccaa tgccatcacg ctcctcctgc aggacggcgt
840

ctccggcctg caggtccagc gcgacggccg gtgggtggcc gtcaacccgg tgcccaacgc
900

cctcgtcatc aacatcggcg atcagttaca ggcgctgagc aacgaccgat acaagagcgt
960

gaaccacaga gtgatcgtca acagcgcgag cgagaggatt tcggtgccga cgttctactg
1020

cccgtcgccg gacacggtgg tcgcgccggc cgacgcgctg gtggacgacg cccaccctcg
1080

ggcctaccag cccttcacgt accaggagta ctacgaggag ttctggaaga tgggccttca
1140

gtcagcaagt tgcctcgaca ggttccgacg gatcgagtga tggacaagac gtgggccgtt
1200

gttatctcct gggccatgag cgttgccgca gccgatgtgt cgccatatgg tggagacgtt
1260

tcctccctcc ggaaaagaaa aataaaacag agtggagacc actagaaccg tcagatagca
1320

tcccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaagtactc tgcgttgtta ccactgctta
1380

atcactagtg aattc
1395

<210> 304
<211> 348
<212> PRT
<213> Lolium perenne

<400> 304

Met Ala Pro Ala Met Ser Asn Pro Leu Leu Ser Asp Arg Val Ala Arg

1 5 10 15

Ser Lys Lys Val Pro Ser Ser His Val Arg Ala Val Gly Asp Arg Pro
20 25 30

Asp Leu Ala Asn Val Asp His Glu Ser Gly Ala Gly Ile Pro Leu Ile
35 40 45

Asp Leu Lys Gln Leu Glu Gly Pro Gly Arg Arg Arg Val Val Glu Ala
50 55 60

Ile Gly Ser Ala Cys Glu Asn Asp Gly Phe Phe Met Val Thr Asn His
65 70 75 80

Gly Ile Pro Glu Ala Val Val Glu Gly Met Leu Ser Val Ala Arg Glu
85 90 95

Phe Phe His Leu Pro Glu Ser Glu Arg Leu Lys Cys Tyr Ser Asp Asp
100 105 110

Pro Lys Lys Ala Val Arg Leu Ser Thr Ser Phe Asn Val Arg Thr Glu
115 120 125

Lys Val Ser Asn Trp Arg Asp Phe Leu Arg Leu His Cys Tyr Pro Leu
130 135 140

Glu Ser Phe Val Asp Gln Trp Pro Ser Asn Pro Pro Ala Phe Arg Gln
145 150 155 160

Val Val Gly Thr Tyr Ser Thr Glu Ala Arg Ala Leu Ala Leu Arg Leu
165 170 175

Leu Glu Ala Ile Ser Glu Ser Leu Gly Leu Glu Arg Gly His Met Val
180 185 190

Lys Ala Met Gly Arg His Ala Gln His Met Ala Val Asn Tyr Tyr Pro
195 200 205

Pro Cys Pro Gln Pro Glu Leu Thr Tyr Gly Leu Pro Gly His Lys Asp
210 215 220

Pro Asn Ala Ile Thr Leu Leu Leu Gln Asp Gly Val Ser Gly Leu Gln
225 230 235 240

Val Gln Arg Asp Gly Arg Trp Val Ala Val Asn Pro Val Pro Asn Ala
245 250 255

Leu Val Ile Asn Ile Gly Asp Gln Leu Gln Ala Leu Ser Asn Asp Arg
260 265 270

Tyr Lys Ser Val Asn His Arg Val Ile Val Asn Ser Ala Ser Glu Arg
275 280 285

Ile Ser Val Pro Thr Phe Tyr Cys Pro Ser Pro Asp Thr Val Val Ala
290 295 300

Pro Ala Asp Ala Leu Val Asp Asp Ala His Pro Arg Ala Tyr Gln Pro
305 310 315 320

Phe Thr Tyr Gln Glu Tyr Tyr Glu Glu Phe Trp Lys Met Gly Leu Gln
325 330 335

Ser Ala Ser Cys Leu Asp Arg Phe Arg Arg Ile Glu
340 345

<210> 305
<211> 1309
<212> DNA
<213> Trifolium repens

<400> 305
gaattcgatt aagcagtggt aacaacgcag agtacgcggg ataaaaactg cactagtgtg
60

tataagtttc ttggtgaaaa aagagtttgt aaattaacat catggctagt atcaaacaaa
120

ttggaaacaa gaaagcatgt gtgattggtg gcactggttt tgttgcatct atgttgatca
180

agcagttact tgaaaagggt tatgctgtta atactaccgt tagagaccca gatagcccta
240

agaaaatatc tcacctagtg gcactgcaaa gtttggggga actgaatcta tttagagcag
300

acttaacagt tgaagaagat tttgatgctc ctatagcagg atgtgaactt gtttttcaac
360

ttgctacacc tgtgaacttt gcttctcaag atcctgagaa tgacatgata aagccagcaa
420

tcaaaggtgt gttgaatgtg ttgaaagcaa ttgcaagagc aaaagaagtt aaaagagtta
480

tcttaacatc ttcggcagcc gcggtgacta taaatgaact caaagggaca ggtcatgtta
540

tggatgaaac caactggtct gatgttgaat ttctcaacac tgcaaaacca cccacttggg
600

gttatcctgc ctcaaaaatg ctagctgaaa aggctgcatg gaaatttgct gaagaaaatg
660

acattgatct aatcactgtg atacctagtt taacaactgg tccttctctc acaccagata
720

tcccatctag tgttggcttg gcaatgtctc taataacagg caatgatttt ctcataaatg
780

ctttgaaagg aatgcagttt ctgtcgggtt cgttatccat cactcatgtt gaggatattt
840

gccgagctca tatatttctt gcagagaaag aatcagcttc tggtagatac atttgctgtg
900

ctcacaatac tagtgttccc gagcttgcaa agtttctcaa caaacgatat cctcagtata
960

aagttccaac tgaatttgat gattgcccca gcaaggcaaa gttgataatc tcttctgaaa
1020

agcttatcaa agaagggttc agtttcaagc atggtattgc cgaaactttc gaccagactg
1080

tcgagtattt taagactaag ggggcactga agaattagat tttgatattt ctaattcaat
1140

agcaaactct aagcttgtta tgtgtttgtg aagttcagag tgaaatatca aatgaataag
1200

tggagagagc acaataagag gagagcacaa taattttgga aaaaaaaaaa aaaaaaaaaa
1260

aaaaaaaagt actctgcgtt gttaccactg cttaatcact agtgaattc
1309

<210> 306
<211> 338
<212> PRT
<213> Trifolium repens

<400> 306

Met Ala Ser Ile Lys Gln Ile Gly Asn Lys Lys Ala Cys Val Ile Gly
1 5 10 15

Gly Thr Gly Phe Val Ala Ser Met Leu Ile Lys Gln Leu Leu Glu Lys
20 25 30

Gly Tyr Ala Val Asn Thr Thr Val Arg Asp Pro Asp Ser Pro Lys Lys
35 40 45

Ile Ser His Leu Val Ala Leu Gln Ser Leu Gly Glu Leu Asn Leu Phe
50 55 60

Arg Ala Asp Leu Thr Val Glu Glu Asp Phe Asp Ala Pro Ile Ala Gly
65 70 75 80

Cys Glu Leu Val Phe Gln Leu Ala Thr Pro Val Asn Phe Ala Ser Gln
85 90 95

Asp Pro Glu Asn Asp Met Ile Lys Pro Ala Ile Lys Gly Val Leu Asn
100 105 110

Val Leu Lys Ala Ile Ala Arg Ala Lys Glu Val Lys Arg Val Ile Leu
115 120 125

Thr Ser Ser Ala Ala Ala Val Thr Ile Asn Glu Leu Lys Gly Thr Gly
130 135 140

His Val Met Asp Glu Thr Asn Trp Ser Asp Val Glu Phe Leu Asn Thr
145 150 155 160

Ala Lys Pro Pro Thr Trp Gly Tyr Pro Ala Ser Lys Met Leu Ala Glu
165 170 175

Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Asp Ile Asp Leu Ile Thr
180 185 190

Val Ile Pro Ser Leu Thr Thr Gly Pro Ser Leu Thr Pro Asp Ile Pro
195 200 205

Ser Ser Val Gly Leu Ala Met Ser Leu Ile Thr Gly Asn Asp Phe Leu
210 215 220

Ile Asn Ala Leu Lys Gly Met Gln Phe Leu Ser Gly Ser Leu Ser Ile
225 230 235 240

Thr His Val Glu Asp Ile Cys Arg Ala His Ile Phe Leu Ala Glu Lys
245 250 255

Glu Ser Ala Ser Gly Arg Tyr Ile Cys Cys Ala His Asn Thr Ser Val
260 265 270

Pro Glu Leu Ala Lys Phe Leu Asn Lys Arg Tyr Pro Gln Tyr Lys Val
275 280 285

Pro Thr Glu Phe Asp Asp Cys Pro Ser Lys Ala Lys Leu Ile Ile Ser
290 295 300

Ser Glu Lys Leu Ile Lys Glu Gly Phe Ser Phe Lys His Gly Ile Ala
305 310 315 320

Glu Thr Phe Asp Gln Thr Val Glu Tyr Phe Lys Thr Lys Gly Ala Leu
325 330 335

Lys Asn

<210> 307
<211> 1005
<212> DNA
<213> Trifolium repens

<400> 307
gaattcgatt aagcagtggt aacaacgcag agtacgcggg gacttaaaca ttgacacaag
60

tcccaaataa aaaagatctg aaacaacata gtcaccccat tttttaacat taaactaaaa 120

atatgtcggc catcaccgca atccaagtcg agaaccttga atttccggct gtggttactt 180

ctccggccac cggtaagtca tattttcttg gtggtgcagg ggagagaggt ttgactattg 240

aaggaaactt catcaagttc actgccatag gagtatattt ggaagatgta gcagtggctt 300

cacttgccac taaatggaag ggtaaatcct ctgaggagtt gcttgagact cttgacttct 360

atagagacat catttcagga ccctttgaaa agttgattcg aggatcgaag attagggaat 420

tgagtggtcc tgagtactca aggaaggtta atgaaaactg cgtggcacac ttaaaatctg 480

ttgggactta tggagatgct gaagctgaag ctatgcaaaa atttgttgaa gccttcaagc 540

ctattaattt tccacctggt gcctctgttt tttacaggca atcacctgat ggaatattag 600

ggcttagttt ctctcaagat gcaagtatac cagaaaagga ggctgcagta atagagaaca 660

aggcagcttc atcggcagtg ttagaaacta tgattggtga acatgctgtt tctcctgatt 720

taaagcgttg tttggctgca agattacctg ccttgttgaa cgagggtact ttcaagattg 780

aatgaaaact gattattatt atctccaaaa gcattgcagc acaagattga gtcatttatg 840

agcatggaca tttttatgtc cacacatgtt taacttttgt atctctcttt agattctcat 900

caatatcaat aatactaata tgaaacgaag tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960

aaaagtactc tgcgttgtta ccactgctta atcactagtg aattc 1005

<210> 308
<211> 220
<212> PRT
<213> Trifolium repens

<400> 308

Met Ser Ala Ile Thr Ala Ile Gln Val Glu Asn Leu Glu Phe Pro Ala
1 5 10 15

Val Val Thr Ser Pro Ala Thr Gly Lys Ser Tyr Phe Leu Gly Gly Ala
20 25 30

Gly Glu Arg Gly Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala
35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Val Ala Ser Leu Ala Thr Lys
50 55 60

Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr
65 70 75 80

Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys
85 90 95

Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Asn Glu Asn
100 105 110

Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Ala
115 120 125

Glu Ala Met Gln Lys Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro
130 135 140

Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly
145 150 155 160

Leu Ser Phe Ser Gln Asp Ala Ser Ile Pro Glu Lys Glu Ala Ala Val
165 170 175

Ile Glu Asn Lys Ala Ala Ser Ser Ala Val Leu Glu Thr Met Ile Gly
180 185 190

Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg Leu
195 200 205

Pro Ala Leu Leu Asn Glu Gly Thr Phe Lys Ile Glu
210 215 220

<210> 309
<211> 1105
<212> DNA
<213> Trifolium repens

<400> 309
gaattcacta gtgattaagc agtggtaaca acgcagagta cgcggggaca ttacaactca
60

caacaccttc tccattacca tctatcttct actaagttca acgagatcaa tggcacttcc
120

ttctgtcacc gctttgaata tcgagaacaa tctattccct cctaccgtca caccaccggg
180

atccaccaac aatttcttcc tcggcggtgc aggagagcgg ggtcttcaaa ttcaagacaa
240

atttgtcaaa ttcaccgcta ttggtgttta tctacaggac attgctgttc cttacctcgc
300

cactaaatgg aagggtaaga ctgctcaaga gctaacggaa actgttcctt tcttcaggga
360

catcgttaca ggtccatttg agaaatttat gcaggtgaca atgatcttgc cattgactgg
420

gcaacaatac tcagagaaag tgtcagaaaa ttgtgtagct atttggaagt ctcttgggat
480

ttataccgac gaagaagcca aagcaattga gaagtttgtt tctgtcttca aagatgaaac
540

attcccacca ggctcctcta tccttttcac agtattaccc aaaggattag gatcactaac
600

gataagtttc tctaaagatg gatccattcc agagaccgag tctgcagtta tagagaataa
660

gctactctca caagctgtgc ttgagtcgat gataggggcg cacggtgtct cccctgcagc
720

aaaacagagt ttggccacca ggttatccga gttattcaac gaggttggtg atgctagcaa
780

ctgattatat caacaaaacg aaaatgaaag tcctttctgc aataaagacc aagcggaaat
840

tttattttag gtgcactttg aaatgacctc tttggcgact ttttcttgta ctaataataa
900

agagtgtgtt tgtatcatgt tgtaatttta ttttagaaaa agtgaggtaa gaaaggagtc
960

cttatgttta tttcaattat tgaaaaatta tttgcatgta taattgattt caactgatgt
1020

tatttaatca cgtttttttct aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gtactctgcg
1080

ttgttaccac tgcttaatcg aattc
1105

<210> 310
<211> 224
<212> PRT
<213> Trifolium repens

<400> 310

Met Ala Leu Pro Ser Val Thr Ala Leu Asn Ile Glu Asn Asn Leu Phe
1 5 10 15

Pro Pro Thr Val Thr Pro Pro Gly Ser Thr Asn Asn Phe Phe Leu Gly
20 25 30

Gly Ala Gly Glu Arg Gly Leu Gln Ile Gln Asp Lys Phe Val Lys Phe
35 40 45

Thr Ala Ile Gly Val Tyr Leu Gln Asp Ile Ala Val Pro Tyr Leu Ala
50 55 60

Thr Lys Trp Lys Gly Lys Thr Ala Gln Glu Leu Thr Glu Thr Val Pro
65 70 75 80

Phe Phe Arg Asp Ile Val Thr Gly Pro Phe Glu Lys Phe Met Gln Val
85 90 95

Thr Met Ile Leu Pro Leu Thr Gly Gln Gln Tyr Ser Glu Lys Val Ser
100 105 110

Glu Asn Cys Val Ala Ile Trp Lys Ser Leu Gly Ile Tyr Thr Asp Glu
115 120 125

Glu Ala Lys Ala Ile Glu Lys Phe Val Ser Val Phe Lys Asp Glu Thr
130 135 140

Phe Pro Pro Gly Ser Ser Ile Leu Phe Thr Val Leu Pro Lys Gly Leu
145 150 155 160

Gly Ser Leu Thr Ile Ser Phe Ser Lys Asp Gly Ser Ile Pro Glu Thr
165 170 175

Glu Ser Ala Val Ile Glu Asn Lys Leu Leu Ser Gln Ala Val Leu Glu
180 185 190

Ser Met Ile Gly Ala His Gly Val Ser Pro Ala Ala Lys Gln Ser Leu
195 200 205

Ala Thr Arg Leu Ser Glu Leu Phe Asn Glu Val Gly Asp Ala Ser Asn
210 215 220

<210> 311
<211> 1272
<212> DNA
<213> Trifolium repens

<400> 311
gaattcgatt aagcagtggt aacaacgcag agtacgcggg gattcaaaca tagctcaaag
60

tgtgtaacaa atttcttaac ttaaaacatt ttcaacccaa caaaaaaaaa caaagacaaa
120

aacatgggta gtgttgaaat tccaacaaag gttcttacta acagttctag tcaagtgaaa
180

atgcctgtgg ttggaatggg atcagcacct gatttcacat gtaagaaaga cacaaaagat
240

gcaatcattg aagccatcaa acagggttat agacactttg atactgctgc tgcttatggc
300

tcagaacaag ctcttggtga aggtttgaaa gaagcaattg aacttggtct tgtcactaga
360

gaagaccttt ttgttacttc taaactttgg gtcactgaaa atcatcctca tcttgttgtt

420

cctgctcttc aaaaatctct caagactctt caattggagt acttggactt gtatttgatc
480

cattggccac ttagttctca gcctggaaag ttttcatttc caattgatgt ggcagatctc
540

ttgccatttg atgtgaaggg tgtttgggaa tccatggaag aaggcttgaa acttggactc
600

actaaagcta ttggtgttag taacttctct gtcaagaaac ttcaaaatct tgtctcagtt
660

gccactgttc ttcctgctgt caatcaagtg gagatgaacc ttgcatggca acaaaagaag
720

cttagagaat tttgcaatgc aaatggaata gtgttaactg cattttcacc attgagaaaa
780

ggtgcaagca ggggaccaaa tgaagttatg gaaaatgata tgcttaaaga gattgcagat
840

gctcatggaa agtctgttgc acaaatttca ttgagatggt tatatgaaca aggagtcact
900

tttgttccca agagctatga taaggaaaga atgggtcaaa atttggctat ctttgattgg
960

acattggcaa aagaagatca tgagaaaatt gatcaaatta agcagaaccg tttgatccct
1020

ggaccaacca agccaggact cagtgaccta tgggatgatg aaatataaag tggaagatgt
1080

taaaagtccc ttaagctcac tcaatatcta tctattgtgt actttttgca tttggggttt
1140

gaaattgagt caccccttgtt tctgtatcga tttaaaattt aaataatcaa tttttcatta
1200

caaaaaaaaa aaaaaaaaaa aaaaaaaaaa agtactctgc gttgttacca ctgcttaatc
1260

actagtgaat tc
1272

<210> 312
<211> 314
<212> PRT
<213> Trifolium repens

<400> 312

Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Ser Ser Ser
1 5 10 15

Gln Val Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
20 25 30

Cys Lys Lys Asp Thr Lys Asp Ala Ile Ile Glu Ala Ile Lys Gln Gly
35 40 45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
50 55 60

Gly Glu Gly Leu Lys Glu Ala Ile Glu Leu Gly Leu Val Thr Arg Glu
65 70 75 80

Asp Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
85 90 95

Leu Val Val Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Glu
100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Gly Leu Lys Leu Gly Leu Thr
145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Asn Leu
165 170 175

Val Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
180 185 190

Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Ala Asn Gly
195 200 205

Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
210 215 220

Pro Asn Glu Val Met Glu Asn Asp Met Leu Lys Glu Ile Ala Asp Ala
225 230 235 240

His Gly Lys Ser Val Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
245 250 255

Gly Val Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Gly Gln
260 265 270

Asn Leu Ala Ile Phe Asp Trp Thr Leu Ala Lys Glu Asp His Glu Lys
275 280 285

Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
290 295 300

Gly Leu Ser Asp Leu Trp Asp Asp Glu Ile

305 310

<210> 313
<211> 1548
<212> DNA
<213> Trifolium repens

<400> 313
gaattcgatt aagcagtggt atcaacgcag agtacgcggg gacaacaact ataacttcct 60

gttattaacc aattgagttc aaattacata catagcagga actatactaa agatatcaac 120

atggttagtg tttctgaaat tcgcaaggct caaagggctg aaggccctgc aactattttg 180

gccattggta ctgcaaatcc agcaaatcgt gttgaccaga gtacatatcc tgatttctac 240

ttcaaaatca ctaacagtga gcataaggtt gagcttaaag agaaatttca gcgcatgtgt 300

gataaatcta tgatcaagag cagatacatg tatctaacag aagagatttt gaaagaaaat 360

cctagtcttt gtgaatacat ggcaccttca ttggatgcta ggcaagacat ggtggtggtt 420

gaggtaccta gacttgggaa ggaggctgca gtgaaagcta tcaaagaatg gggtcaacca 480

aagtcaaaga ttactcactt aatcttttgc accacaagtg gtgttgacat gcctggtgcc 540

gattaccaac tcacaaaact cttaggtctt cgcccatatg tgaagaggta catgatgtac 600

caacaagggt gctttgcagg tgggacggtt cttcgtttgg ccaaggattt ggccgagaac 660

aacaaaggtg ctcgtgtgtt ggttgtttgc tctgaagtaa ccgcagtcac attccgcggc 720

cccagtgaca ctcatttgga cagtcttgtt ggacaagcac tattcggaga tggagctgct 780

gcactcattg ttggctcaga cccagtacca gaaattgaga agccaatatt tgagatggtt 840

tggaccgcac agacaattgc tccagatagt gaaggtgcca ttgatggtca tcttcgtgaa 900

gctggactaa catttcatct tcttaaagat gttcctggga ttgtctcaaa gaacattgat 960

aaggcattgg ttgaggcatt ccaaccatta aacatctctg attacaattc aatcttttgg 1020

attgctcatc caggtggtcc tgcaattcta gaccaagttg agataaagtt gggcttaaaa 1080

cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat gtcaagtgca 1140

tgtgtattgt tcatcttaga tgagatgaga aagaaatcgg ctgaaaatgg acttaaaacc
1200

acaggagaag gacttgactg gggtgtgttg tttggatttg ggcccggact taccattgaa
1260

actgttgttc tacatagtgt ggctatatga gaatgagaga cttgatttgt ttttattgta
1320

ttgtattgta ttactttaaa tcttggttga acctccattt taagaataaa tatggagttc
1380

aatatggacc atcctgttaa aataatatat cgttaatagc tattatttta gtgtctgttt
1440

ctttttacta aactatttta ttttagtatt tgtttttgac caaaaaaaaa aaaaaaaaaa
1500

aaaaaaagta ctctgcgttg ttaccactgc ttaatcacta gtgaattc
1548

<210> 314
<211> 389
<212> PRT
<213> Trifolium repens

<400> 314

Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Ala Asn Arg Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
35 40 45

Lys Val Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr

145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
210 215 220

Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
225 230 235 240

Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
260 265 270

Gly Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln
275 280 285

Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
290 295 300

Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ile Lys Leu Gly Leu Lys
305 310 315 320

Pro Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Glu Tyr Gly Asn
325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
340 345 350

Ser Ala Glu Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
370 375 380

His Ser Val Ala Ile
385

<210> 315
<211> 1447
<212> DNA

<213> Trifolium repens

<400> 315
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acgcatatta tatatatata tatatagtct ataattgaaa gaaactgcta aagatattat 120

taagatatgg tgagtgtagc tgaaattcgc aaggctcaga gggctgaagg ccctgcaacc 180

attttggcca ttggcactgc aaatccacca aaccgtgttg agcagagcac atatcctgat 240

ttctacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa gttccaacgc 300

atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga gattttgaaa 360

gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca agacatggtg 420

gtggttgagg tacctagact tgggaaggag gctgcagtca aggccattaa agaatggggt 480

caaccaaagt caaagattac tcacttaatc ttttgcacca caagtggtgt tgacatgcct 540

ggtgctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa aaggtatatg 600

atgtaccaac aaggttgttt tgcaggaggc acggtgcttc gtttggcaaa agatttggcc 660

gagaacaaca aaggtgctcg tgtgctagtt gtttgttctg aagtcaccgc agtcacattt 720

cgcggcccca gtgatactca cttggacagt cttgttggac aagcattgtt tggagatgga 780

gccgctgcac taattgttgg ttctgatcca gtgcctgaaa ttgagaaacc aatatttgag 840

atggtttgga ctgcacaaac aattgctcca gacagtgaag gtgccattga tggtcatctt 900

cgtgaagctg ggctaacatt tcatcttctt aaagatgttc ctgggattgt atcaaagaac 960

attaataaag cattggttga ggctttccaa ccattaggaa tttctgacta caactcaatc 1020

ttttggattg cacacccggg tggacctgca attcttgatc aagtagaaca aaagctagcc 1080

ttgaagcccg aaaagatgag ggccacgagg gaagttctaa gtgaatatgg aaacatgtca 1140

agcgcatgtg tattgttcat cttagatgag atgcggaaga aatcggctca aaatggactt 1200

aagacaactg gagaaggact tgattggggt gtgttgttcg gcttcggacc aggacttacc 1260

attgaaaccg ttgttcttcg tagcgtggct atataagatg tgtgattgtt tttattttaa
1320

tgtattactt ttaatcttgc tgccttgaat ttcgatttaa gaataaataa atatatcttt
1380

tgataaaaaa aaaaaaaaaa aaaaaaaaaa aagtactctg cgttgttacc actgcttaat
1440

cgaattc
1447

<210> 316
<211> 389
<212> PRT
<213> Trifolium repens

<400> 316

Met Val Ser Val Ala Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Pro Asn Arg Val Glu
20 25 30

Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
210 215 220

Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
225 230 235 240

Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
260 265 270

Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
275 280 285

Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
290 295 300

Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys
305 310 315 320

Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
340 345 350

Ser Ala Gln Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
370 375 380

Arg Ser Val Ala Ile
385

<210> 317
<211> 2394
<212> DNA
<213> Trifolium repens

<400> 317
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60

aaattcactc attgcataga aaaccataca catttgatct tgcaaagaag aaatatggga
120

gacgaaggta tagtgagagg tgtcacaaag cagacaaccc ctgggaaggc tactatattg
180

gctcttggca aggcattccc tcaccaactt gtgatgcaag agtgtttagt tgatggttat
240

tttagggaca ctaattgtga caatcctgaa cttaagcaga aacttgctag actttgtaag
300

acaaccacgg taaaaacaag gtatgttgtt atgaatgagg agatactaaa gaaatatcca
360

gaacttgttg tcgaaggcgc ctcaactgta aaacaacgtt tagagatatg taatgaggca
420

gtaacacaaa tggcaattga agcttcccaa gtttgcctaa agaattgggg tagatcctta
480

tcggacataa ctcatgtggt ttatgtttca tctagtgaag ctagattacc cggtggtgac
540

ctatacttgt caaaaggact aggactaaac cctaaaattc aaagaaccat gctctatttc
600

tctggatgct cgggaggcgt agccggcctt cgcgttgcga aagacgtagc tgagaacaac
660

cctggaagta gagttttgct tgctacttcg gaaactacaa ttattggatt caagccacca
720

agtgttgata gaccttatga tcttgttggt gtggcactct ttggagatgg tgctggtgca
780

atgataattg gctcagaccc ggtatttgaa actgagacac cattgtttga gctgcatact
840

tcagctcagg agtttatacc agacaccgag aagaaaattg atgggcggct gacggaggag
900

ggcataagtt tcacactagc aagggaactt ccgcagataa tcgaagacaa tgttgaggga
960

ttctgtaata aactaattga tgttgttggg ttggagaata aggagtacaa taagttgttt
1020

tgggctgtgc atccaggtgg gcctgcgata ttgaatcgcg tggagaagcg gcttgagttg
1080

tcgccgcaga agctgaatgc tagtagaaaa gctctaatgg attatggaaa tgctagcagc
1140

aatactattg tttatgtgct ggaatatatg ctagaagagg aaaagaagat taaaaaggcg
1200

ggtggaggag attctgaatg gggattgata cttgcttttg gacctggaat tacttttgag
1260

gggattctag caaggaactt gtgtgcatga agtcttatac aattgtgatg catgacttat
1320

actcttattt ctactaatta ttatattaag caaattcaga acttttaagt aatgatttaa
1380

tgaagaatac ttatagtata ttgactttat tcactttcaa agcaagttta tgatcctaag
1440

acatggtaga acttgagcat gtggaatagt tgtaacaaaa actctaagca aatagagact
1500

ttatgtagta taaagcattt ccagacatga taaataatgg tacctcagaa cataaaatat
1560

atttagctat ctttcatccc caactttaca catccaccaa ggtacagaat aagcatatgt
1620

caacacaaaa tgtactctaa gtctaacatg agtaaccaaa catgatgcct gattaagtta
1680

aaagaaaaga aaatctgagg gcatagatct tcaatcacac cactccagag ggaaggcgta
1740

gaacaagctg tccgccgaaa acactgcaat tcaataaata tcattaggac aacagtgcag
1800

agtcatgcgg gaaatgtctt aagtcactgt actaaaaata taggattata ttatgaacta
1860

tactaacctt ttcacataat agtaacagaa atcagctaag atgaatgtct ggacaatttc
1920

tgagataaga accatgacgg ccataagcca taccccaagg caaccaataa atgtccacgg
1980

gtatctaaca cctgttgcaa gaaatagtaa gttattagga gatgtgcggt tacgaaattc
2040

aagctacaca acaaaaggag gccagaacaa cagcaatctt gtaaccagat gacaacaata
2100

aaatgtaaac ttaaagagac cgaacacaca aacattgcaa ctcagatgga attgctgcca
2160

tgtaactagt aggagatttg ggacgtcaaa tcagtatatt atgcaaatac aaggtatgac
2220

cgccttgtct attgtagcat acaacaaacg tacagtgggt ttgtccctct caaaatggca
2280

ggatctttac agcacaatat ttggttttgt catacttata ccataaaaaa aaaaaaaaaa
2340

aaaaaaaaaa aaagtactct gcgttgttac cactgcttaa tcactagtga attc
2394

<210> 318
<211> 391
<212> PRT
<213> Trifolium repens

<400> 318

Met Gly Asp Glu Gly Ile Val Arg Gly Val Thr Lys Gln Thr Thr Pro
1 5 10 15

Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
20 25 30

Val Met Gln Glu Cys Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
35 40 45

Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
50 55 60

Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
65 70 75 80

Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
85 90 95

Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
100 105 110

Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
115 120 125

Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
130 135 140

Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
145 150 155 160

Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
165 170 175

Asp Val Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
180 185 190

Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
195 200 205

Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
210 215 220

Ile Gly Ser Asp Pro Val Phe Glu Thr Glu Thr Pro Leu Phe Glu Leu
225 230 235 240

His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
245 250 255

Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
260 265 270

Pro Gln Ile Ile Glu Asp Asn Val Glu Gly Phe Cys Asn Lys Leu Ile
275 280 285

Asp Val Val Gly Leu Glu Asn Lys Glu Tyr Asn Lys Leu Phe Trp Ala
290 295 300

Val His Pro Gly Gly Pro Ala Ile Leu Asn Arg Val Glu Lys Arg Leu
305 310 315 320

Glu Leu Ser Pro Gln Lys Leu Asn Ala Ser Arg Lys Ala Leu Met Asp
325 330 335

Tyr Gly Asn Ala Ser Ser Asn Thr Ile Val Tyr Val Leu Glu Tyr Met
340 345 350

Leu Glu Glu Glu Lys Lys Ile Lys Lys Ala Gly Gly Gly Asp Ser Glu
355 360 365

Trp Gly Leu Ile Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile
370 375 380

Leu Ala Arg Asn Leu Cys Ala
385 390

<210> 319
<211> 1663
<212> DNA
<213> Trifolium repens

<400> 319
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tttctttttg agtccttgct acgtggcttt accaaaaaac gttgctaagt catcaaccat
120

tccaattcct taatataacc tatcagtact caccatcttt tcttcctccc tgctaacttt
180

agactcagag aagatggtga atgttaatga gatccgccag gcacagagag ctgaaggccc
240

tgccaccgtg ttggcaatcg gcactgcaac tcctccaaac tgtgtcgatc agagtacata
300

cccagactac tacttccgca tcacaaacag tgagcacaag acagagctca aagaaaaatt
360

ccagcgcatg tgtgacaaat ctatgattaa gaagagatac atgcatttga cagaagagat
420

tttgaaggag aatccaagtt tatgtgagta catggcacct tcattggatg caagacaaga
480

catggtggtt gtggaagtac caaggctagg aaaagaggct gcaacaaagg ctatcaagga
540

atggggtcaa cctaagtcca agattactca cctcatcttt tgcaccacaa gtggtgtgga
600

catgcctggc gccgactatc agcttacaaa gcttttaggc cttcgtccgc atgtgaagcg
660

ttatatgatg taccaacaag gttgtttcgc tggtggtacg gtgcttcgtt tggctaaaga
720

cttggctgaa aacaacaaag gtgcccgtgt gttggtggtt tgttcagaga tcactgcggt
780

tactttccgt ggacccagtg acactcatct tgatagcctt gtggggcaag cattgtttgg
840

agatggtgca gcagctgtga ttgtaggttc agacccatta ccacaagttg agaagccctt
900

gtttgaattg gtatggactg ctcaaacaat ccttccagac agtgaaggag ccattgatgg
960

gcaccttcgt gaagtcgggc tgacattcca tctcctcaag gatgttcctg gactcatctc
1020

aaagaacatt gagaaagctc ttgttgaggc ctttcaacct ttaggtatct ctgattacaa
1080

ttctatattt tggatcgcac atcctggtgg acctgcaatt ctggaccaag tggaagccaa
1140

attaagctta aagccagaga aaatgcaagc cacccggcat gtgcttagcg agtatggtaa
1200

catgtcaagt gcatgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga
1260

tggacttgcc acaacaggcg aggggctgga atggggtgta ctattcggtt ttggacccgg
1320

actcactgtt gagactgtat tgctccatag tgttgccact taaattgcct agatatgcta
1380

taactatatg cttatttaat tctttgtttc tgggggattt tatcttcact tacttcactg
1440

agcatttgaa taaagtttgt tttaattatt cataatgtaa tatggtgttg cttaatgtac
1500

ccatccatat aatatttgta atacatatat taatcaactt gcaatttcat gaaaaaaaaa
1560

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaggaaaaaa aaaaaaaaaa aaaaaaaaaa
1620

aagtactctg cgttgttacc actgcttaat cactagtgaa ttc
1663

<210> 320
<211> 389
<212> PRT
<213> Trifolium repens

<400> 320

Met Val Asn Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Thr Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro His Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Val Ile Val
210 215 220

Gly Ser Asp Pro Leu Pro Gln Val Glu Lys Pro Leu Phe Glu Leu Val
225 230 235 240

Trp Thr Ala Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
260 265 270

Gly Leu Ile Ser Lys Asn Ile Glu Lys Ala Leu Val Glu Ala Phe Gln
275 280 285

Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
290 295 300

Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ala Lys Leu Ser Leu Lys
305 310 315 320

Pro Glu Lys Met Gln Ala Thr Arg His Val Leu Ser Glu Tyr Gly Asn
325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Arg Lys
340 345 350

Ser Lys Glu Asp Gly Leu Ala Thr Thr Gly Glu Gly Leu Glu Trp Gly
355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr Val Leu Leu
370 375 380

His Ser Val Ala Thr
385

<210> 321
<211> 1653
<212> DNA
<213> Trifolium repens

<400> 321
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60

ttgtttccat aacacaagaa ctagtgtttg cttgaatctt aagaaaaaat gcctcaaggt
120

gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc tactcaggga
180

aaggcaacga tacttgcatt aggaaaggct ttccccgccc aggtcctccc tcaagagtgc
240

ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa ggagaaattg
300

gagcgtcttt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc aaaggagatc
360

ttagacaact atccagagct agccatagat ggaacaccaa caataaggca aaagcttgaa
420

atagcaaatc cagcagtagt tgaaatggca acaagagcaa gcaaagattg catcaaagaa
480

tggggaaggt cacctcaaga tatcacacac atagtctatg tttcctcgag cgaaattcgt
540

ctacccggtg gtgaccttta tcttgcaaat gaactcggct taaacagcga tgttaatcgc
600

gtaatgctct atttcctcgg ttgctacggc ggtgtcactg gcttacgtgt cgccaaagac
660

atcgccgaaa ataaccctgg tagtagggtg ttactcacaa catccgagac cactattctc
720

ggttttcgac caccgagtaa agctagacct tatgacctcg ttggcgctgc acttttcggt 780

gatggcgccg ctgctgcaat aattggaaca gaccctatat tgaatcaaga atcacctttc 840

atggaattga accatgcagt ccaaaaattc ttgcctgata cacaaaatgt gattgatggt 900

agaatcactg aagagggtat taattttaag cttggaagag accttcctca aaaaattgaa 960

gacaatattg aagaattttg caagaaaatt atggctaaaa gtgatgttaa ggaatttaat 1020

gacttatttt gggctgttca tcctggtggg ccagctatac tcaataagct agaaaatata 1080

ctcaaattga aaagtgataa attggattgt agtaggaagg cattaatgga ttatggaaat 1140

gttagtagca atactatatt ctatgtgatg gagtatatga gagattattt gaaggaagat 1200

ggaagtgaag aatggggatt aggattggct tttggaccag ggattacttt tgaaggggtt 1260

ctcctccgta gcctttaatc ttgaaataat aattcatatg aaattacttg tcttaagatt 1320

gtgataggaa gatgaatatg tattggatta atattgatat ggtgttattt taagttgatt 1380

ttaaaaaaag tttattaata aagtatgatg taacaattgt tgtttgaatg ttaaaaggga 1440

agtatactat tttaagttct tgaccatact gatttttttct ttacacattt tcatatctaa 1500

aattgttcta tgatatcttc attgttgata ctgtaataat ataatatcta atttggctgg 1560

caaaatgaaa gatttttcac cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtactctg 1620

cgttgttacc actgcttaat cactagtgaa ttc 1653

<210> 322
<211> 389
<212> PRT
<213> Trifolium repens

<400> 322

Met Pro Gln Gly Asp Leu Asn Gly Ser Ser Ser Val Asn Gly Ala Arg
1 5 10 15

Ala Arg Arg Ala Pro Thr Gln Gly Lys Ala Thr Ile Leu Ala Leu Gly
20 25 30

Lys Ala Phe Pro Ala Gln Val Leu Pro Gln Glu Cys Leu Val Glu Gly
35 40 45

Phe Ile Arg Asp Thr Lys Cys Asp Asp Thr Tyr Ile Lys Glu Lys Leu
50 55 60

Glu Arg Leu Cys Lys Asn Thr Thr Val Lys Thr Arg Tyr Thr Val Met
65 70 75 80

Ser Lys Glu Ile Leu Asp Asn Tyr Pro Glu Leu Ala Ile Asp Gly Thr
85 90 95

Pro Thr Ile Arg Gln Lys Leu Glu Ile Ala Asn Pro Ala Val Val Glu
100 105 110

Met Ala Thr Arg Ala Ser Lys Asp Cys Ile Lys Glu Trp Gly Arg Ser
115 120 125

Pro Gln Asp Ile Thr His Ile Val Tyr Val Ser Ser Ser Glu Ile Arg
130 135 140

Leu Pro Gly Gly Asp Leu Tyr Leu Ala Asn Glu Leu Gly Leu Asn Ser
145 150 155 160

Asp Val Asn Arg Val Met Leu Tyr Phe Leu Gly Cys Tyr Gly Gly Val
165 170 175

Thr Gly Leu Arg Val Ala Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser
180 185 190

Arg Val Leu Leu Thr Thr Ser Glu Thr Thr Ile Leu Gly Phe Arg Pro
195 200 205

Pro Ser Lys Ala Arg Pro Tyr Asp Leu Val Gly Ala Ala Leu Phe Gly
210 215 220

Asp Gly Ala Ala Ala Ala Ile Ile Gly Thr Asp Pro Ile Leu Asn Gln
225 230 235 240

Glu Ser Pro Phe Met Glu Leu Asn His Ala Val Gln Lys Phe Leu Pro
245 250 255

Asp Thr Gln Asn Val Ile Asp Gly Arg Ile Thr Glu Glu Gly Ile Asn
260 265 270

Phe Lys Leu Gly Arg Asp Leu Pro Gln Lys Ile Glu Asp Asn Ile Glu
275 280 285

Glu Phe Cys Lys Lys Ile Met Ala Lys Ser Asp Val Lys Glu Phe Asn
290 295 300

Asp Leu Phe Trp Ala Val His Pro Gly Gly Pro Ala Ile Leu Asn Lys
305 310 315 320

Leu Glu Asn Ile Leu Lys Leu Lys Ser Asp Lys Leu Asp Cys Ser Arg
325 330 335

Lys Ala Leu Met Asp Tyr Gly Asn Val Ser Ser Asn Thr Ile Phe Tyr
340 345 350

Val Met Glu Tyr Met Arg Asp Tyr Leu Lys Glu Asp Gly Ser Glu Glu
355 360 365

Trp Gly Leu Gly Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Val
370 375 380

Leu Leu Arg Ser Leu
385

<210> 323
<211> 1600
<212> DNA
<213> Trifolium repens

<400> 323
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60

caacaccatt aataaccttc caaattctcg ttacctcacc aaatctcatt tttcattata
120

tatcttgggt acatcttttg ttacctccaa caaaaaaatg gtgaccgtag aagagattcg
180

taacgcccaa cgttcaaatg gccctgccac tatcttagct tttggcacag ccactccttc
240

taactgtgtc actcaagctg attatcctga ttactacttt cgtatcacca acagcgaaca
300

tatgactgat cttaaggaaa aattcaagcg gatgtgtgat agatcaatga taaagaaacg
360

ttacatgcac ctaacagaag actttctgaa ggagaatcca aatatgtgtg aatacatggc
420

accatcacta gatgtaagac gagacatagt ggttgttgaa gtaccaaagc taggtaaaga
480

agcagcaaaa aaagccatat gtgaatgggg acaaccaaaa tccaaaatca cacatcttgt
540

tttctgcacc acttccggtg ttgacatgcc gggagccgat taccaactca ccaaactttt
600

aggcttaaaa ccttctgtca agcgtctcat gatgtatcaa caaggttgtt tcgctggcgg
660

cacagttctc cgcttagcaa aagaccttgt tgagaataac aaaaatgcaa gagttcttgt
720

tgtttgttct gaaattactg cggttacttt tcgtggacca tcggatactc atcttgattc 780

gctcgtggga caggcgcttt ttggtgatgg agccgcagca atgattattg gtgcggatcc 840

tgatttaacc gtggagcgtc cgattttcga gattgtttcg gctgctcaga ctattcttcc 900

tgattctgat ggcgcaattg atggacatct tcgtgaagtg gggctcactt ttcatttatt 960

gaaagatgtt ccggggatta tttcaaagaa cattgaaaaa agtttagttg aagcttttgc 1020

gcctattggg attaatgatt ggaactcaat attttgggtt gcacatccag gtggaccggc 1080

tattttagac caggttgaag agaaactcca tcttaaagag gagaaactcc ggtccacccg 1140

gcatgtgctt agtgaatatg gaaatatgtc aagtgcatgt gttttattta ttttggatga 1200

aatgagaaag aggtctaaag aggaagggat gattacaact ggtgaagggt tggaatgggg 1260

tgtgttgttt gggtttggac cgggtttaac tgttgaaacc gttgtgcttc atagtgttcc 1320

ggttcagggt tgaatttatt atacatagat tggaaaataa aatttgcctg ccgagagatg 1380

tgaactaact ttgtaggcaa gctcaaatta aagtttgaga taatattgtg ctttagttat 1440

tatggtatgt aatgtaatgt ttttactttt ttcgaaattc atgtaatttg atatgtaaag 1500

taatatgttt gggttggaat ataattattt gttaactaaa aaaaaaaaaa aaaaaaaaaa 1560

aaaaagtact ctgcgttgtt accactgctt aatcgaattc 1600

<210> 324
<211> 391
<212> PRT
<213> Trifolium repens

<400> 324

Met Val Thr Val Glu Glu Ile Arg Asn Ala Gln Arg Ser Asn Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Phe Gly Thr Ala Thr Pro Ser Asn Cys Val Thr
20 25 30

Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Met Thr Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp Arg Ser Met

50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Asp Phe Leu Lys Glu Asn
65 70 75 80

Pro Asn Met Cys Glu Tyr Met Ala Pro Ser Leu Asp Val Arg Arg Asp
85 90 95

Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Glu Ala Ala Lys Lys
100 105 110

Ala Ile Cys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Val
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Lys Pro Ser Val Lys Arg Leu Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Val Glu Asn Asn Lys Asn Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Met Ile Ile
210 215 220

Gly Ala Asp Pro Asp Leu Thr Val Glu Arg Pro Ile Phe Glu Ile Val
225 230 235 240

Ser Ala Ala Gln Thr Ile Leu Pro Asp Ser Asp Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
260 265 270

Gly Ile Ile Ser Lys Asn Ile Glu Lys Ser Leu Val Glu Ala Phe Ala
275 280 285

Pro Ile Gly Ile Asn Asp Trp Asn Ser Ile Phe Trp Val Ala His Pro
290 295 300

Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Glu Lys Leu His Leu Lys
305 310 315 320

Glu Glu Lys Leu Arg Ser Thr Arg His Val Leu Ser Glu Tyr Gly Asn
325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Arg
340 345 350

Ser Lys Glu Glu Gly Met Ile Thr Thr Gly Glu Gly Leu Glu Trp Gly
355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr Val Val Leu
370 375 380

His Ser Val Pro Val Gln Gly
385 390

<210> 325
<211> 1333
<212> DNA
<213> Trifolium repens

<400> 325
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gcagttatca aacacaacag tcttccactt gagctctgtt tctccacatg tcgaagctag
120

tttgcgtcac cggcggcagc ggatgcatcg gttcatggct agtccatctc cttctcctcc
180

gcggctacac tgttcacgcc accgtccaaa atctcaatga tgagaacgaa acgaagcatc
240

tagaagctct cgaaggagca caaactaatc tccgtctctt ccagatcgat ctccttaact
300

acgacacaat cctcgctgct gtccgcggtt gcgtcggaat tttccacctc gcttcacctt
360

gcactgtaga caaagttcat gatcctcaga aggagctttt ggatcctgca attaaaggga
420

ctttgaatgt gcttactgca gctaaggaag taggggtgaa gcgtgtggtt gttacctcgt
480

ctgtctcggc gattactcct agtcctgatt ggccttctga tgttgttaaa agagaggatt
540

gttggactga tgttgaatat tgcaagaaaa aagagttgtg gtatccgttg tccaaaacat
600

tggctgagaa agctgcgtgg gatttttcca aagaaaatgg tttggatgtt gttgtggtga
660

atcccggtac tgtgatgggt cctgttattc caccacggca taatgcaagc atgctcatgc
720

ttgtgagact tcttgaaggc tgcgctgaaa catttgaaga ctattttatg ggattggtcc
780

acttcaaaga tgtagcattg gcgcatattt tggtgtatga gaacaaagaa gcatctggta
840

gacatgtgtg tgttgaaact atctctcact acggtgattt tgtggcaaaa gttgctgaac
900

tttatccaga atatagtgtt cctaggatgc agcgagatac gcaacctgga ttgttgagag
960

cgaatgatgg atcaaagaag ctcatagatt tgggtttgga attcattcca atggagcaaa
1020

ttatcaagga tgctgtagag agtttgaaga acaaaggatt catttcttga atgatgttac
1080

tgttctttgg agaaccctat agttaccaga gtatagacta aataatatat aggtgatggg
1140

tcagagaatg agtacttatg tcatgagttg tgtctgtata atatgttttc tcaattctta
1200

tatgttaaat tgctaatgtt aacttcaata tttatcagcc agtattgttt ttttaataaa
1260

atattgaagc aaaaaaaaaa aaaaaaaaaa aaaaaaaagt actctgcgtt gttaccactg
1320

cttaatcgaa ttc
1333

<210> 326
<211> 320
<212> PRT
<213> Trifolium repens

<400> 326

Met Ser Lys Leu Val Cys Val Thr Gly Gly Ser Gly Cys Ile Gly Ser
1 5 10 15

Trp Leu Val His Leu Leu Leu Leu Arg Gly Tyr Thr Val His Ala Thr
20 25 30

Val Gln Asn Leu Asn Asp Glu Asn Glu Thr Lys His Leu Glu Ala Leu
35 40 45

Glu Gly Ala Gln Thr Asn Leu Arg Leu Phe Gln Ile Asp Leu Leu Asn
50 55 60

Tyr Asp Thr Ile Leu Ala Ala Val Arg Gly Cys Val Gly Ile Phe His
65 70 75 80

Leu Ala Ser Pro Cys Thr Val Asp Lys Val His Asp Pro Gln Lys Glu
85 90 95

Leu Leu Asp Pro Ala Ile Lys Gly Thr Leu Asn Val Leu Thr Ala Ala
100 105 110

Lys Glu Val Gly Val Lys Arg Val Val Val Thr Ser Ser Val Ser Ala
115 120 125

Ile Thr Pro Ser Pro Asp Trp Pro Ser Asp Val Val Lys Arg Glu Asp
130 135 140

Cys Trp Thr Asp Val Glu Tyr Cys Lys Lys Lys Glu Leu Trp Tyr Pro
145 150 155 160

Leu Ser Lys Thr Leu Ala Glu Lys Ala Ala Trp Asp Phe Ser Lys Glu
165 170 175

Asn Gly Leu Asp Val Val Val Val Asn Pro Gly Thr Val Met Gly Pro
180 185 190

Val Ile Pro Pro Arg His Asn Ala Ser Met Leu Met Leu Val Arg Leu
195 200 205

Leu Glu Gly Cys Ala Glu Thr Phe Glu Asp Tyr Phe Met Gly Leu Val
210 215 220

His Phe Lys Asp Val Ala Leu Ala His Ile Leu Val Tyr Glu Asn Lys
225 230 235 240

Glu Ala Ser Gly Arg His Val Cys Val Glu Thr Ile Ser His Tyr Gly
245 250 255

Asp Phe Val Ala Lys Val Ala Glu Leu Tyr Pro Glu Tyr Ser Val Pro
260 265 270

Arg Met Gln Arg Asp Thr Gln Pro Gly Leu Leu Arg Ala Asn Asp Gly
275 280 285

Ser Lys Lys Leu Ile Asp Leu Gly Leu Glu Phe Ile Pro Met Glu Gln
290 295 300

Ile Ile Lys Asp Ala Val Glu Ser Leu Lys Asn Lys Gly Phe Ile Ser
305 310 315 320

<210> 327
<211> 1470
<212> DNA
<213> Trifolium repens

<400> 327
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cttaaacctc acaaaaaata aaccacacaa cacacaaaca ccaaaaacag agcaccgttt
120

ccatcatcaa acaatggcac cagccaaaac tctaagttat ctctcacaac aaaacactct
180

cgagtcaagt ttcgttaggg aagaagatga gcgtccaaaa gttgcctaca ataacttcag
240

caacgagatt ccaatcattt ctcttgctgg aattgatgag gttgatggtc gtagaacaga
300

gatatgtaac aagattgttg aagcttgtga gaattggggt atttttcagg ttgttgatca
360

tggtgttgat acaaaacttg tttctgagat gacccgtttt gctagagagt tttttgcttt
420

gccaccggaa gagaagctcc ggtttgacat gtccggtggt aaaaagggtg gtttcattgt
480

ctctagtcat cttcaaggag aagcagtgaa ggattggaga gagctagtga catatttttc
540

atacccaatt aaacaaagag attattcaag gtggccagac aagccagaag gatggaaaga
600

ggtaacagaa aaatacagtg aaaacctaat gaatttagct tgcaagctat tggaagtttt
660

atcagaagca atgggtttag aaaaagaagc tctaacaaaa gcatgtgttg atatggatca
720

aaaagttgtt ataaattatt acccaaaatg ccctgaacct gacctcacac ttggccttaa
780

acgtcacact gaccctggca caattactct tttgcttcaa gatcaagttg gtggtcttca
840

agctaccaaa gataatggta agacgtggat tacagttcaa ccagttgaag gtgcttttgt
900

tgttaatctt ggagaccatg gtcactatct aagtaatgga cggttcaaaa atgctgacca
960

tcaagcagtg gtgaattcga actacagccg tttatcaata gcaacatttc aaaatccagc
1020

tccagatgca actgtgtacc ctttgaagat tagagatggt gaaaaatctg tgttggaaga
1080

accaatcact tttgctgaaa tgtatagaag gaagatgacc aaagaccttg aaattgctag
1140

gatgaagaag ttggctaagg aacaacaact tagggacttg gaggagaaca agactaaata
1200

tgaggccaaa cctttgaatg agatctttgc ttaattaatt agtcttaatt taaataataa
1260

attttagact taatttacat ataataattt taatttttg ttcaattaat ctatgtttaa
1320

tttgtcgtta ttgtccacgt gtattaagct gcttggttgt gtgtgccttg gagaataatc
1380

aataatatta catctatgtt taattataaa aaaaaaaaaa aaaaaaaaaa gtatctgcgt
1440

tgttaccact gcttaatcac tagtgaattc
1470

<210> 328
<211> 366
<212> PRT
<213> Trifolium repens

<400> 328

Met Ala Pro Ala Lys Thr Leu Ser Tyr Leu Ser Gln Gln Asn Thr Leu
1 5 10 15

Glu Ser Ser Phe Val Arg Glu Glu Asp Glu Arg Pro Lys Val Ala Tyr
20 25 30

Asn Asn Phe Ser Asn Glu Ile Pro Ile Ile Ser Leu Ala Gly Ile Asp
35 40 45

Glu Val Asp Gly Arg Arg Thr Glu Ile Cys Asn Lys Ile Val Glu Ala
50 55 60

Cys Glu Asn Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Thr
65 70 75 80

Lys Leu Val Ser Glu Met Thr Arg Phe Ala Arg Glu Phe Phe Ala Leu
85 90 95

Pro Pro Glu Glu Lys Leu Arg Phe Asp Met Ser Gly Gly Lys Lys Gly
100 105 110

Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Ala Val Lys Asp Trp
115 120 125

Arg Glu Leu Val Thr Tyr Phe Ser Tyr Pro Ile Lys Gln Arg Asp Tyr
130 135 140

Ser Arg Trp Pro Asp Lys Pro Glu Gly Trp Lys Glu Val Thr Glu Lys
145 150 155 160

Tyr Ser Glu Asn Leu Met Asn Leu Ala Cys Lys Leu Leu Glu Val Leu
165 170 175

Ser Glu Ala Met Gly Leu Glu Lys Glu Ala Leu Thr Lys Ala Cys Val
180 185 190

Asp Met Asp Gln Lys Val Val Ile Asn Tyr Tyr Pro Lys Cys Pro Glu
195 200 205

Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
210 215 220

Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala Thr Lys Asp

225 230 235 240

Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly Ala Phe Val
245 250 255

Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
260 265 270

Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Tyr Ser Arg Leu Ser
275 280 285

Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val Tyr Pro Leu
290 295 300

Lys Ile Arg Asp Gly Glu Lys Ser Val Leu Glu Glu Pro Ile Thr Phe
305 310 315 320

Ala Glu Met Tyr Arg Arg Lys Met Thr Lys Asp Leu Glu Ile Ala Arg
325 330 335

Met Lys Lys Leu Ala Lys Glu Gln Gln Leu Arg Asp Leu Glu Glu Asn
340 345 350

Lys Thr Lys Tyr Glu Ala Lys Pro Leu Asn Glu Ile Phe Ala
355 360 365

<210> 329
<211> 2515
<212> DNA
<213> Trifolium repens

<400> 329
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tattccttta attctttcat ataatcattt gaatttccat tctccctaaa aattctatag
120

ctaccacatc acacaacata acaaattaag aaatatttat tactatatta agatatggaa
180

gtagtagcag cagcaatcac aaaaaacaat ggcaagattg attcattttg cttgaatcat
240

gctaatgcta ataacatgaa agtgaatggt gctgatcctt tgaattgggg tgtggctgct
300

gaggcaatga agggaagtca cttggatgag gtgaagcgta tggtggagga ataccggaaa
360

ccggttgtcc gtcttggtgg cgagacacta accatttctc aggtggctgc cattgctgca
420

cacgatggtg caacggtgga gctatcggaa tctgctagag ccggcgttaa ggcaagcagt
480

gactgggtta tggagagtat gaacaaaggt accgacagct acggtgtccc aacagggttc

540

ggcgctacct cgcaccgccg aaccaaacaa ggtggtgctt tgcagaaaga gctcataagg
600

tttttgaatg ctggaatatt tggaaatgga actgagtcaa gccacacact accacacaca
660

gccacaagag ctgccatgct agtgagaatc aacacacttc tccaaggcta ttcaggaatt
720

agatttgaaa tcttagaagc tatcaccaag cttcttaaca acaatgtcac cccatgttta
780

ccgcttcgcg gtacaatcac agcttcagga gatttagtcc ctctttctta cattgctggt
840

ttactaaccg gacgaccaaa ttccaaggct catggacctt ctggagaagt acttaatgca
900

aaacaagctt ttcaatcagc tggaatcgat gccgagttct ttgaattaca accaaaagaa
960

ggccttgccc ttgttaacgg aaccgctgtt ggttctggtt tagcttctat tgttcttttt
1020

gaggctaata tattggcggt gttgtctgaa gttctatctg caattttcgc tgaagttatg
1080

caagggaagc ccgaatttac cgatcatttg acacataagt tgaaacatca ccctggtcaa
1140

attgaggctg ctgctattat ggaacacatt ttggatggga gtgcttatgt taaagacgct
1200

aagaagttgc atgagatgga tcctttacag aagccaaaac aagatagata tgcacttagg
1260

acttcgccac aatggcttgg tcctttgatt gaagtgatta gattctctac caagtcaatt
1320

gagagagaga tcaactctgt caatgacaat cctttgattg atgtttcaag gaacaaggct
1380

ttgcatggtg gaaattttca aggaacacct atcggagtat ccatggataa tacacgtttg
1440

gctcttgcat caattggcaa acttatgttt gctcaattct ctgagcttgt caatgatttt
1500

tacaacaatg gattgccatc aaatctctct gctagtagaa atccgagctt ggattatggg
1560

ttcaagggat ccgaaattgc catggcttct tattgttccg agttgcaata tcttgcaaat
1620

ccggttacaa ctcatgtcca aagtgcggaa caacacaacc aagatgtcaa ctctttgggt
1680

ttgatttctt ctagaaaaac ttatgaagca attgagatcc ttcaattgat gtcttccaca
1740

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1800

tcggtcaaaa ataccgtaag ccaagtggcc aaaaagacac taaccatagg tgtcaatgga

1860

gaacttcatc cttcaagatt ttgtgaaaaa gacttattga aagtggttga tagggaacat
1920

gtctttgcct acattgatga tccttgtagt gctacatacc cattgatgca aaaactcagg
1980

caagtactag tggatcatgc attagttaat ggagaaagtg agaagaattt gaacacatca
2040

atcttccaaa agattgcaac ttttgaggaa gagttgaaaa acctttgcca aaagaggttg
2100

aaagtgcaag gattgcatat gaaagtggaa attcaacaat tccaaacaag atcaatggat
2160

gcagatctta tccactctac aattttgtga gaaaggagtt gggaactggt ttgctaactg
2220

gagaaaatgt catttcaccg ggtgaagagt gtgacaaact attcacagct atgtgtcaag
2280

gaaaaatcat tgatcctctt cttgaatgct tgggagagtg gaacggtgct cctcttccaa
2340

tttgttaact ttgattgtta gttcataaaa tgttttattt gtatttatca tttgtattta
2400

tgcgagtgta gtaataatga ttaggtgttt tgtgccttta atgaaaaaaa aaaaaaaaaa
2460

aaaaaaaaaa aaaagtactc tgcgttgtta ccactgctta atcactagtg aattc
2515

<210> 330
<211> 671
<212> PRT
<213> Trifolium repens

<400> 330

Met Glu Val Val Ala Ala Ala Ile Thr Lys Asn Asn Gly Lys Ile Asp
1 5 10 15

Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Gly
20 25 30

Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Val
50 55 60

Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Thr Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110

Thr Asp Ser Tyr Gly Val Pro Thr Gly Phe Gly Ala Thr Ser His Arg
115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Leu
130 135 140

Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Ser His Thr Leu Pro
145 150 155 160

His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile Asn Thr Leu Leu
165 170 175

Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Ala Ile Thr Lys
180 185 190

Leu Leu Asn Asn Asn Val Thr Pro Cys Leu Pro Leu Arg Gly Thr Ile
195 200 205

Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala Gly Leu Leu
210 215 220

Thr Gly Arg Pro Asn Ser Lys Ala His Gly Pro Ser Gly Glu Val Leu
225 230 235 240

Asn Ala Lys Gln Ala Phe Gln Ser Ala Gly Ile Asp Ala Glu Phe Phe
245 250 255

Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr Ala Val
260 265 270

Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala Asn Ile Leu Ala
275 280 285

Val Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val Met Gln Gly
290 295 300

Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys His His Pro
305 310 315 320

Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu Asp Gly Ser
325 330 335

Ala Tyr Val Lys Asp Ala Lys Lys Leu His Glu Met Asp Pro Leu Gln
340 345 350

Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln Trp Leu

355 360 365

Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile Glu Arg
370 375 380

Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser Arg Asn
385 390 395 400

Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser
405 410 415

Met Asp Asn Thr Arg Leu Ala Leu Ala Ser Ile Gly Lys Leu Met Phe
420 425 430

Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn Gly Leu Pro
435 440 445

Ser Asn Leu Ser Ala Ser Arg Asn Pro Ser Leu Asp Tyr Gly Phe Lys
450 455 460

Gly Ser Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu Gln Tyr Leu
465 470 475 480

Ala Asn Pro Val Thr Thr His Val Gln Ser Ala Glu Gln His Asn Gln
485 490 495

Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg Lys Thr Tyr Glu Ala
500 505 510

Ile Glu Ile Leu Gln Leu Met Ser Ser Thr Phe Leu Ile Ala Leu Cys
515 520 525

Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Leu Lys Asn Ser Val
530 535 540

Lys Asn Thr Val Ser Gln Val Ala Lys Lys Thr Leu Thr Ile Gly Val
545 550 555 560

Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp Leu Leu Lys
565 570 575

Val Val Asp Arg Glu His Val Phe Ala Tyr Ile Asp Asp Pro Cys Ser
580 585 590

Ala Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu Val Asp His
595 600 605

Ala Leu Val Asn Gly Glu Ser Glu Lys Asn Leu Asn Thr Ser Ile Phe
610 615 620

Gln Lys Ile Ala Thr Phe Glu Glu Glu Leu Lys Asn Leu Cys Gln Lys
625 630 635 640

Arg Leu Lys Val Gln Gly Leu His Met Lys Val Glu Ile Gln Gln Phe
645 650 655

Gln Thr Arg Ser Met Asp Ala Asp Leu Ile His Ser Thr Ile Leu
660 665 670

<210> 331
<211> 2667
<212> DNA
<213> Trifolium repens

<400> 331
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120

attactttct acaccccccc ctctcaacta ttattaacta acataatgga gggaattacc
180

aatggccatg ctgaagcaac tttttgcgtg accaaaagtg ttggtgatcc actcaactgg
240

ggtgcagccg cggagtcgtt gatggggagt catttggatg aggtgaagcg tatggtggag
300

gaataccgta atccattggt taaaattggc ggcgagacgc ttaccattgc tcaggtggct
360

ggaattgctt ctcatgatag tggtgtgagg gtggagctgt ctgagtccgc cagggccggc
420

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480

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540

aaggagctaa ttaggttttt gaatgccgga atatttggca atggtacaga atctaactgt
600

acactaccac acacagcaac cagagctgca atgcttgtga gaatcaacac tcttcttcaa
660

ggatattctg gaattagatt tgaaattttg gaagctatca caaagcttct aaacaacaac
720

attaccccat gtttaccact tcgtggtaca atcacggctt ccggtgatct cgttccgctt
780

tcctacattg ccggtttgtt aaccggtaga ccgaactcca aagccgttgg accctccgga
840

gaaattctca atgcaaaaga agcttttcaa cttgccggca ttggttctga gtttttttgaa
900

ttgcagccaa aagaaggtct tgctcttgtt aatggtactg ctgttggttc tggtttagct
960

tctattgttc tgtttgaagc aaatgtacta gctgttttgt ctgaagttat gtcggcgatt
1020

ttcgctgaag ttatgcaagg gaaaccagaa ttcactgatc atttgactca taagttgaaa
1080

catcaccctg gtcaaattga agctgctgca attatggaac atattttgga tggaagtgct
1140

tatgttaaag cagctaagaa attacacgaa accgatcctt tacaaaagcc gaaacaagat
1200

cgttatgcac ttagaacttc acctcaatgg cttggtcctt tgattgaagt gataagattt
1260

tcaactaagt caattgagag agaaattaac tctgtcaatg ataacccttt gattgatgtt
1320

tcaaggaaca aggccattca cggtggtaat tttcaaggaa cacctattgg agtttcaatg
1380

gataacacac gtttagctct tgcttcaatt ggtaaactca tgtttgctca attctctgaa
1440

cttgttaatg atttttacaa caacgggtta ccttcgaatc ttactgctag taggaaccca
1500

agcttggatt acggtttcaa gggatcggaa attgccatgg cttcttattg ttctgagtta
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU02/01345

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. [7]: C12N 15/29, 15/52, 15/53, 15/55, 15/60, 15/61; A01H 5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
SEE ELECTRONIC DATABASE BOX BELOW

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
SEE ELECTRONIC DATABASE BOX BELOW

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
PEPTIDE DATABASES (SWISSPROT, GENBANK, EMBL, PIR) DGENE: SEQ ID NOS 2,9,14,18,24,65,70,79,92,96,109,111,118,136,148,154,156,160,162,164,169,186,195,197,203,246,248,250,279,287,294,299,304,308,310,312,314,318,320,322,324,326,328,334

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO 02 18604 A (THE SALK INSTITUTE FOR BIOLOGICAL STUDIES) 7 March 2002 Fig 1D shares ~92% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-19, 25, 27
X	US 6 054 636 A (FADER GM) 25 April 2000 Fig 2 shares ~81% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-27

[X] Further documents are listed in the continuation of Box C [X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 November 2002	05 DEC 2002

Name and mailing address of the ISA/AU
AUSTRALIAN PATENT OFFICE
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E-mail address: pct@ipaustralia.gov.au
Facsimile No. (02) 6285 3929

Authorized officer
TERRY MOORE
Telephone No : (02) 6283 2632

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 36543 A (PIONEER HI-BRED INTERNATIONAL, INC.) 22 July 1999 SEQ ID NO 2 shares ~81% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-17, 21, 22, 24-27
X	Genbank Acc No AAB41524 chalcone isomerase (*Medicago sativa*) 29 January 1997 (See also Medline Abstract 8193301) 92% identity with SEQ ID NOS 18, 310	1-3, 13-18, 24-27
X	Genbank Acc No CAA74847 anther-specific protein (*Nicotiana sylvestris*) (See also Medline Abstract 99084767) 83% identity with SEQ ID NOS 96, 322 and 67% identity with SEQ ID NOS 318, 70	1, 2, 4, 13-18, 24-26, 28
X	Genbank Acc No CAC14061 chalcone synthase (*Ruta graveolens*) 27 October 2000 ~87% identity with SEQ ID NOS 24, 65, 79, 92, 102, 107, 314, 316, 320, 324	1, 2, 4, 13-18, 24-26, 28
X	Genbank Acc No AAB41556 chalcone reductase (*Medicago sativa*) 30 January 1997 ~95% identity with SEQ ID NOS 109, 118, 312	1, 2, 5, 13-18, 20, 24-26, 29
X	Genbank Acc No CAA11226 chalcone reductase (*Sesbania rostrata*) 3 July 2001 90% identity with SEQ ID NO 111	1, 2, 5, 13-18, 24-26, 29
X	Genbank Acc No AAK52955 dihydro-flavonoid reductase-like protein (*Zea mays*) 14 May 2001 69% identity with SEQ ID NOS 287, 160 and 53% identity with SEQ ID NO 148	1, 2, 6, 13-18, 24-26, 30
PX	WO 02 063021 A (PIONEER HI-BRED INTERNATIONAL, INC.) 15 August 2002 SEQ ID NO 1 shares 74% identity with SEQ ID NOS 148, 160, 287	1, 2, 6, 13-18, 24-26, 30
X	Genbank Acc No AAD54273 dihydroflavonol-4-reducatse DFR1 (*Glycine max*) 10 September 1999 81 % identity with SEQ ID NO 169	1, 2, 6, 13-18, 24-26, 30
X	WO 95 27790 A (CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE) 19 October 1995 SEQ ID NO 1 shares 43% identity with SEQ ID NOS 136, 156, 326, 39% identity with SEQ ID NO 154 and 51% identity with SEQ ID NO 294.	1, 2, 6, 13-18, 24-26, 30
PX	WO 02 10210 A (BAYER AKTIENGESELLSCHAFT) 7 February 2002 SEQ ID NO 2329 shares 51% identity with SEQ ID NO 164, SEQ ID NO 636 shares 62% identity with SEQ ID NO 186, SEQ ID NO 1573 shares 49% identity with SEQ ID NOS 246, 248, SEQ ID NO 2091 shares 57% identity with SEQ ID NOS 304, 299	1, 2, 7, 9, 13-17, 24-26, 31, 32
X	WO 99 14351 (E.I. DU PONT DE NEMOURS AND COMPANY) 25 March 1999 SEQ ID NO 1 shares 56% identity with SEQ ID NO 162	1, 2, 6, 13-17, 21, 22, 24-26, 30

INTERNATIONAL SEARCH REPORT

International application No. **PCT/AU02/01345**

C (Continuation)	DOCUMENTS CONSIDERED TO BE RELEVANT	
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO 02 26994 A (AGRICULTURE VICTORIA SERVICES PTY LTD) 4 April 2002 Fig 39 shares 72% identity with SEQ ID NO 294	1, 2, 6, 13-18, 21, 22, 24-26, 30
X	WO 97 12982 A (CENTRE NATIONAL DE LA RECHERCHE SCEINTIFIQUE) 10 April 1997 SEQ ID NO 5 shares 55% identity with SEQ ID NO 294	1, 2, 6, 13-17, 24-26, 30
X	Genbank Acc No CAA80265 flavonoid 3',5'-hydroxylase (*Petunia x hybrida*) 7 December 1993 70% identity with SEQ ID NO 197	1, 2, 8, 13-18, 24-26, 32
X	EP 1 033 405 (CERES INCORPORATED) 6 September 2000 SEQ ID NO 49742 shares 57% identity with SEQ ID NO 195	1, 2, 8, 13-18, 24-26, 32
X	Genbank Acc No AAF23859 DFR-like protein (*Arabidopsis thaliana*) 11 January 2000 61% identity with SEQ ID NO 186	1, 2, 7, 13-18, 24-26, 31
X	Genbank Acc No BAB01697 oxidase-like protein (*Arabidopsis thaliana*) 27 December 2000 50% identity with SEQ ID NOS 246, 248	1, 2, 9, 13-18, 24-26, 33
X	TREMBL Acc No CAB63776 F3'H1 protein (*Glycine max*) 1 May 2000 85% identity with SEQ ID NO 328, 203	1, 2, 9, 13-18, 24-26, 33
X	Genbank Acc No CAB78172 flavanone 3-beta-hydroxylase (*Arabidopsis thaliana*) 16 March 2000 57% identity with SEQ ID NOS 304, 299	1, 2, 9, 13-17, 24-26, 33
X	Genbank Acc No AAG49298 Flavonoid 3'-hydroxylase (*Callistephus chinensis*) 16 January 2001 68% identity with SEQ ID NO 250	1, 2, 10, 13-18, 20, 24-26, 34
X	Genbank Acc No AAA99500 Phenylalanine ammonia lyase (*Stylosanthes humilis*) 15 May 1996 88% identity with SEQ ID NOS 254, 259, 269, 271, 273, 275, 330, 332, 334	1, 2, 11, 13-18, 24-26, 35
X	Genbank Acc No CAA41169 phenylalanine ammonia lyase (*Medicago sativa*) 5 May 1995 87% identity with SEQ ID NOS 254, 259, 269, 271, 273, 275, 330, 332, 334	1, 2, 11, 13-18, 24-26, 35
X	Genbank Acc No AAB41550 vestitone reductase (*Medicago sativa*) 30 January 1997 (See also Medline abstract 7625843) 95% identity with SEQ ID NOS 336, 279	1, 2, 12-18, 21, 22, 24-26, 36

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU02/01345

Box I **Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :

   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos :

   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos :

   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II **Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

See supplemental Box

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

Supplemental Box 1
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (lack of unity)

The international application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept. The fundamental test for unity of invention is specified in Rule 13.2 of the Regulations under the PCT.

"Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only where there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features. The expression "special technical feature" shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, make over the prior art."

The problem addressed by the application is the modification of flavonoid biosynthesis (see page 2, line 29-page 3, line 7). The solution provided by the claims resides in the use of 56 specific polypeptides from clover, medic, ryegrass or fescue species (claim 25) and the nucleic acids or fragments coding for these polypeptides (claim 1). These 56 specific polypeptides fall within the following ten groups:

1.	Chalcone isomeras (CHI)	(SEQ IDS 2,9,14,18,308,310)
2.	Chalcone synthase (CHS)	(SEQ IDS 24,65,70,79,92,96,102,107,314,316,318,322,324)
3.	Chalcone reductase (CHR)	(SEQ IDS 109,111,118,312)
4.	Dihydroflavonol 4-reductase (DFR)	(SEQ IDS 136,148,154,156,160,162,164,169,287,294,326)
5.	Leucoanthocyanidin reductase (LCR)	(SEQ ID 186)
6.	Flavonoid 3',5' hydrolase (F3'5'H)	(SEQ IDS 195,197)
7.	Flavanone 3-hydrolase (F3H)	(SEQ IDS 203,246,248,299,304,328)
8.	Flavonoid 3'-hydroxylase (F3'H)	(SEQ ID 250)
9.	Phenyalanine ammonia-olyase (PAL)	(SEQ IDS 254,259,269,271,273,275,330,332,334)
10.	Vestitone reductase (VR)	(SEQ IDS 279,336)

The application acknowledges that representatives of these enzyme species, and the nucleotides that encode them, are known and have been isolated from other plant species (see page 2 lines 29-31). This is supported by the following documents, which disclose the isolation and characterisation of a number of these enzymes from a range of species, including clover and medic and rye.

EMBL CAA63306	*Secale cereale* chalcone synthase (CHS) (5 March 1999)
GENBANK AAA17993	*Trifolium subterraneum* phenylalanine ammonia-lyase (PAL) (10 May 1994)
PIR S66262	*Medicago sativa* vestitone reductase (VS) (12 November 1999)
SWISSPROT P51109	*Medicago sativa* dihydroflavanol 4-reductase (DHR) (1 October 1996)
SWISSPROT P51088	*Trifolium subterraneum* chalcone synthase (CHS) (15 July 1999)
PIR S44371	*Medicago sativa* chalcone isomerase (CHI) (16 July 1999)
Medline Abstract 11164576	altered pigmentation using CHS and DFR
Medline Abstract 7981963	altered plant stress response using CHS and PAL

These documents disclose not only flavonoid biosynthesis enzymes in a range of plant species they also disclose manipulation of these sequences to modify features such as pigmentation and stress responses. Thus features such as the 10 listed enzyme families, the isolation of representative of these families from a range of plant species and modification of flavonoid pathway enzymes are known. Furthermore, the enzymes isolated from the 4 specific species: clover, medic, ryegrass and fescue, do not appear to contribute any advantage or produce any unexpected result in comparison to known members of the same families isolated from other species. Thus these features are known or are obvious and cannot be regarded as "special technical features" conferring unity on the separate inventions.

Supplemental Box 1
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (lack of unity)

In the absence of an obvious special technical feature, it is appropriate to use the Markush approach.

Claims 1 and 26 are written as claims directed to alternatives, in a so-called Markush style of drafting. The application of the test for Markush claims gives the following result:

(A) the common property is modification of the flavonoid biosynthesis pathway.

(B) (1) no common structure is evident as the structures of the polypeptides are not revealed

(B) (2) there is no single recognised class of compounds embracing all the polypeptides, as the polypeptides belong to different classes ie CHI, CHS, CHR, DFR, LCR F3'5'H, F3H, F3'H, PAL,VR, each carrying out different biological functions.

The species of origin of the polypeptides does not provide a legitimate classification as proteins are primarily classified by their activity not their origin. Thus the polypeptides can be grouped into 10 classes CHI, CHS, CHR, DFR, LCR F3'5'H, F3H, F3'H, PAL, VR, based on their activities, and represent 10 different inventions. Each of these inventions can only be searched using independent search strategies and thus each search requires significant additional effort.

As a service to the Applicant, multiple inventions, as specified by the Applicant, were searched for a single search fee with the proviso that the total number of amino acid sequences associated with the combination of inventions was no greater than 10. This offer was independent of unity consideration and was provided solely as a service to the Applicant. For five additional search fees all the inventions, totalling 56 sequences were searched.

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member					
US	6 054 636	AU	94934/98	EP	1 015 614	WO	99 14351
WO	99 36543	AU	22321/99	EP	1 045 909		
WO	99 14351	AU	94934/98				
WO	97 12892	EP	0 853 672	FR	2739395		

END OF ANNEX